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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 3, 2005, 04:08:02; Search time 64.5137 Seconds (without alignments) 1990.064 Million cell updates/sec Run on:

US-10-631-958-2 1717 Perfect score:

1 PKHLLVFINPFGGKGQGKRI......KCSRFNFLRFLIRHTNQQDQ 326 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1774312 seqs, 393823214 residues

Searched:

Total number of hits satisfying chosen parameters:

1774312

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Published Applications AA:\*

1: \cgn2\_6\ptodata/2\pubpaa/USO7\_PUBCOMB.pep:\*

2: \cgn2\_6\ptodata/2\pubpaa/USO7\_NEW\_PUB-pep:\*

3: \cgn2\_6\ptodata/2\pubpaa/USO6\_NEW\_PUB-pep:\*

4: \cgn2\_6\ptodata/2\pubpaa/USO6\_NEW\_PUB-pep:\*

5: \cgn2\_6\ptodata/2\pubpaa/USO6\_NEW\_PUB-pep:\*

6: \cgn2\_6\ptodata/2\pubpaa/USO6\_NEW\_PUB-pep:\*

7: \cgn2\_6\ptodata/2\pubpaa/USO8\_NEW\_PUB-pep:\*

8: \cgn2\_6\ptodata/2\pubpaa/USO8\_NEW\_PUB-pep:\*

9: \cgn2\_6\ptodata/2\pubpaa/USO8\_NEW\_PUB-pep:\*

10: \cgn2\_6\ptodata/2\pubpaa/USO8\_PUBCOMB.pep:\*

11: \cgn2\_6\ptodata/2\pubpaa/USO9\_PUBCOMB.pep:\*

11: \cgn2\_6\ptodata/2\pubpaa/USO9\_PUBCOMB.pep:\*

12: \cgn2\_6\ptodata/2\pubpaa/USO9\_PUBCOMB.pep:\*

13: \cgn2\_6\ptodata/2\pubpaa/USO9\_PUBCOMB.pep:\*

14: \cgn2\_6\ptodata/2\pubpaa/USO9\_PUBCOMB.pep:\*

15: \cgn2\_6\ptodata/2\pubpaa/USO9\_PUBCOMB.pep:\*

16: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

16: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

16: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

17: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

18: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

19: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

10: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

10: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

11: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

12: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

13: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

14: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

15: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

16: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

17: \cgn2\_6\ptodata/2\pubpaa/USO0\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	Luck 11 April 200	Sequence 2. Appli	Sequence 2, Appli		Sequence 6, Appli	Sequence 6, Appli	Sequence 10, Appl	Sequence 40, Appl	Sequence 10, Appl	Sequence 121, App	Sequence 11, Appl
SOLUTION	ΙD	118-09-784-8108-11	US-09-969-896-2	US-10-631-958-2	US-10-876-281-11	US-09-784-810A-6	US-10-876-281-6	US-09-969-896-10	US-10-262-511-40	US-10-631-958-10	US-10-618-941-121	US-09-969-896-11
	DB	0	, 61	16	18	σ	18	10	15	16	16	10
	Length	305	326	326	326	471	471	537	537	537	537	295
dip	Query Match Length DB 1	0 001	100.0	100.0	100.0	100.0	100.0					
	Score	1717	1717	1717	1717	1717	1717	1640.5	1640.5	1640.5	1640.5	1640.5
	Result No.	C	<u>ښ</u>	m	4	S	9	7	80	6	10	11

## ALIGNMENTS

Sequence 11, Application US/09784810A

Patent No. US20020082203A1

GENERAL INFORMATION:

TATLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING

TITLE OF INVENTION: SAME

TITLE OF INVENTION: SAME

FILE REFERENCE: 10716-08

CURRENT APPLICATION NUMBER: US/09/784,810A

CURRENT PILING DATE: 2001-02-14

PRIOR PELING DATE: 2000-02-14

PRIOR FILING DATE: 2000-02-14

PRIOR FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTIN VET: 2.1

SEQ ID NO 11 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-784-810A-11 US-09-784-810A-11

ö 9 9 1 PKHLLVPINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE Gaps ö 100.0%; Score 1717; DB 9; Length 326; 100.0%; Pred. No. 2.8e-172; Live 0; Mismatches 0; Indels 0 Matches 326; Conservative Query Match Best Local Similarity ઠે g

TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120

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Query Match
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kossida, Sophia
TITLE OF INVENTION: Regulation of human sphingosine
TITLE OF INVENTION: Kinase-Like Protein
FILE OF INVENTION: Kinase-Like Protein
FILE OF INVENTION: Kinase-Like Protein
FILE REFERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO :
LENGTH: 326
                                                                                                                                                                                                                     DLILIRKCSRFNFLRFLIRHTNOODO 326
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US-09-969-896-2
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RESULT 3 US-10-631-958-2 ., Sequence 2, Application US/10631958

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WS-10-876-281-11
Sequence 11, Application US/10876281
Fublication No. US20050123942A1
GENERAL INFORMATION:
APPLICANT: RASTELLI, LUCA
TITLE OF INVENTION: SAME
CURRENT APPLICATION NUVBER: US/10/876,281
CURRENT APPLICATION NUMBER: US/09/784,810
FRIOR APPLICATION NUMBER: US/09/784,810
FRIOR APPLICATION NUMBER: US/09/784,810
FRIOR APPLICATION NUMBER: 00/182,360
FRIOR APPLICATION NUMBER: 60/182,360
FRIOR APPLICATION NUMBER: 60/182,360
FRIOR FILING DATE: 2000-02-14
FRIOR APPLICATION NUMBER: 60/182,360
FRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATCH IN Ver. 2.1
SEQ ID NO 11
SEQ ID NO 11
SERGITH: 326
TYPE: PRI
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APPLICANT: ACSSIGN:
APPLICANT: ACSSIGN:
TITLE OF INVENTION: Regulation of human Sphingosine;
TITLE OF INVENTION: Regulation of human Sphingosine;
FILE REPERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/10/631,958
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US/09/969,896
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 326; Conservative
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APPLICANT: RASTELLI, LUCA
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
FILE REFERENCE: 10716-08
CURRENT APPLICATION NUMBER: US/10/876,281
CURRENT FILING DATE: 2004-06-24
FRIOR APPLICATION NUMBER: 60/182,360
FRIOR PILING DATE: 2000-02-14
FRIOR PILING DATE: 2000-02-14
FRIOR PILING DATE: 2000-03-12
FRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VUMER: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SED ID NO 6
    DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK 292
                                                                        QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 352
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Publication No. US20030125533A1;
GAPLICANT: Kossida, Sophia
TITLE OF INVENTION: Regulation of human Sphingosine;
TITLE OF INVENTION: Kinase-Like Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-969-896-10
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Patent No. US20020082203A1
GENERAL INFORMATION:
APPLICANT RASTELLI, LUCA
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                            DSEKKRILGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCROSK
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                                                                                                                                                    1 PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
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                                                               Query Match 100.0%; Score 1717; DB 18; Length 326; Best Local Similarity 100.0%; Pred. No. 2.8e-172; Matches 326; Conservative 0; Mismatches 0; Indels 0;
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100.0%; Score 1717; DB 9;
Best Local Similarity 100.0%; Pred. No. 4.7e-172;
Matches 326; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT FILING DATE: 2001-02-14
FRIOR APPLICATION NUMBER: 60/182,360
PRIOR FILING DATE: 2000-02-1412,261
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SLENGTH: 471
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j ORGANISM: Homo sapiens
US-10-876-281-11
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ORGANISM: Homo sapiens
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US-09-784-810A-6
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US-09-784-810A-6
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61 TLYBINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
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                                                                                                                                                                                                                                                               95.5%; Score 1640.5; DB 10; Length 537; 96.3%; Pred. No. 6.9e-164; ive 1; Mismatches 0; Indels 11;
            CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT FILING DATE: 2001-10-04
FRIOR APPLICATION NUMBER: US 60/238,005
FRIOR APPLICATION NUMBER: US 60/314,113
FRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLILIRKCSRFNFLRFLIRHTNOODO 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
Gorman, Linda
Zerhusen, Bryan D.
Anderson, David W.
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
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FILE REFERENCE: 004974.00594
                                                                                                                                                                                                                                                                                 Best Local Similarity 96.3
Matches 314, Conservative
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                 ; ORGANISM: HOT
US-09-969-896-10
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APPLICANT: ROCHENDES, MARK E.
APPLICANT: Leach, Mark E.
APPLICANT: Age, Michele L.
APPLICANT: Beach, Mark E.
APPLICANT: Beach, Michele L.
APPLICANT: Begraphs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE OF INVENTION: NOVEL 18/10/262,511
CURRENT PILING DATE: 2003-6-28
PRIOR PILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/337,815
PRIOR PILING DATE: 2001-10-04
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-05
PRIOR PILING DATE: 2002-04-17
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96.3%; Pred. No. 6.9e-164;
tive 1; Mismatches 0;
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; Sequence 10, Application US/10631958
; Publication No. US20040192580A1
; GENERAL INFORMATION:
; APPLICANT: Kossida, Sophia
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Best Local Similarity 96.3
Matches 314; Conservative
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US-10-262-511-40
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TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
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APPLICANT: KOSSIGN.

TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Riase-Like Protein
FILE REPERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR APPLICATION NUMBER: US 60/314,113
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2010-108-3
NUMBER OF SEC ID NOS: 16
SOFTWARE: FastSEC for Windows Version 4.0
SEC ID NO 11.
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Pred. No. 7.4e-164;
1; Mismatches 0;
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; Publication No. US20030125533A1
; GENERAL INFORMATION:
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ilarity 96.3%;
Conservative 1
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US-09-969-896-11
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Best Local Simi
Matches 314;
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TYPE: PRT
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; TITLE OF INVENTION: Regulation of human Sphingosine; TITLE OF INVENTION: Kinase-Like Protein; FILE REFERENCE: 004974,00594; CURRENT APPLICATION NUMBER: US/10/631,958; CURRENT FILING DATE: 2003-08-01; PRIOR APPLICATION NUMBER: US/09/969,896; PRIOR FILING DATE: 2000-10-04; PRIOR FILING DATE: 2000-10-06; PRIOR RILING DATE: 2000-10-06; PRIOR APPLICATION NUMBER: US 60/314,113; PRIOR RILING DATE: 2001-08-23; NUMBER OF SEQ ID NOS: 16; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 10; SEQ ID NO 10; TYPE: PRI T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
95.5%; Score 1640.5; DB 1
Best Local Similarity 96.3%; Pred. No. 6.9e-164;
Matches 314; Conservative 1; Mismatches 0;
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Publication No. US20040197792A1

GENERAL INFORMATION:
APPLICANT: WANNING, GERAED
APPLICANT: MANNING, GERAED
TITLE OF INVENTION: NOVEL KINASES
ITLE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT PILING DATE: 2003-07-15
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.2
SEQ ID NO 121
LENGTH: 537
TYPE: PRT
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Best Local Similarity 96.3
Matches 314; Conservative
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US-10-618-941-121
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SOFTWARE: Patentin Ver. 2.0; SRQ ID NO 2.1.ELNGTH: 537
TYPE: PRT
NUMBER OF SEQ ID NOS: 4
                                                                                    ORGANISM: Homo sapiens
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FEATURE:
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US-10-425-115-361076
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US-10-315-597A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10315597A
Publication No. US20030162206A1
GENERAL INFORMATION:
APPLICANT: Sugiura, Masako
APPLICANT: Kohama, Takafumi
APPLICANT: Kohama, Takafumi
TITLE OF INVENTION: Ceramide Kinase and DNA Encoding It
FILE REFERENCE: 02658CIP/HG
CURRENT APPLICATION NUMBER: US/10/315,597A
CURRENT FILING DATE: 2002-12-10
PRIOR PILING DATE: 2000-06-14
                                                                                                                                                                       TITLE OF INVENTION: Regulation of human Sphingosine;
TITLE OF INVENTION: Regulation of human Sphingosine;
TITLE OF INVENTION: Rinase-Like Protein;
FILE REFERENCE: 004974,00594
CURRENT APPLICATION NUMBER: US/10/631,958
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US/09/969,896
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-08-23
NUMBER: OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO III: 562
                  DLILIRKCSRFNFLRFLIRHTNQQDQ 326
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                                                                                      RESULT 12
US-10-631-958-11
Sequence 11, Application US/10631958
; Publication No. US20040192580A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-958-11
                                                                                                                                                              GENERAL INFORMATION:
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US-10-315-597A-2
301
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Sequence 361076, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Rovalic, David K.
APPLICANT: Zao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5522)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 361076
LENGTH: 588
                                                                                                                                                                                                                                                 239 GPIDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 298
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                                                                                                                                                                                   130 PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDII------VTEHANQAKE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 300
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      DB 14; Length 537;
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Query Match 95.1%; Score 1632.5; DB 14
Best Local Similarity 95.7%; Pred. No. 4.8e-163;
Matches 312; Conservative 2; Mismatches 1;
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US-10-425-115-361076
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OTHER INFORMATION: unsure at all Xaa locations
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Sequence 29, Application US/09784810A

Sequence 29, Application US/09784810A

Patent No. US2002082203A1

GENERAL INFORMATION:

APPLICANT: RASTELLI, LUCA

TITLE OF INVENTION: SAME

FILE REFERENCE: 10716-08

CURRENT PELING DATE: 2001-02-14

PRIOR PELICATION NUMBER: 60/182,360

PRIOR PELICATION NUMBER: 60/182,360

PRIOR FILING DATE: 2000-03-22

PRIOR FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTION VENER: 201

SEQ ID NOS: 29

SEQ ID NO 29
234 TLSSLSDIELKAFDGVVAVGGDGLFNEILNGILSSRHKVSYPFTPEGFGYVGSSDNCEEQ 293
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                                                                           294 TRNWVNFSKPTPDSGNAVFLGNPSKCDDQEPLLSTSHPSELEIPSNSTKEPCIGDQDNPV 353
                                                                                                                          113 -----LRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNST---- 161
                                                                                                                                              162 ---LLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQH 218
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US-09-784-810A-29
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ORGANISM: Unknown Organism
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Search completed: September 3, 2005, 04:32:26 Job time : 66.5137 secs This Page Blank (uspto)

Run on:

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Aas77730 DNA encod
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Ab140823 Human sph
Aas77727 DNA encod
Ab125705 Drosophil
Ab125705 Drosophil
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Aa76592 Human sph
Ab140829 Human imm
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Ab140828 Human sph
Adj9559 Human lip
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Abx70921 Novel hum
Aba68945 Human Cer
Adh62844 Human Nov
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Ab159533 Human sph
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/product= "sphingosine kinase-like protein"
/note= "start and stop codons are not indicated"
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ADS10370
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ABC40823
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ABA96945
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-Q2092005 165814 4497/app_query.fasta_1.1941
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-Q2/cgn2_1/USPTO_spool/US10631958/runat_02092005 165814 4497/app_query.fasta_1.1941
-DB=N Geneseq_16Deco4 -QFWT=fastap -SUFFIX=rng -MINNATCH=0.1 -LOOPCL=0
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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR_MIN=0 -ALIGN=15
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-USRB=-USRGEQUERY -NGG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMBOUT=120 -WARN TIMBOUT=0 -THREADS=1 -XGAPOP=10 -LONGLOG
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                      Compugen Ltd
                                                     OM protein - nucleic search, using frame plus p2n model
           GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compug
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                                                                                      CAGCAGCTGGAGGAGGAGGAGGAAGAAAGAAAGCACTGTATGGTTTTGGAAGCTGCGGAGGACGTG
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                                                                     PheLeuSerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrVal
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22-MAR-2000; 2000US-0191261P.
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P-PSDB; AAE07884
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                                                                                                                                                                                                                                 The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g asthma), autoimmune diseases (e.g rheumatoid arthritis) and central and peripheral nervous system disorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein
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Conservative:
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23-AUG-2001; 2001US-0314113P
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Best Local Similarity:
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 GlySerProArgAspArgLysProCysArgAlaGlyCysPheValCysArgGlnSerLys
                                985 CAGCAGCTGGAGGAGGAGCAGAAGAAAGCACTGTATGGTTTGGAAGCTGCGGAGGACGTG
                                                                                                                         GluGluTrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSerCys
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                                                                                                                                                                                                                                                    301 AspLeulleLeulleArgLysCysSerArgPheAsnPheLeuArgPheLeulleArgHis
                                                             nGlnLeuGluGluGluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia, cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
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76. .1689
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2001US-0327449P.
2001US-0328024P.
2001US-0328044P.
2001US-0328044P.
2001US-0328044P.
2001US-0328144P.
2001US-0330414P.
2001US-0330309P.
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2002US-0373260P.
2002US-0373815P.
2002US-0373817P.
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2001US-0343629P.
2001US-0349575P.
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05-0CT-2001; 2
09-0CT-2001; 2
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09-0CT-2001; 2
12-0CT-2001; 2
15-0CT-2001; 2
14-0CT-2001; 2
22-0CT-2001; 2
24-0CT-2001; 2
24-0CT-2001; 2
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19-APR-2002;
19-APR-2002;
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                                                      The present invention relates to sphingosine kinase (SphK) polypeptides and nucleic acids encoding them. SphK is useful for treating a SphK-associated disorder sepecially cancers such as leukaemia, lymphoma, ovarian, breast, lung, colon, testicular, stomach and skin, atherosclerosis, restenosis or ischaemia and cell proliferative disease or disorder associated with vascular diseases. SphK gene is used in gene therapy and antisease-therapy. Sphingolipids serving as signalling molecules, have recently emerged as regulators of cell growth, differentiation, diverse cell phenotypes and cell death. Activation of SphK by tumour necrosis factor (TNF) -lipha inhibits apoptosis in human andothelian.
 restenosis or ischemia in a human.
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Indels:
Gaps:
 especially cancer,
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                              Claim 8; Page 94-95; 107pp; English.
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disorder
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RE 12-ARR-2002; 2002U3-031393P.

RE 12-ARR-2002; 2002U3-031393P.

RE 16-MAY-2002; 2002U3-03139P.

RE 16-MAY-2002; 2002U3-031393P.

RE 16-MAY-2002; 2002U3-031392P.

RE 25-MAY-2002; 2002U3-031393P.

RE 25-MAY-2002; 2002U3-0313P.

RE 25-MAY-2002; 2002U3-0314P.

RE 25-MAY-2002; 2002U3-0314P.

RE 25-MAY-2002

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Sequence 1740 BP; 389 A; 476 C; 530 G; 345 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches:

1.26e-170 1640.50 96.63% 96.32%

> Percent Similarity: Best Local Similarity:

GACAGTGAGAAGAAACGGTGGGTTTTGCCAGATACGACTTTTCAGGTTTAAAGACC 1029 GACCTCATCCTCATCCGGAAATGCTCCAGGTTCAATTTTTCTGAGATTTCTCATCAGGCAC 1389 240 GluGluTrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSerCys 280 AlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSer 300 derrerececedadececeadodecererecedecedecederresadadedecentrer 1329 AspLeuIleLeuIleArgLysCysSerArgPheAsnPheLeuArgPheLeuIleArgHis 320 200 100 729 120 140 849 909 ThrieuLeukgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspIleIleLys 180 609 699 789 LeuHisIleValValGlyAspSerLeuAlaMetAspValSerSerValHisHisAsnSer 160 ACACTCCTTCGCTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCATCAAAG 969 CCAAAGCATTTACTGGTATTTATCAACCCGTTTGGAGGAAAAGGACAAGGCAAGCGGATA 522 80 GAGGAGTGGCAAGTCGTCTGTGGGAAGTTTCTGGCCATCAATGCCACAAACATGTCCTGT ProLysHisLeuLeuValPheIleAsnProPheGlyGlyLysGlyGlnGlyLysArglle ATGITTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGAGGAGCGCCGGGGTCGAC CAGAACCACCCCGGGCTGTGTGTCCCCCAGTAGCCTCCGGATTGGAATCATTCCCGCA GlySerProArgAspArgLysProCygArgAlaGlyCygPheValCygArgGlnSerLyg MetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp GlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAla CTGCATATCGTTGTTGGGGACTCGCTGGCCATGGATGTGTCCTCAGTCCACCACAACAACA AspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThr GlnGlnLeuGluGluGluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspVal 41 AsnLysPheTyrValAsnTyrValGluValIleThrGluHisAlaAsnGlnAlaLysGlu ACTCTGTATGAGATTAACATAGACAAATACGACGGCATCGTCTGTGTCGGCGGAGATGGT GlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAla PheLeuSerHisKHisKisKogTyrGluGlyThrValSerPheLeuProAlaGlnHisThrVal 1 Indels: US-10-631-958-2 (1-326) x ADA05679 (1-1740) Accadecadeaceae 1407 ThrasnGlnGlnAspGln 326 1030 241 1270 21 523 580 63 610 81 670 101 730 121 790 141 850 161 910 181 970 201 221 1090 1150 261 1210 281 301 1390 Query Match: DB: 셤 g a ò 유 g g 8 ద ð 셤 à D ò 셤 ò 셤 ò 원 ઠે 셤 ઠે a 8 ઠે 유 8 ઠે 8 ò à

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                                                                                      292 CAGAACCACCCCGGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGAATCATTCCGCA
                                                                                                                                            GGGTCAACGGACTGCGTGTGTTACTCCACCGTGGGCACCCAGGAAACCTCGGCG
                                                                                                                                                                   LeuHislleValValGlyAspSerLeuAlaMetAspValSerSerValHisHishsAsnSer
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ACTCTGTATGAGATTAACATAGACAAATACGACGCCATCGTCTGTGTCGCGGAGATGGT
                        MetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp
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                                                                                                                    Human; enzyme; haemostatic; sphingosine kinase 4;
platelet transfusion; platelet stabiliser; gene;
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                                                                                                                                                                              Location/Qualifiers
1. .1251
1. stag= a /*tag= a /product= "Sphingosine kinase
                                                                                            Human Sphingosine kinase 4 coding sequence
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                      DNA; 3975 BP
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P-PSDB; ABR56301.
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                     ACC70838 standard;
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                                              ACC70838;
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GlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAla 120
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                                                                           GlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAla
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                      CAGAACCACCCCCGGGCTGTGCTGGTCCCCCAGTAGCCTCCGGATTGATCATTCCCGCA
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cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma;
autoimmune disease; rheumatoid arthritis; Parkinson's disease; ss.
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/note= "see ABB07857"
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                                                                                                                                                                                                                                                                                        New human sphingosine kinase A, B and C polynucleotides and polypeptides useful in e.g. chromosome and gene mapping, and detecting inflammation or disease associated with abnormal levels of sphingosine kinase expression.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heart, lymphoid or tissues of the nervous system
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                                                                                                                                                                                             Falzone GR
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1640.50
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                                                                           02-MAR-2000; 2000WO-CA000223
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P-PSDB; AAY96059.
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Best Local Similarity:
Query Match:
DB:
WO200052173-A2
                                                                                                                 02-MAR-1999;
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Pred. No.:
                                    08-SEP-2000
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  GGGTCAACGGACTGCGTGTGTTACTCCACCGTGGGCACCAGCGACGCAGAAACCTCGGCG
                                                                          CTGCATATCGTTGGGGACTCGCTGGCCATGGATGTGTCCTCAGTCCACCACAGC
                                                                                                                                          ThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyBap1leIleLye
                                                                                                                                                                        ACACTCCTTCGCTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCAAG
                                                                                                                                                                                                                                     AspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene; ds; kinase; human; SNP; single nucleotide polymorphism; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease; cardiovascular disease; brain; neuronal associated disease; metabolic; inflammatory disorder; cytostatic; neuroprotective; immunomodulator; antiinflammatory; lipid kinse; KIAA1646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSer
                                                 LeuHisIleValGlyAspSerLeuAlaMetAspValSerSerValHisHisAsnSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lipid kinse KIAA1646 DNA SeqID 55.
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replace(3020,c)
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/standard_name=
replace(3769,c)
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replace(2577,g)
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variation
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                                                                                                                                                                                                                                                                                                                                                                                                                          New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynuclectide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g asthma), autoimmune diseases (e.g rheumatoid arthritis) and central and peripheral nervous system disorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProLysHisLeuLeuValPhelleAsnProPheGlyGlyLysGlyGlnGlyLysArgile
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/note= "see ABB07856"
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                                                                                                                                          05-OCT-2001; 2001WO-EP011516
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                                                                                                                                                                                                                                                                                                                                 ACACTCCTTCGCTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCATCAAG
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GlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAla
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                                                                                                                             GGGTCAACGGACTGCGTGTTTACTCCACCGTGGGCACCACGACGAGAAACCTCGGCG
                                                                                                                                                                                                 LeuHisIleValValGlyAspSerLeuAlaMetAspValSerSerValHisHisAsnSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions and be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polynucleotide sequence is a human kinase DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * nucleic acid molecule encoding a kinase polypeptide, useful for
sparing a composition for treating diseases or disorders, e.g., cancer,
neurological, immunological or inflammatory disorders.
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                          Other;
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P-PSDB; ADJ96664.
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The present invention describes an isolated PRO nucleic acid (1). Also described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide; (5) a chimeric molecule comprising the composition of matter comprising a polypeptide of (4); an agonist or antagonist of the polypeptide or an antibody that binds to the composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the polypeptide or an antibody that binds to the comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a comprising a method for determining the presence of a PRO polypeptide or an ammal; (10) a method of determining the polypeptide; (11) a method of dentifying a compound that inhibite or mammal; (12) a method of stimulating the immune response in a mammal; (12) a method of stimulating the immune response in a mammal; (13) a method of stimulating the immune response in a mammal. The pRO sequences have antialleragic, antianament, antiathritic, antialiabetic, antianament, antiathritic, antialiabetic, antianament, antiathritic, antiathroid, (18) dermatological, gastrointestinal, computed activities, and can be used in gene therapy. The nucleic acid of virucide activities, and can be used in gene therapy. The nucleic acid of the encoded polypeptides, compositions, kits and methods are cuseful in diagnosing and treating an immune response. The present sequence represents a human composition and present invention.
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                                                                                                                                                                                                    New PRO polymucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.
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                                                                                            Schoenfeld J, Williams PM;
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                                                                                            Gurney AL,
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                                                                                        Aggarwal S, Clark H,
Wood WI, Wu TD;
                                                       (GETH ) GENENTECH INC
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Huntington's disease; amyotrophic lateral sclerosis, haemophilia;
Huntington's disease; parkinson's disease; Alzheimer's disease;
autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound;
ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke;
fibrosis; reperfusion injury; infection; allergic rhinitis; asthma;
coagulation disorder; cancer; tumour; inflammatory disease; septic shock;
Crohn's disease; anaphylaxis; proliferation; chemotactic;
differentiation; stem cell growth factor; haematopoiesis; chemokinetic;
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Met PheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp
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                                                                                           CAGAACCACCCCCGGGCTGGTGGTCCCCCAGTAGCCTCCGGATTGGAATCATTCCGCA
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                                                                                             ThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIleValCysValGlyGlyAspGly
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neurological disease; inflammation; human immunodeficiency virus;
HIV infection; type 2 diabetes; obesity; sepsis; arteriosclerosis;
cancer; neuroprotective; antiinflammatory; anti-HIV; antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to the CDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic atteral sclerosis); neurodegenerative disease (e.g. parkinson's disease, anyotrophic clateral sclerosis, neurodegenerative disease (e.g. parkinson's disease, anyotrophic clateral sclerosis, reumatoid arthritis, insulin-dependent diabetes mellitus) erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus); wounds, ulcars, burns; bone disorders (e.g. osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head trauma); lung or luver fibrosis, reperfusion injury in various tissues; bacterial, viral or fungal infections; allergic conditions such as allergic rhinitis, asthma; coagulation disorders (e.g. septic shock, Crohn's disease, anaphylaxis). The protein may be used to inhibit the growth, crimites, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have

Cycles of rhythms. The protein may also have

Cycles of rhythms. The protein may also have

Cycles of rhythms. The coopin, stem cell growth factor, haematopoiesis

Crequlation, immune stimulating or suppressing, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, and antinflammatory

Crecombinant protein for analysis. The present sequence is an expressed of the invention, this sequence is an expressed of sequence tag (EST) and was identified using subtractive hybridisation
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haemostatic; antiinflammatory; expressed sequence tag;
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T, Wang J,
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Wehrman 7
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Xue AJ, Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                       HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents cDNA encoding a human ceramide kinase designated hCERKI. The invention relates to hCERKI, nucleic acids encoding it, expression vectors and host cells containing hCERKI nucleic acids, the recombinant production of hCERKI and antibodies specific for hCERKI. The invention also encompasses methods of isolating hCERKI from samples, the use of hCERKI in drug screening, and the use of hCERKI uncleic acid sequences in gene therapy. hCERKI mediates the ATP-dependent 1-phosphorylation of ceramides and can be used to screen for therapeutic and preventive agents for a wide range of disorders. Such disorders include neurological disease, inflammation, human immunodeficiancy virus (HIV) infection, type 2 diabetes, obesity, sepsis, arteriosclerosis and
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anorectic; antibacterial; antiseptic; antiarteriosclerotic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ceramide kinase gene and the enzyme encoded by it for screening substances as drugs for neurological, inflammatory and other disorders.
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                                                                                                                                                                                                          /product= "Human ceramide kinase hCERK1"
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1632.50
96.32%
95.71%
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Pred. No.:
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Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease

WPI; 2004-213931/20.

P-PSDB; ADN62845

Claim 20; SEQ ID NO 39; 395pp; English

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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Otr T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
      02-OCT-2001; 2001US-0326483P.
05-OCT-2001; 2001US-0327443FP.
05-OCT-2001; 2001US-0327449FP.
09-OCT-2001; 2001US-032794PP.
09-OCT-2001; 2001US-032804PP.
12-OCT-2001; 2001US-032804FP.
12-OCT-2001; 2001US-032804FP.
15-OCT-2001; 2001US-032904FP.
17-OCT-2001; 2001US-033904FP.
18-OCT-2001; 2001US-033916FP.
24-OCT-2001; 2001US-033926FP.
17-APR-2002; 2001US-0339256FP.
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2002US-0373817P.
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2002US-0381037P.
2002US-0381038P.
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2002US-0383656P
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
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STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
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ZERHUSEN B D.
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PATTURAJAN M.
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BERGHS C.
DIPIPPO V A.
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PEYMAN J A.
KEKUDA R.
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19-APR-2002; 2
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The invention relates to isolated NoVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abbrrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and cativity of NOVX by supplementing the patient our polymucleotides may be used to treat disorders associated with decreased complements of NOVX by supplementing the patient our control or activity of NOVX by supplementing the patient our problements and preventing their expression. NOVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polymucleotide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious colleges, ancer, associated cancex, and excepting the presence of NOVX in samples. NOVX polypeptides and polymucleotides may be used in this way to prevent, diagnoses, ancrexia, cancer, cancer-associated cancexia, neurodegenerative ciseases, ancrexia, cancer-associated cancexia, neurodegenerative ciseases, ancrexia, cancer, cancer-associated cancexia, metabolic disorders, bisorders, metabolic disorders, bisorders, metabolic disorders, bisorders, and the various dyslipidaemias, metabolic wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence

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Matches:
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96.02%
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Ji W, Miller Shimkets RA, Eisen A, Gan

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                                                                                                   The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haemacopoletic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic DNA of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
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                                   New polynucleotide, useful in preparing a composition for diagnosing or treating inflammatory, neurodegenerative or stem cell disorders, e.g., aplastic anemia or cancer for promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                 GACGAGGTGTCTGTCCTCTGGCCCTGTGTCTGGCCCCCGAGGGTGGCGGCATGGTGCTAC
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                                                                                                                                                                                                                                Sequence 4702 BP; 970 A; 1226 C; 1364 G; 1118 T; 0 U; 24 Other;
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276
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1414.50
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P-PSDB; ADS11054.
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aLeuHisIleValValGlyAspSerLeuAlaMetAspValSerSerValHisHisAsnSe
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Wang J, Ghosh M,
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Then R, Zhao QA, 1
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us-10-631-958-2.rng

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c in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cannot acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence dor this patent did not appear in the printed specification, but was obtained in the control of contro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging
                                                                                                                                                                                                                                                  CysSerArgPheAsnPheLeuArgPheLeuIleArgHisThrAsnGlnGlnAspGln 326
                                                    ProCysArgAlaGlyCysPheValCysArgGlnSerLysGlnGlnLeuGluGluGluGln
                                                                       LysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspValGluGluTrpGlnValValCys
                                                                                                                   AAGAAAGCACTGTATGGTTTGGAAGCTGCGGAGGACGTGGAGGAGGAGGAGTCGCTCTGT
                                                                                                                                             GlyLyBPheLeuAlaIleAsnAlaThrAsnMetSerCysAlaCyBArgArgSerProArg
          GluGlyThrValSerPheLeuProAlaGlnHisThrValGlySerProArgAspArgLys
                                                                                                                                                                                                                                                                                                                                                                                                   mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostice, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity.
                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #13534.
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23-AUG-2000; 2000US-00649167
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P-PSDB; ABG13543.
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            of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications. It is that disgnostics, forensics, gene mapping, identification of mutations are promisible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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treating disc
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Matches:
Conservative:
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
dermatological; immunosuppressive; antidiabetic; hypotensive;
dermatological; antifumgal; antifrheumatic; antidiabetic; hypotensive;
antiviral; antifungal; antifrheumatic; antidiabetic; hypotensive;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
cardiant; thrombolytic; coagulant; vasotropic; antidiabeticial;
cardiant; thrombolytic; coagulant; vasotropic; antidiabeticiant
cardiant; thrombolytic; coagulant; or antidinease of or predisposition
corteins in be used for determining the presence of or predisposition
corteins in gene therapy vectors. The proteins and nucleic acids may be
used to treat cancers, proliferative disorders, neurodegenerative
disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
storage, systemic lupus erythematosus, severe combined immunodeficiency
(SCID), AlDS, viral, bacterial or fungal infection, malaria, autoimmune
disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
cartilage damage, nocturnal haemoglobinuria, antinfilammatory disease; to
                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 2392; 5507pp; English.
                                                                                                                                           99US-0127607P
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P-PSDB; AAB41822.
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                     WO200058473-A2
                                                                                                                                           31-MAR-1999;
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                                                                                                                                                                                                                                                 TCAGTCCACCACAACAGCACACTCCTTCGCTACTCCGTGTCCCTGCTGGGCTACGGCTTC 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nooturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                     ATCGTTGTTGGCTGCCCCCGAGGCTCGGAAACCACCGCGTCCCGCCATACTGCCTGT 782
                                                                                                   783 GGCAGTGGGCACGGGCAGCTGTGCCTGGGCTGCGAGCTGTGGAACGCATGCCTCTGTGAG 842
                                                                                                                                             -----GlyAspSerLeuAlaMetAspValSer 154
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                                                                                                                                             Homo sapiens
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                                 Sequence 753 BP; 165 A; 195 C; 207 G; 186 T; 0 U; 0 Other;
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Mus musculus 3 days neonate thymus CDRA, RIKEN full-length enriched library, clone:A630056Dll product:DA59H18.2 (NOVEL PROTEIN SIMILAR TO HUMAN, MOUSE, YEAST, WORM AND PLANT (PREDICTED) PROTEINS)
(FRAGMENT) homolog [Homo sapiens], full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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               Group Phase I & II Team.

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Rukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Rukuda, S., Furuno, M., Hiramcto, K., Hiraoka, T., Hiozane, T.,

Haysshida, K., Hayteu, N., Hiramcto, K., Hiraoka, T., Kaukawa, T.,

Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tanaka, T., Tanaka, A., Takahashi, F., Takaku-Akahira, S.,

Huramatsu, M., and Hayashizaki, Y.
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ATNNSCACPRS PGGLS PFAHLGDGSSDLILI RKCSRRNFLRFI RHTNQBDQPPFTV
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PAIEVRVHCQLVRLFARGIEBES"
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PNHPRAVLVPSTLRIGIIPAGSTDCVCYSTVGTNDAETSALHIIGDSLAIDVSSVHY
HNTLLRYSVSLLGYGFYGDLIKDSEKKRMMGLVRYDFSGLKTFLSHQYYBGTLSFLPA
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/note="unnamed protein product; DA59H18.2 (NOVEL PROTEIN
SIMILAR TO HUMAN, MOUSE, YEAST, WORM AND PLANT (PREDICTED)
PROTEINS) (FRAGMENT) homolog [Homo sapiens] (SPTR|Q9UGE5,
evidence: FASTY, 86.5%ID, 100%length, match=945)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="3 days neonate"
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-ULL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose Trust/MRC building Addenbrookes Hospital Cambridge) whose passistance we gratefully acknowledge.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/.

URL:http://fantom.gsc.riken.jp/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
FANTOM Consortium and the RIKEN Genome Exploration Research
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Length 1824; Indels

Score 1116.8; DB 3; Pred. No. 1.3e-279; 0; Mismatches 302; I

Query Match 69.2%; Best Local Similarity 81.2%; Matches 1309; Conservative

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HNTLLRXSVSLLGYGFYGDLIKDSEKKRWMGLVRYDFSGLKTPLSHQYYEGTLSFLPA
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                                                                                                                                                                                                                                                                                       Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                                                                               Exploration Research Group Phase II Team and the
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                                                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research
  RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                               Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://gonome.goc.riken.jp/
URL:http://fantom.goc.riken.jp/.
Location/Qualifiers
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/organism="Mus musculus"

/mol type="mRNA"

/strain="C57BL/6J"

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/db_xref="FAXON:10090"

/clone="D330016D08"
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4248 bp mRNA linear HTC 03-APR-2004 Mus musculus 13 days embryo heart CDNA, RIKEN full-length enriched library, clone:D330016D08 product:DA59H18.2 (NOVEL PROTEIN SIMILAR TO HUMAN, MOUSE, YEAST, WORM AND PLANT (PREDICTED) PROTEINS) (FRAGMENT) homolog [Homo sapiens], full insert sequence.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AGENCOURT 6418742 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502281 5', mRNA Fequence.
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 CAGCAGGACCAGTITGACTITGACTITIGITGAAGTITATCGCGTCAAGAAATTCCAGTIT 1380
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(Dases 1 to 1063)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbe-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM12140 row: c column: 18
High quality sequence stop: 665.
1. .1063
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                                                     Length 4248
                                                   69.1%; Score 1115.2; DB 3; Length
81.1%; Pred. No. 4.2e-279;
ive 0; Mismatches 303; Indels
                                                                  Best Local Similarity 81.1
Matches 1308; Conservative
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/mol_type="mRNA"
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/clone="IMAGE:5803668"
/clone="IMAGE:5803668"
/tlssue type="lymphoma, cell line"
/tlssue type="lymphoma, cell line"
/tlssue type="lymphoma, cell line"
/tlssue type="lymphoma, cell line"
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/clone lib="NIH MGC 99"
/noce="Organ: lympho, Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/AnoI sites using the following S: dagptor:
GGACGAG(G). Size-selected >500bp for average insert size into Reb. Library constructed by Ling Hong in the laboratory of Gerald M: Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
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Homo sapiens cDNA clone IMAGE:5803668
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1 (bases 1 to 1059)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                     841 CTCATCAGGACACACCCAGCAGGACAGTTTGACTTCCCCTTTTGGTTGAAGTTTATC
                                                                                                       1361 GCGTCAAG--AAATTCCAGTTTACGTCGAAGCACATGGAGGATG-----AGGACAGCGA
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CTCATCAGGCACACCAGCAGGACCAGTTTGACTTCAC--TTTTGTTGAAGTTTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Standt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can bettp://image.library by: A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2040 row: a column: 13
High quality sequence stop: 601.
Location/Qualifiers
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Pred. No. 4.2e-189;
0; Mismatches 6;
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                                                                                                                                                                  CCTCAAGGAGGGGGG 1428
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Best Local Similarity 99.1
Matches 784; Conservative
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            /mol type="mana" office...
//mol type="mana" office...
/db xref="taxon:9606"
/clone="IMAGE:550281"
/tissue_type="retinoblastoma"
/lab host="DHINB (phage-resistant)"
/lone="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
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organism="Homo sapiens"
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         23
High quality sequence stop: 640.
Location/Qualifiers
                                                                   /organism="Homo sapiens"
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Abases 1 to 1078)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Lo Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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AGENCOURT_6873251 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5925382
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                                                                                                                                                                                         GGATIGGAAICAITCCCGCAGGGTCAACGGACIGCGTGTGTTACTCCACCGTGGGCACCA 372
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                                                     TCTGTGTCGGCGGAGATGGTATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGC
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Homo sapiens
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1 (bases 1 to 797)

1088 National Institutes of Health, Mammalian Gene Collection (MGC)

1080 Marional Institutes of Health, Mammalian Gene Collection (MGC)

1081 Marional Cancer Genomics

1081 Marional Cancer Institute / NIH

1082 Mational Cancer Institute / NIH

1083 Mational Cancer Institute / NIH

1084 Mational Cancer Institute / NIH

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1087 Mational Cancer Institute / NIH

1088 Mational Cancer Institute / NIH

1089 Mational Cancer Institute / NIH

1080 Mational Cancer Institute / NIH

1080 Mational MacColone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

1080 Mational Mational Mational Cancer Colone distribution information can be later NPAHI/13 zev. column: 20

1081 High quality sequence stop: 656.

1082 Mation/Matifiates

1083 Mational Mational Formal Mational Mationa
                                                                                                                                                                                                                           CK000755 797 bp mRNA linear EST 26-NOV-2003 AGENCOURT 16363467 NIH MGC 221 Homo sapiens cDNA clone MRNA Sequence.
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                  TCCTTCCTCCCTGCACACACACGG--TGGGATCTCCAAGGGA--TAGGAAGCCCTGCCG
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Pred. No. 2.3e-181;
0; Mismatches 21; Indels
                                                                                              1044 GGCAGGATGCTTTGTTTG 1061
                                                                                                                                 GGCCAGGGATGCCTTTG 798
                                                                                                                                                                                                                                                                                                                 CK000755.1 GI:38526789
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (base 1 to 1047)
S NIH-MGC http://mgc.nci.nih.gov/.
I Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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133 GTGTCGGCGGAGATGGTATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGAGGAGGAGA
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                                                                                         GTGTCGGCGGAGATGGTATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGA
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/u.v.f.a
/u.ganism="Homo sapiens"
/wol_type="mRNA"
/wol_type="mRNA"
/do_txef="taxon:9606"
/clone="INAGE:30708699"
/clone="INAGE:30708699"
/clone="INAGE:30708699"
/clone="INAGE:30708699"
/clone="Organ: mixed; Vector: pVX-Asc; Site 1: EcoRI;
/note="Organ: mixed; Vector: pVX-Asc; Vector: Areage with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according tomRNA size fraction, ligated with EcoR I adaptor; digested with Not I and then cloned directionally into pXX-Asc vector. Average insert size 4-SKD. Adaptors 5'(AATTCGGCACGAGGS)' and 5'd
/cCTCGGCCG)' 3' 1. Linker sequence - GCGCCCCTGAGAGCC T18. Sequencing primers 3' end: T3 promoter primer 5'd
/ATTAACCCTCACTAAAGGGA)' 5' End: T7 promoter primer 5'd
/TAATACGCCTCACTAAAGGGS)' Library was constructed in the library"
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AGENCOURT 16369000 NIH MGC 221 Homo sapiens cDNA clone IMAGE:30708597 5', mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Nutional Institutes of Health, Mammalian Gene Collection (MGC)
Upubblished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
Bldg. 31 RmloAo7 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencian by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM1075 row: a column: 22
High quality sequence stop: 689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 713)

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Pred. No. 3.4e-172;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                           CCCGGCTGCCCACTTGGGAGGACGGGTCTTCT 1254
                                                                                                                                                                                                                                                    CCCGGCTGCCCAATTTGGGGAAGGAAGGGTCCT 881
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Best Local Similarity 99.9%;
Matches 705; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
Homo sapiens
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
COMMENT
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CK000525
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                                                                                                                                                                       /clone="INGES:5812382"
/tissue_type="lymphoma, cell line"
/lab host="NHIOB (phage-remistant)"
/clone lib="NHI MGC 99"
/note="Organ: lymph; Vector: pOTB7; Site_l: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/AhoI sites using the following S; adaptor:
GGACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               754
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Pred. No. 2.1e-174;
0; Mismatches 35;
http://image.llnl.gov
Plate: LLCM2062 row: 1 column: 15
High quality sequence stop: 535.
Location/Qualifiers
                                                                                                           'organism="Homo sapiens"
'mol_type="mRNA"
'db xref="taxon:9606"
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94.78;
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AGGGACAGTGTCCTTCCTCCCTGCACAACACGGGGATCTCCAAGGGATAGGAAGCC 1037
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC c
can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: NDAM512 row: k column: 18
High quality sequence stop: 673.
                                                                                                                                                                                                          /tissue type="Embryonic Stem cells"
/cell line="WAOI"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NIA Human H1 Embryonic Stem Cell cDNA Library
(Long)"
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71 GCTGGCCATGGATGTGTCCTCAGTCCACACACACACACTCCTTCGCTACCCGTGTC
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                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                      /clone="IMAGE:30426593"
                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                    Location/Qualifiers
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(bases 1 to 820)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.
                                                                               188 CAGGAGGATCTCCAAGGGATAGGAAGCCCTGCCGGGCAGGATGCTTGTTGTAGGCA
                                                                                                                                                                                                                                                                                                                                                                           GGACGTGGAGGAGGTGGCAAGTCGTGGGAAGTTTCTGGCCATCAATGCCACAAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                            368 GTCCTGTGCTTGTCGCCGGAGCCCCAGGGGCCTCTCCCCGGCTGCCCACTTGGGAACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               548 GAAATTCCAGTTTACGTCGAAGCACATGGAGGATGAGGACAGCGACCTCAAGGAGGGGG
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                                   8 CAACAGCACACTCCTTCGCTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGGACAT
                                                                                                                                                   AAGCAAGCAGCAGCTGGAGGAGGAGCAGAAGAAAGCACTGTATGGTTTTGGAAGCTGCGGA
                                                                                                                                                                                                                                                                                                                       248 AAGCAAGCAGCAGCAGAAGAAGAAGAAAAAGCACTGTATGGTTTGGAAGCTGCGGA
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National Cancer Institute / NIH
Bldg. 31 RmlOA07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
CDNA Library Preparation: Yulan Piao and Minoru Ko
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Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of lowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
771: 319 315 8250
Fax: 319 315 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Louis Standt
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfi.html
Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CF135528 732 bp mRNA linear EST 09-SEP-2003 UI-HF-BN0-amf-g-10-0-UI.rl NIH MGC_50 Homo sapiens cDNA clone IMAGE:3090211 5', mRNA sequence.
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AGGGACAGTGTCCTTCCTCCTGCACAACACACGGTGGGATCTCCAAGGGATAGGAAGCC 310
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                                                                                                                                  GAAGTTTCTGGCCATCAATGCCACAAACATGTCCTGTGCTTGTCGCCGGAGCCCCAGGGG
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/organism="Homo sapiens"
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BX952302 653 bp mRNA linear EST 01-MAR-2004 DKFZp781L11183 rl 781 (synonym: hlcc4) Homo sapiens cDNA clone DKFZp781L11183 5', mRNA sequence.
BX952302 BX952302.1 GI:43428907
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/note="Turner from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
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                                                                                                                                                                                                                                                                                                             Score 684.4; DB 7;
Pred. No. 5.5e-167;
0; Mismatches 1;
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1487

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17000532197874 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
CN296312
                                                           541 GAAGAAGCGCTTTGGGCACATTTGCAGCAGCCACCCTCCTGCTGCTGCACCGTCTCCAA 600
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481 GAAATICCAGITIACGICGAAGCACAIGGAGGAIGAGGACAGCGACCICAAGGAGGGGGGG 540
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I (bases 1 to 661)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Blotechnol. 22 (6), 707-716 (2004)
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Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
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Insert Length: 661 Std Error: 0.00.
Location/Qualifiers
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/mol_type="mRNA"
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                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 653)
1 (bases 1 to 653)
Mambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
EST (Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., et al.)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type=taxon:9606"
/db xref=taxon:9606"
/clone="URF2PSILI1183"
/dev_stage="URF2PSILI1183"
/lab_host="UR108"
/clone="lib="781 (synonym: hlcc4)"
/note="Vector: pSportl_Sfi; Site_1: SfilB; cDNA-collection"
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                                                                                                                                                                                                                            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5. sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZ)781Li183) is available at the RZPD in Berlin. Please contact the RZPD Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERNANY; Email: clone@rzpd.de.
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1. (bases I to 584)

Suzuki, Y., Yamashita, R., Shirota, M., Sakahibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
                                                                                                                                                                        GCGTGTGTTACTCCACCGTGGGCACCAGCGACGCAGAAACCTCGGCGCTGCATATCGTTG
                                                                                           GGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGAATCATTCCCGCAGGGTCAACGGACT
                                                                                                                 GGGCTGTGCTGCTCCCCAGTAGCCTCCGGATTGGAATCATTCCGCAGGGTCAAACGGACT
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                     TGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGCGCCGGGGTCGACCAGAACCACCCCC
                                                                                                                                                                                                                                                                       241 TIGGGGACTCGCTGGCCATGGAIGTGTCCTCAGTCCACCACCACAGCACACTCCTTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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/db xref="taxon:9606"
/clone="nRR01274"
/tissue type="brain"
/clone_lib="Sugano cDNA library, brain"
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Pred. No. 1.4e-139;
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                                     ACGTGGAGGAGTGGCAAGTCGTCTGTGGGAAGTTTCTGGCCATCAATGCCACAAACATGT 1189
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581 bp mRNA linear EST 15-SEP-2004
BP224560 Sugano cDNA library, lymphocyte Daudi Homo sapiens cDNA
clone DAT01067, mRNA sequence.
BP224560
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241 GCAAGCAGCAGCTGGAGGAGCAGAAGAAGCACTGTATGGTTTGGAAGCTGCGGAGG 300
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Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 581)

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/clone\_lib="Sugano cDNA library, brain'

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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 584)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Contact: Yutaka Suzuki
Department of Wirology
Institute of Madical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukielms. Lickyo.ac.jp.
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/clone="NRR01216"
/tissue_type="brain"
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Pred. No. 2.7e-137;
0; Mismatches 2;
                                0;
Query Match 35.3%;
Best Local Similarity 99.5%;
Matches 582; Conservative 0
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Perfect score:

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Sequence:

Scoring table:

Minimum DB Maximum DB

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Sequence 3122, Ap Sequence 12897, A Sequence 12897, A Sequence 1349, Ap Sequence 1937, Ap Sequence 166, App Sequence 154, App Sequence 40, App Sequence 40, App Sequence 40, App Sequence 2, Appli
 Sequence 399, App Sequence 30448, A Sequence 30448, A Sequence 12677, A Sequence 253, App Sequence 31476, A Sequence 31476, A Sequence 11079, App Sequence 188, App Sequence 1961, App Sequence 1479, App Sequence 159, Appli
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Sequence 748, App
Sequence 1002, Ap
Sequence 4, Appli
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FILE REFERENCE: 802

CURRENT APPLICATION NUMBER: US/09/774,528

CURRENT APPLICATION NUMBER: US/09/774,528

CURRENT PILING DADS: 441

SOFTWARE: PL_Genes Version 2.0

TITLE OF 100 148
US-09-750-580-1
US-09-270-767-28485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 148, Application US/09774528; Patent No. 6743619; GENERAL INFORMATION:
                               ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1129)..(2817)
US-09-774-528-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                           US-09-774-528-148
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    100.5
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     Command line parameters:
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Sequence 15155, A
Sequence 13, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
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                                                                                                  5, 2005, 19:28:44; Search time 184.39 Seconds (without alignments) 2892.921 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 PKHLLVFINPFGGKGGGKRI......KCSRFNFLRFLIRHTNQQDQ 326
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                         OM protein - nucleic search, using frame_plus_p2n model
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US-09-970-516-3
US-09-817-676A-13
US-09-817-676A-11
US-09-949-016-1155
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US-09-205-258-90
US-09-248-796A-1756
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                                                                                                                                                                                                                                                                                                        1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Matches:
Conservative:
Mismatches:
Indels:
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                                                           US-09-270-767-14306

Sequence 14306, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of TITLE OF INVENTION: Nucleic acids and proteins of CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 14306

LENGTH: 2064
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             Percent Similarity:
Best Local Similarity:
Query Match:
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 Length:
Matches:
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Best Local Similarity:
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DB:
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|--------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|------------------------------------------------|-------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------|-------------------------------------------------------------------------|------------------------------------------------------------------|--------------------------------------------------------|--------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|
| ::::::<br>      ::::::<br>  1174 CTGAaTAATGGGGGTATGACGCCGAACTGAGAAGAGAGCCCGATCTTCTACTG<br> | 1234 ACCACGCCGCTGGAGGACATTCCGCAGAGTCCGCGTAGTGTGTGCTCGCTGGGAGAGTCA  226ArglysProcysArgAlaGlyCysPheValCys | DB 1294 GIGCCAICCGAIGCCAAIGCCAAGGGCIGCAGGCTCGCCAGCAGGAA 1353 Qy 237 ArgGlnSerLysGlnGlnLeuGluGluGluGlnChrysAlaLeuTyrGlyLeuGluAla 256 Dh 1354 CACCAATCTCAATTCAAAACAAAAAAAAAAAAAAAAAA | 257 AlagluAspValGlu                                                     | 261                                                                     | OY 262GluTrpGlnValVaSGlyLy8PheLeuAlaIleAshArhsn 277                     | 278 MetSerCysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAsp :::    | 298 GlySerSerAspLeulleLeulleArgLysCysSerArgPheAsnPheLeuArgPheLeu  1.    | 318 Ile 318 :::                                | Db 1702 CTC 1704<br>RESULT 3<br>US-09-270-767-15155/c | ; Sequence 15155, Application US/09270767<br>; Patent No. 6703491<br>; GENERAL INFORMATION:<br>; APPLICANT: Homburger et al. | Red<br>TM<br>199                                                              | ; NUMBER OF SEQ ID NOS: 62517<br>; SOFTWARE: PatentIn Ver. 2.0<br>; SEQ ID NO 15155<br>; IRMGTH: 1084 | S   | Cores:                                                           | 2e-65 Length:<br>566.00 Matches:<br>49.58\$ Conservative:               | : 34.35%<br>32.96%<br>4                                          | US-10-631-958-2 (1-326) x US-09-270-767-15155 (1-1084) | Qy         2 LysHisLeuLeuValPhelleAsnProPheGlyGlyLysGlyGlnGlyLysArglleTyr         21           n | 22 GluargiysValalaProLeuPheThrieuAlaSerileThrThraspileileGlyAsn      |

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Sequence 13, Application US/09817676A

Patent No. 6800470

GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT PILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/194,318
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 15
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TITLE: Molecular cloning and functional characterization
TITLE: movel mammalian sphingosine kinase type 2 isoform
JOHRNAL: J. Biol. Chem.
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DATABASE ACCESSION NUMBER: AF245447
DATABASE ENTRY DATE: 2000-06-27
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (7)..(1860)
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PAGES: 19513-19520
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Patent No. 6610534
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polymucleotides encoding sphingosine kinases
FILE REFERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCTTCACACTGGGCTGCTGGGCCTCGCCACACTGCACCTACCGCGGACGCCTC 1020
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Conservative:
Mismatches:
Indels:
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47.41%
28.88%
14.15%
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(18) OTHER INFORMATION US-09-970-516-3
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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Pred. No.:
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FACELIA NO. 1901.33.

FARENTAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

FRIOR FILING DATE: 2000-04-14

PRIOR PLILNG DATE: 2000-10-20

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRESCR FOR WINDOWS VERBION 4.0

SEQ ID NO 1155

LENGTH: 1793
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                                                                   44 TyrvalAsnTyrvalGluValIleThrGluHisAlaAsnGlnAlaLysGluThrLeuTyr 63
   24 LysValAlaProLeuPheThrLeuAlaSerIleThrThrAspIleIleGlyAsnLysPhe 43
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; Patent No. 6812339
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US-09-949-016-1155
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; ORGANISM: Huma:
US-09-949-016-1155
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                        172 TyrGlyPheTyrGlyAsplleIleLysAspSerGluLysLysArgTrpLeuGlyLeuAla 191
   ---ThrVal 131
                                                               GlyThrSerAspAlaGluThrSerAlaLeuHisIleValValGlyAspSerLeuAlaMet 151
                                                                                                                                  AspValSerSerValHisHisAsnSerThrLeuLeuArgTyrSerValSerLeuLeuGly 171
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APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Takafumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 60/194,318
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11.
LENGTH: 2698
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PUBLICATION INFORMATION:
TITLE: Molecular cloning and functional characterization of TITLE: movel mammalian sphingosine kinase type 2 isoform JOURNAL: J. Biol. Chem.
VOLUME: 275
PAGES: 19513-19520
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GlySerThrAspCysValCysTyrSer-
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09817676A Patent No. 6800470 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATABASE ACCESSION NUMBER: AF245448
DATABASE ENTRY DATE: 2000-06-27
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ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
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Best Local Similari
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| Aliqnment Scores                                   |                       |                                     |                                                  |                                                                  |                 |   | Ор                 | 1165 ATGGGC                                 |
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| ••                                                 |                       | 29e-19                              | Length:                                          | 1783                                                             |                 |   | δ                  | 307 Lys                                     |
| Score.<br>Percent Similarity<br>Rest Local Similar |                       | 220:00<br>41.47%<br>25.88%          | Conservative:<br>Wiemetchee.                     | - 55 c<br>- 3 - 3 - 3 - 3 - 3 - 3 - 3 - 3 - 3 - 3                |                 |   | ΩD                 | 1210 GCGGGA                                 |
| Query Match:<br>DB:                                |                       | . 28 %                              | Indels:<br>Gaps:                                 | 13,<br>13                                                        |                 |   | RESULT<br>US-09-   | RESULT 8<br>US-09-970-516-1                 |
| US-10-631-958-2                                    | (1-326) x             | US-09-949-016-1155                  | 6-1155 (1-1783)                                  |                                                                  |                 |   | ; Seque<br>; Pater | Sequence 1, Applic<br>Patent No. 6610534    |
| 1 Pr                                               | rolysHisLeu           | ProLysHisLeuLeuValPhelleAsnProPheGl | AsnProPheGlyGly                                  | YLYSG1YG1nG1YLYSArg11                                            | rgile 20        |   | ; GENE             | LICANT: No. 6                               |
| 376 CC                                             | <br>  CTGCCGCGTG      | CTGGTGCTGCTG                        | AACCCGCGCGGCGG                                   |                                                                  | 4GCTC 435       |   |                    | LE OF INVENTI<br>LE OF INVENTI              |
| 21 TY                                              | yrGluArgLys           | WalAlaProLeu                        | PheThrLeuAlaSer                                  | TyrGluArgLysValAlaProLeuPheThrLeuAlaSerIleThrThrAspIleIleGly     | leGly 40        |   | CONT.              | CURRENT APPLICATI                           |
| 436 TT                                             | rccgaagtcac           | Grecaecccrrr                        | Trecggagteacdideagecectriticgeteagectgaaate      | ATC                                                              | 477             |   | MUM.               | NUMBER OF SEQ ID                            |
| 41 As                                              | snLysPheTyr           | .ValAsnTyrVal                       | GluValIleThrGlu                                  | AsnLysPheTyrValAsnTyrValGluValIleThrGluHisAlaAsnGlnAlaLysGlu     | yaglu 60        |   | SEO                |                                             |
| 478                                                |                       | TCCTTCACG                           | CTGATGCTCACTGAG                                  | -rccttcacgctgatgctcactgagcggcggaaccacgcgggag                     | GGGAG 522       |   |                    | TYPE: DNA                                   |
| 61 Th                                              | nrLeuTyrGlu           | illeAsnileAsp                       | LysTyrAspGlyIle                                  | ThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIleValCysValGlyGlyAspGly     | spGly 80        |   | FE                 | FEATURE:                                    |
| 523 CT                                             | regrecearce           | GAGGAGCTGGGC                        | CGCTGGGACGCTCTG                                  | cregrecercesageseresececreseacercresresresresresresages          | ACGGG 582       |   | ğ E                |                                             |
| 81 Me                                              | etPheSerGlu           | ValLeuHisGly                        | LeulleGlyArgThr                                  | MetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp     | alasp 100       |   | -60-SA             | US-09-970-516-1                             |
| 583 CI                                             | rgargcacgag           | GTGGTGAACGGG                        | CTCATGGAGCGGCCT                                  | ::<br>crgargcacGagGrgGrgGracGGGCrcarGGGGCCrGACrGGGAGACCGCCArCcAG | rccag 642       |   | Alignme            | Alignment Scores:                           |
| 101 G1                                             | lnAsnHisPrc           | oArgAlaValLeu                       | ValProSerSerLeu                                  | GlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAla     | roAla 120       |   | Score:             |                                             |
| 643 AA                                             | aag                   |                                     |                                                  | :::<br>ccccrgrgragccrcccagca                                     | CAGCA 666       |   | Percen<br>Best L   | Percent Similarity:<br>Best Local Similarit |
| 121 G                                              | GlySerThrAspCysValCys | CysValCys                           |                                                  | TyrSerThrvalGly                                                  | alGly 132       |   | Query Match<br>DB: | Match:                                      |
| 667 GG                                             | <br>GCTCTGGCAAC       | : ::<br>GGCGCTGGCAGCT'              | TCCTTGAACCATTAT                                  | ::: :::<br>GGCTCTGGCAACGCGCTGCCTTGAACCATTATGCTGGCTATGAGCAGGTCACC | II<br>FCACC 726 |   | US-10-             | US-10-631-958-2 (1-3                        |
| 133 Th                                             | hrSerAspAla           | GluThrSerAla                        | LeuHisIleValVal                                  | ThrSerAspAlaGluThrSerAlaLeuHisIleValValGlyAspSerLeuAla-          | Met 151         |   | ò                  | 1 ProLys                                    |
| 727 AA                                             | ATGAAGACCTC           | CTGACCAACTGC                        | ACGCTATTGCTGTGC                                  | AATGAAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCGCCGGCTGCTGTCACCCAT      | CCATG 786       |   | QQ                 | 40 CCCTGC                                   |
| 152 A8                                             | spvalSerSer           | :ValHisHisAsn                       | AspvalSerSerValHisHisAsnSerThrLeuLeuArgTyrSerVal | TyrSerValSerLeuLeuGly                                            | euGly 171       |   | ò                  | 21 TyrGlu                                   |
| 787 AA                                             | Accrecrerci           | rcrecacaceger                       | rcececrecere                                     | Aaccrecreferecacacacerredesecrecrecrerereresecresecresecres      | recc 846        |   | qq                 | 100 TTCCGG                                  |
| 172 Ty                                             | yrGlyPheTyr           | GlyAspileile                        | LysAspSerGluLys                                  | TyrGlyPheTyrGlyAspIleIleLysAspSerGluLysLysArgTrpLeuGlyLeuAla     | euAla 191       |   | λ                  | 41 AsnLys                                   |
| 847 TG                                             | GGGCTTCATI            | rgcrgatgrggac                       | CTAGAGAGTGAGAAG                                  | TGGGGCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAGATG     | AGATG 906       |   | qq                 | 142                                         |
| 192 Ar                                             | rgTyrAspPhe           | SerGlyLeuLys'                       | ThrPheLeuSerHis                                  | ArgTyrAspPheSerGlyLeuLysThrPheLeuSerHisHisGysTyrGluGlyThrVal     | hrVal 211       |   | ò                  | 61 ThrLeu                                   |
| 907 CG                                             | SCTICACICIC           | secencerecte                        | CGTCTGGCAGCCCTG                                  | cecticacteteggcaceticeggeggcagecetegggacetacegggcacta            | SACTG 966       |   | Д                  | 187 CTGGTG                                  |
| 212 Se                                             | erPheLeuPro           | AlaGlnHisThr                        | ValGlySerProArg                                  | SerPheLeuProAlaGlnHisThrValGlySerProArgAspArgLysProCysArgAla     | rgAla 231       |   | λõ                 | 81 MetPhe                                   |
| 967 GC                                             | ccraccrccc            | rgtaggaaga                          | GCCTACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCTGCCTCCCCC | .corecorococo                                                    | 1014            | 4 | qд                 | 247 CTGATG                                  |
| 232 G1                                             | lyCysPheVal           | CysArgGlnSer                        | LysGlnGlnLeuGlu                                  | GlyCysPheValCysArgGlnSerLysGlnGlnLeuGluGluGluGlnLysLysAlaLeu     | laLeu 251       |   | ò                  | 101 GlnAsn                                  |
| 1015                                               | GTTGTG                | GTCCAGCAGGG                         | -GTTGTGGTCCAGGGCCCGGTAGATGCACA-                  | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                          | CTT 1050        |   | q                  | 307 AAG-                                    |
| 252 Ty                                             | yrGlyLeuGlu           | AlaAlaGluAsp                        | ValGluGluTrp                                     | TyrGlyLeuGluAlaAlaGluAspValGluGluTrpGlnValValCysGlyLys-<br>      | ys 269          |   | ò                  | 121 GlySer                                  |
| 1051 GT                                            | Greccacregae-         | ;                                   | GTGCCCTCTCACTGG                                  | -dagccagtgcccrcrcacrdgacaarggrdcccgacgagac                       | AGGAC 1104      | 4 | qq                 | 331 GGCTCT                                  |
| 270                                                | Phe                   | eLeuAlaIleAsn                       | AlaThrAsnMetSer                                  | -PheLeuAlaIleAsnAlaThrAsnMetSerCysAlaCysArgArgSerPro             | erPro 286       | _ | ò                  | 133 ThrSer                                  |
| 1105 TT                                            | TTGTGCTAATC           | creecacrecre                        | CACTCGCACCTGGGC                                  | TTTGTGCTAATCCTGGCTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCC       | CACCC 1164      | 4 | qq                 | 391 AATGAA                                  |
| 287 AI                                             | rgGlyLeuSer           | rProAlaAlaHis                       | LeuGlyAspGlySer                                  | ArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSerAspLeuIleLeuIleArg     | learg 306       |   | ò                  | 152 AspVal                                  |
|                                                    | =                     | =                                   | -                                                |                                                                  | <del>-</del>    |   |                    |                                             |

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5610534artis AG
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10N: Induction of blood vessel formation through administration of
10N: polynucleotides encoding sphingosine kinases
4-316.7
11ON NUMBER: US/09/970,516
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2 NOS: 6
2 NOS: 6
                                                  1165 ATGGGCCGCTGTGCAGCT------GGCGTCATGCATCTGTTCTACGTGCGG 1209
                              -CysSerArgPheAsnPheLeuArgPheLeuIle------ArgHis 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uTyrGluIleAsnIleAspLysTyrAspGlyIleValCysValGlyGlyAspGly 80
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igggrcgGaggacgcrgggacgcrcrggrggrcgrcgrggrcgrcgrggrcgrcgacgacgacgg 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               raspalaGluThrSerAlaLeuHisIleValValGlyAspSerLeuAla---Met 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGTCACGTGCAGCCCCTTTTGGCTGAGCTGAATC-------141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sPheTyrValAsnTyrValGluValIleThrGluHisAlaAsnGlnAlaLysGlu
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| Qy         81 MetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp 100           :::                                                                                                                                                                                                                                           | 423 483 483 483 152 172 172 192 192 202 202 202 202 202 202 202 202 202 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | US-09-970-516-5  Alignment Scores:                                                        |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------|
| Db 451 AACCTGCTGTCTCTGCACACGGCTTCGGGGCTGCTCTTCTCTGTGCTCGGCC 510  Qy 172 TyrGlyPheTyrGlyAspileIleLysAspSerGluLysLysArgTrpLeuGlyLeuAla 191  :::        Db 511 TGGGCTTCATTGCTGATGTGGACTTGAGAGTATCGGCGTCTGGGGGAGATG 570  Qy 192 ArgTyrAspPheSerGlyLeuLysThrPheLeuSerHisHisCysTyrGluGlyThrVal 211     :::     :::     :::::            :::: | NESULT 9 105-09-59-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997-1 105-00-595-997- | 4 Gaps: 8-2 (1-126) x US-09-959-897-1 (1-1205) 1 ProLysHisLeuLeuValPheIleAsnProPheGlyGlyI |

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EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,875
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511 TGGGCCTTTGTTGCTGACGTGGACCTCGAGAGTGAGAAGTACAGGCGCTTGGGGGAGATT 570
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571 CGTTTCACAGTGGGCACCTTTTGGCCTAGCAAGCCTGCGCATCTACCAAGGCCAACTG 630
                                                                                                                                                                                                                              81 MetPheSerGluvalLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp 100
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41 AsnLysPheTyrValAsnTyrValGluValIleThrGluHisAlaAsnGlnAlaLysGlu 60
                                                                                                                                                                     61 ThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIleValCysValGlyAspGly 80
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
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; Sequence 90, Application US/09205258
; Patent No. 6525174
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Patent No. 6747137
GENERAL PAPLICANTION: Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
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Matches:
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LOCATION: (1522)
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FEATURE:
NAME/KEY: SITE
LOCATION: (1527)
OTHER INFORMATION: n
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Query Match:
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US-09-248-796A-1756
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Pred. No.:
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      FOR DIAGNOSTICS AND THERAPEUTICS
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Matches:
Conservative:
Mismatches:
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553 AAAATCTTACCAATATTACAAGCGGCT------
FILLE OF INVENTION: FUR DIAGNOSILLE.

FULE REFERENCE: 107196.13

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 1756
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216.00
42.95%
24.76%
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Best Local Similarity:
Query Match:
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ORGANISM: (
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                                                                                                                                         159 AsnSerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspIle 178
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                                                           142 HislleValValGlyAspSerLeuAlaMetAspVal-----SerSerValHisHis 158
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TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR PRILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL FL_Genes Version 1.0
SEQ ID NO 796
LENGTH: 2462
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Matches:
Conservative:
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Patent No. 6569662
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
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Wang, Jian-Rui
Zhou, Ping
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Zhang, Jie
Ren, Feiyan
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Liu, Chenghua
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ORGANISM: Homo sapiens
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  230 ArgAlaGlyCysPheValCysArgGlnSerLysGlnGlnLeuGluGluGluGlnLysLys 249
                                                                                250 AlaLeuTyrGlyLeuGluAlaAlaGluAspVal---GluGluTrpGln-ValValCysGl 268
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                                                                                                                                                          268 yLysPheLeuAlaileAsnAlaThrAsnMetSerCysAlaCysArgArgSerProArg-- 287
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Matches:
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Mismatches:
Indels:
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APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTH
TITLE OF INVENTION: NUCLEIC ACID
FILE REFERENCE: 16516.075
CURRENT APPLICATION NUMBER: US/09/614,221A
CURRENT FILING DATE: 2000-07-12
PRIOR FILING DATE: 1999-07-12
SEQ ID NOS: 626
SEQ ID NOS: 626
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Sequence 399, Application US/09614221A
Patent No. 6723837
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Karunanandaa, Balasulojini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae
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US-09-614-221A-399
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Patent No. 6703491

GREERAL INFORMATION:

APPLICANT: Homburst et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REPERENCE: File Reference: 7326-094

CURRENT PAPLICANTION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 30448

LENGTH: 901

TYPE: DNA
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                                                                                     LysHisLeuLeuValPhelleAsnProPheGlyGlyGlyGlyGlyGlyLysArglleTyr
                                                                                                                                                                   42 LysPheTyrValAsnTyrValGluValIleThrGluHisAlaAsnGlnAlaLysGluThr
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Local Similarity:
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                                                                                                        -------ArgLysProCysArgAlaGlyCysPheValCys-------
                                                                                            LysThrPheLeuSerHisHisCysTyrGluGlyThrValSerPheLeu-
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| Cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US06_PUBF_PUB.seq:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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SUMMARIES

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|        | 18              | 432.5                                           |         | 2079               | 18           | -10-425-114-3453                     | , ,               |
|        | 19              | 2                                               |         | 2079               | 20           | ١٠                                   | , ω               |
|        | 20              | 4                                               |         | 564                | 22           | -10-477-445-46                       | ۸.                |
|        | 21              | m                                               |         | 1833               | 13           | -10-437-963-3065                     | ,                 |
|        | 5 5             | 334.5                                           |         | 2166               | 20           | -10-425-115-6489                     | Ψ,                |
|        | 2 4 5           | 456                                             |         | 2084               | ם מ          | -10-425-114-3408<br>-10-424-599-4739 | ., ,              |
|        | 52              | 330                                             |         | 1869               | 18           | -10-425-114-3480                     |                   |
| O      | 7               | 321.5                                           |         | 2189               | 19           | -10-437-963-9280                     | ٠.                |
|        | 27              | r ;                                             |         | 3362               | 20           | -10-425-115-2900                     |                   |
|        | 788             | 78                                              |         | 1512               | 700          | 10-425-115-6489                      | Ψ.                |
|        | 2 6             | מ מ                                             |         | 1857               | 9 4          | -10-424-599-5941<br>-10-425-114-3213 | .,                |
|        | 31              | 305.5                                           |         | 2247               | 25           | 1 -                                  | Sequence 97849, A |
|        | 32              | 3                                               |         | 167                | 10           | 9-968-696-60-                        | w                 |
|        | 33              | ω,                                              |         | 167                | 13           | 급.                                   | •                 |
|        | 4. 5            | 300.5                                           |         | 1306               | 9 5          | 10-115-635-247                       |                   |
|        | 9 6             | 291                                             |         | 2629               | 1 6          | -10-437-963-3290                     | • • •             |
|        | 37              | 89                                              |         | 1468               | 16           | ٠.                                   | , –               |
|        | 38              | 288.5                                           |         | 2284               | 20           | -10-425-115-7942                     |                   |
|        | 39              | 87                                              |         | 3008               | 13           | -10-437-963-7789                     |                   |
|        | 0 ,             | 282                                             |         | 2629               | 17           | ς.                                   |                   |
|        | 4 4             | 282                                             |         | 6297               | ا د<br>و د   | US-10-622-U11-24                     | v u               |
| t      | 7               | 273                                             |         | 522                | 9 0          | 10-423-113-6621<br>09-784-8108-7     | mence 7           |
| טנ     | 4               | 273                                             |         | 522                | , 2          | US-1                                 | Sequence 7, Appl  |
| ı      | 4               | 270.5                                           |         | 2609               | 17           | -10-348-052-                         | e 25,             |
|        |                 |                                                 |         |                    |              | OHIVENING I I                        |                   |
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| RE     | RESULT          | 1                                               |         |                    |              |                                      |                   |
| Sn     | -09-9(<br>Segue | JS-09-969-896-1<br>: Sequence 1, Application US | policat | ion US/            | 9660         | 9686                                 |                   |
| ٠.     | Publi(          | cation N                                        | o. US20 | 0301255            | 33A1         | 5533A1                               |                   |
|        | GENER           | AL INFOR                                        | MATION: | South              |              |                                      |                   |
|        | TITL            | E OF INV                                        | ENTION: | Requia             | tion         | 5                                    |                   |
| . •-   | TITL            | E OF INV                                        | ENTION: | Kinase-I           | e-Like       | Protein                              |                   |
| •• •   | FILE RE         | REFEREN<br>FNT ADDI                             | CE: 004 |                    | 94           | 968 696/60/8                         |                   |
|        | CURRENT         | ENT FILI                                        | NG DATE | 2001               | 1-10-        | 04                                   |                   |
| ••     | PRIOR           | R APPLIC                                        | ATION N | UMBER:             | us e         | 60/238,005                           |                   |
| ٠      | PRIOR           | R FILING                                        | DATE:   | 2000-10<br>TIMBER: | -06<br>115 6 | £11 412/0                            |                   |
| - •-   | PRIOR           | OR FILING DATE: 2001-08-23                      | DATE:   | 2001-08            | -23          | 11/11/10/0                           |                   |
| •-     | NUMBER          | ER OF SE                                        | ON GI Ö | S: 16              |              |                                      |                   |
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GlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAla 120
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                                                                                               Sequence 1, Application US/10631958

Sequence 1, Application US/10631958

Publication No. US20040192580A1

GENERAL INFORMATION:
TITE OF INVENTION: Kinase-Like Protein

FILE REFERENCE: 004974.00594

CURRENT APPLICATION WUMBER: US/09/969,896

PRIOR FILING DATE: 2001-10-04

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2001-06

PRIOR FILING DATE: 2001-06

PRIOR FILING DATE: 2001-06

PRIOR FILING DATE: 2001-06

PRIOR FILING DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 16

SOFWARE: FastSEQ for Windows Version 4.0

TYPE: DNA
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Matches:
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Pred. No.:
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 979
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                       TYPE: DNA ORGANISM: Homo sapiens
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Percent Similarity:
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                                                 AACAAATTCTATGTTAACTATGTAGAAGTAATTACTGAACATGCTAATCAGGCCAAGGAG
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US-10-631-958-2 (1-326) x US-09-784-810A-5 (1-1840)
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US-10-876-281-5
; Sequence 5, Application US/10876281
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Fatent No. US20020082203A1
GENERAL INPORMATION:
FALLE PAPLICANT: RASTELL, LUCA
TITLE OF INVENTION: SAME
FILE REFERENCE: 10716-08
CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT APPLICATION NUMBER: 60/182,360
FRIOR PEPLICATION NUMBER: 60/182,360
FRIOR FILING DATE: 2000-02-14
FRIOR FILING DATE: 2000-03-14
FRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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Percent Similarity:
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| 9942A1                                                   | Db 865 TICCTCTCCCACCACTGCTATGAAGGGACAGTGCTCCTTCCT                                                                                                                                     |
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| SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING           | Qy         221 GlySerProArgAspArgLysProCysArgAlaGlyCysPheValCysArgGlnSerLys         240           Db         925 GGATCTCCAAGGAAAGCCCTGCCGGCCAGGATGCTTTGCTTTGCAGGCAAAGCAAG         984 |
| 0/8                                                      | 241 GlnGlnLeuGluGluGlnGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspVal                                                                                                                      |
| . 60/182,360<br>22-14<br>1. 60/191,261<br>33-22          | Qy 261 GluGluTrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSerCys 280<br>                                                                                                           |
| 2.1                                                      | Qy         281 AlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSer         300                                                                                               |
|                                                          | Qy 301 AspleulleLeulleArgLysCysSerArgPheAsnPheLeuArgPheLeulleArgHis 320<br>                                                                                                           |
| 100% Conservative: 0                                     | Qy         321 ThrAsnGlndspGln 326                                                                                                                                                    |
| Indels:<br>Gaps:<br>Gaps: (1-1840)                       | RESULT 5<br>US-09-969-896-9; Sequence 9, Application US/09969896<br>; Sequence 9, Application US/0995896                                                                              |
| uValPheIleAsnPro<br>                                     | ; GENERAL INFORMATION:<br>; APPLICANT: Kossida, Sophia<br>; TITLE OF INVENTION: Regulation of human Sphingosine<br>; TITLE OF INVENTION: Kinase-Like Protein                          |
| alalaproLeuPheThrLeualaSerIleThrThraspIleIleGly 40       | ; FILE REPERENCE: 004974.00594 ; CURRENT APPLICATION NUMBER: US/09/969,896 ; CURRENT FILING DATE: 2001-10-04 ; PRIOR APPLICATION NUMBER: US 60/238,005                                |
| alasntyrvalgluvalllethrgluHisalaAsnGlnAlaLysGlu 60<br>   | ; FRIOR FILING DATE: 2000-10-06; PRIOR PELICATION NUMBER: US 60/314,113; PRIOR FILING DATE: 2001-08-23; NUMBER OF SEQ ID NOS: 16                                                      |
| I   I   I   I   I   I   I   I   I   I                    | ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO. ; LENCTH: 1614 ; TYPE: DNA.                                                                                                  |
| albeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp 100<br>  |                                                                                                                                                                                       |
| rgalavalLeuvalProserSerLeuargIleGly11eIleProala 120<br>  | Pred. No.: 2.22e-201 Length: 1614 Score: 1640.50 Matches: 314 Percent Similarity: 96.33 Conservative: 1 Best Local Similarity: 96.32\$ Mismatches: 0                                  |
| ysValCysTyrSerThrValGlyThrSerAspalaGluThrSerAla 140<br>  | 95.54% Indels:<br>10 Gaps:<br>1 x US-09-969-896-9 (1-1614)                                                                                                                            |
| alglyaspserLeualametAspValSerSerValHisHisAssnSer 160<br> | Oy 1 ProLysHisLeuVeuValPhelleAsnProPheGlyGlyLysGlyGlnGlyLysArglle 20                                                                                                                  |
| yrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspileileLys 180<br>  | Oy 21 TyrGluargLysValAlabroLeuPheThrLeuAlaSerIleThrThrAspIleIleGly 40<br>                                                                                                             |
| ysargTrpLeuGlyLeuAlaargTyrAspPheSerGlyLeuLysThr 200<br>  | Qy         41 AsnLysPheTyrValAsnTyrValGluValIleThrGluHisAlaAsnGlnAlaLysGlu 60           :::                                                                                           |
| isCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrVal 220      | Oy 61 ThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIleValCysValGlyAspGly 80                                                                                                                    |

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GlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAla
                                                                       CTGCATATCGTTGTTGGGGACTCGCTGGCCATGGATGTGTCCTCAGTCCACCACAGC
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Publication No. US20040192580A1
GENERAL INPORMATION:
TERRETAIN TROSSIDER
TITLE OF INVENTION: Regulation of human Sphin TITLE OF INVENTION: Regulation of human Sphin TITLE OF INVENTION: Regulation of human Sphin TITLE OF INVENTION: Regulation of human Sphin TITLE OF INVENTION: Regulation of human Sphin TITLE OF INVENTION: Rinase-Like Protein CURRENT APPLICATION NUMBER: US/09/969,896; PRIOR FILING DATE: 2003-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-06
WUMBER OF SEQ ID NOS: 16
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SOFTWARE: FastSEQ for Windows Version
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LENGTH: 1614
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                                      TYPE: DNA ORGANISM: Homo sapiens
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* NAME/KEY: CDS

* LOCATION: (76).

US-10-262-511-39
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AlaCysArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSer 300
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APPLICANT: Miler, Charles E.
APPLICANT: Ratelli, Luca
APPLICANT: Bacelli, Luca
APPLICANT: Brone, David J.
APPLICANT: Brene, Carol E. A.
APPLICANT: Bene, David J.
APPLICANT: Brene, Mark E.
APPLICANT: Brene, Mark E.
APPLICANT: Brene, Mark E.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Berghs, Constance
ITHLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPRENCE: 2102-402-462.
CURRENT APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-00-26.
PRIOR FILING DATE: 2001-00-39
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/321,629
PRIOR FILING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR PRILING DATE: 2002-06-19
PRIOR PLILING DATE: 2002-04-19
PRIOR PRILING DATE: 2001-00-09
PRIOR PRILING DATE: 2001-00-09
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PRIOR PRILING DATE: 2001-00-09
PRIOR FILING DATE: 2001-00-09
PRIOR PRICATION NUMBER: 60/373,60
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Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glemda
APPLICANT: Millet, Isabelle
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Ju, Jingfang
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Telana
Gorman, Linda
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Catterton, Elina
Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
Stone, David J.
Shenoy, Suresh G.
Shimkets, Richard A.
Shenok, Mark E.
Leach, Martin D.
Agee, Michele L.
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Anderson, David W.
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   790 GGGTCAACGGACTGCGTGTGTTACTCCACCGTGGGCACCAGCGACGCAAACCTCGGCG 849
                                                CTGCATATCGTTGTGGGGACTCGCTGGCCATGGATGTGTCCTCAGTCCACAAAAAGC 909
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                                LeuHislleValValGlyAspSerLeuAlaMetAspValSerSerValHisHisAsnSer
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Publication No. US20040192580A1
GENERAL INPORMATION:
TERLE LINCORMATION:
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Kinase-Like Protein
FILE REFERENCE: 004974.005969.
CURRENT APPLICATION NUMBER: US/10/631,958
CURRENT FILING DATE: 2003-08-01
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-06
PRIOR PRILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 4413
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US-10-631-958-16
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                                              1270 GCTTGTCGCCGGAGCCCCAGGGCCCTCTCCCCCGGCTGCCCACTTGGGAGACGGGTCTTCT
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Publication No. US20030125533A1

GENERAL INFORMATION:
APPLICANT: Kossida, Sophia
TITLE OF INVENTION: Kegulation of human Sphingosine
TITLE OF INVENTION: Kinase-Like Protein
FILE REFERENCE: 004974, 00594
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-0-0-6
PRIOR FILING DATE: 2001-0-0-6
PRIOR FILING DATE: 2001-0-0-6
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 4413
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1640.50
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ORGANISM: Homo sapiens
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Percent Similarity:
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Pred. No.:
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US-09-969-896-16
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           US-10-631-958-2 (1-326) x US-10-631-958-16 (1-4413)
Gaps:
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Matches:
Conservative:
Mismatches:
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Sequence 55, Application US/10618941
Publication No. US20040197792A1
GENERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: CAREFREIL, SEAN
TITLE OF INVERTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT APPLICATION WUMBER: US/10/618,941
CURRENT APPLICATION WUMBER: 60/395,632
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SEQ ID NO 55
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1640.50
96.63$
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ORGANISM: Homo sapiens
US-10-618-941-55
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Percent Similarity:
Best Local Similarity:
Query Match:
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 AsnLysPheTyrValAsnTyrValGluValIleThrGluHisAlaAsnGlnAlaLysGlu :::|||||||||||||||||||
                                                                                                        MetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp
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Sequence 1, Application US/10315597A
GENERAL INFORMATION:
APPLICANT: Sugiura, Masako
APPLICANT: Kono, Keita
APPLICANT: Kono, Keita
TITLE OF INVENTION:
FILE REFERENCE: 02658CIP/HG
CURRENT APPLICANTON UNMBER: US/10/315,597A
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: JP 2000-178039
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US-10-315-597A-1
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Sequence 148, Application US/10120988

Publication No. US20030219745A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Liu, Chenghua

APPLICANT: Drmanac, Radoje T.

ITLE OF INVENTION: No. US20030219745A1e1 Nucleic Acids and

ITLE OF INVENTION: Polypeptides

FILE REFERENCE: 802CON

CURRENT APPLICATION NUMBER: US/10/120,988

FILE REFERENCE: 802CON

CURRENT APPLICATION NUMBER: 09/774,528

FRIOR FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 441

SOFTWARE: PLELGENE Version 2.0

SEQ ID NO 148

LENGTH 4432
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US-10-120-988-148
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ORGANISM: Homo sapiens
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US-10-120-988-148
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                                    GCGCTGCATATCGTTGGTTGGTCGCTCGCTGGCCATGGTGTCCTCAGTCCACCACCACAAC
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                                                                                                                                                                                                                                                                    ACCAACCAGCAGGACCAG 1455
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TYPE: DNA
ORGANISM: Homo sapiens
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Query Match:
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95.71$
PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO I
LENGTH: 4463
                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                          ) NAME/KEY: unsure
; LOCATION: 3371
; OTHER INFORMATION:
US-10-315-597A-1
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Sequence 176413, Application US/10425115

Sequence 176413, Application US/10425115

Sequence 176413, Application No. US20040214272A1

Septiment information:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 176413

LENGTH: 2657
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.000 CTAGAGATACCATTCTACTAAAGAACCATGTATTGGAGATCAGGATAACCCAGTT 1059
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Best Local Similarity:
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US-10-425-115-176413
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ORGANISM: Zea mays
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                         US-10-51-938-4
; Sequence 4, Application US/10631958
; Publication No. US20040192580A1
; GENERAL INFORMATION:
   APPLICANT: KOSSIGA, Sophia
; TITLE OF INVENTION: Requlation of human Sphingosine
; TITLE OF INVENTION: Kinase-Like Protein
; FILE REFERENCE: 004974.00594
; CURRENT APPLICATION NUMBER: US/10/631,958
; CURRENT FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2001-10-04
; PRIOR FILING DATE: 2001-10-04
; PRIOR FILING DATE: 2001-10-06
; PRIOR FILING DATE: 2001-10-06
; PRIOR FILING DATE: 2001-00-06
; PRIOR FILING DATE: 2001-00-08-23
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 4
; LENGTH: 474
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                                                                                                                                                                                                                                                              226 -----Arglyspro------CysArgAlaGlyCysPheValCysArgGlnSer 239
                                                                                                                                                                                                                                                                                                   240 LysGlnGlnLeuGluGluGluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAsp 259
                                                                                                                                                                                                                                                                                                                                       260 ValGluGluTrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSer 279
                                    127 CysTyrSerThrValGlyThrSerAspAlaGluThrSerAlaLeuHisileValValGly 146
                                                                         147 AspSerLeuAlaMetAspValSerSerValHisHisAsnSerThr-------- 161
                                                                                                                                                                                      199 LysThrPheLeuSerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHis 218
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Search completed: September 6, 2005, 10:47:27 Job time : 951.291 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 3, 2005, 04:10:49; Search time 14.4126 Seconds (without alignments) 2176.332 Million cell updates/sec Run on:

Title: Perfect score:

US-10-631-958-2 1717 1 PKHLLVFINPFGGKGGGKRI......KCSRFNFLRFLIRHTNQQDQ 326 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79: \* 1: pir1: \* 2: pir2: \* 3: pir3: \* 4: pir4: \* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description           | hypothetical prote | cal    | _      | _      | _      | _      |        | _          | ρ.     | conserved hypothet | conserved hypothet | hypothetical prote | conserved hypothet |        |        | conserved hypothet | hypothetical prote |        | ш      | hypothetical prote | hypothetical prote | conserved hypothet | hypothetical prote | cathepsin Q (EC 3. | hypothetical prote | hypothetical prote | indoleacetamide hy | fibroblast growth | conserved hypothet |
|-----------|-----------------------|--------------------|--------|--------|--------|--------|--------|--------|------------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| SUMMARIES | ID                    | T33517             | T05162 | T38776 | S51398 | T19707 | AG1665 | 867059 | AI1293     | AH1769 | AH1528             | F69795             | A83894             | G95120             | AF1171 | AE1394 | C97990             | F84898             | D83734 | E69678 | S75948             | A96719             | A89978             | T16422             | JC7183             | H70861             | H69995             | B25493             | C145              | F72386             |
|           | DB                    | 7                  | ~      | ~      | ~      | ~      | ~      | ~      | ~          | ~      | ~                  | 7                  | ~                  | ~                  | ~      | ~      | ~                  | ~                  | ~      | ~      | 7                  | 2                  | 7                  | 7                  | ~                  | ~                  | ~                  | Н                  | Н                 | ~                  |
|           | Query<br>Match Length | 549                | 1240   | 458    | 687    | 473    | 310    | 624    | 310        | 306    | 309                | 303                | 295                | 294                | 309    | 306    | 311                | 364                | 295    | 345    | 433                | 1028               | 315                | 732                | 343                | 309                | 309                | 455                | S                 | 304                |
| مه        | Query                 | ထ                  | 21.3   | -      | _      | -      | 7      | 10.6   | 10.4       | 7.6    | 7.6                | 7.5                | 7.3                | 7.3                | 7.2    | 7.0    | •                  | •                  | 9.9    |        | •                  | ٠                  | •                  | 6.1                |                    | 5.9                |                    | 5.5                | 5.4               | 5.4                |
|           | Score                 | 486.5              | 365.5  | 226    | 220.5  | 219.5  | 185.5  | 181.5  | 178.5      | 131    | 130                | 129                | 125.5              | 125                | 123.5  | 121    | 121                | 116.5              | 113    | 111.5  | 110                | 107                | 105                | 105                | 102                | 101                | 97.5               | 95                 | 93                | 92.5               |
|           | Result<br>No.         | н                  | 73     | m      | 4      | Ŋ      | 9      | 7      | <b>6</b> 0 | 6      | 10                 | 11                 | 12                 | 13                 | 14     | 15     | 16                 | 17                 | 18     | 19     | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 | 56                 | 27                 | 28                | 29                 |

RESULT : T05162

| hypothetical prote |        | hypothetical prote |        | amiloride sensitiv | transcription repr | peptidylprolyl iso | probable membrane | hypothetical prote | hypothetical prote | hypothetical prote | chitin synthase (E | multidrug resistan | conserved hypothet | scavenger receptor | 6-phosphofructokin |
|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AB2166             | E64975 | G71901             | AI2397 | 139196             | A39564             | S72485             | S60932            | T20987             | F85835             | D90990             | T31097             | F69595             | A86842             | T14893             | S73860             |
| ~                  | ~      | ~                  | 7      | 7                  | 7                  | ~                  | ~                 | 7                  | ~                  | ~                  | ~                  | ~                  | ~                  | ~                  | 7                  |
| 315                | 299    | 338                | 223    | 638                | 789                | 551                | 1511              | 279                | 299                | 299                | 1041               | 297                | 304                | 2153               | 328                |
| 5.4                | 5.3    | 5.3                | 5.3    | 5.2                | 5.2                | 5.1                | 5.1               | 2.0                | 4.9                | 4.9                | 4.9                | 4.9                | 4.9                | 4.9                | 4.9                |
|                    |        |                    |        |                    | Z.                 | 'n                 | 5.                | 98                 | 84.5               | 'n.                | r.                 | 84                 | 84                 | 34                 | 'n                 |
| 92.5               | 91.5   | 91                 | 90.5   | 88                 | 88                 | 87.                | 87                |                    | 84                 | 84                 | 84                 | -                  | -                  | _                  | 83.5               |

## ALIGNMENTS

| RESULT T33517 hypoth hypoth hypoth C.Spec. C.Pate C.Acce R.Acce R.A.Refe A.Refe A.Refe A.Refe A.Resi | RESULT 1 T33517 hypothetical protein T10B11.2 - C C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_rev C;Accession: T33517 Swhinx, Pr; Kemp, K. Submitted to the EMBL Data Librar A;Description: The sequence of C. A;Reference number: 221363 A;Reference number: 221363 A;References: Preliminary; translated A;Molecule type: DNA A;Residues: 1-549 cMIN> A;Residues: 1-549 cMIN> A;Residues: 1-549 cMIN> A;Cross-references: UNIPROT:Q9TZI A;Experimental source: strain Bric;Cenetics: A;Genetics: A;Map position: 1 A;Introns: 26/1; 76/2; 109/3; 159, | RESULT 1 T33517 Hypothetical protein T10B11.2 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Accession: T33517 C; Accession: T33517 Swhinx, P.; Kemp, K. Submitted to the EMBL Data Library, October 1998 A; Description: The sequence of C. elegans cosmid T10B11. A; Reference number: Z21363 A; Reference number: Z21363 A; Reference number: Z21363 A; Residues: 1-549 «MIN- A; Mesidues: 1-549 «MIN- A; Mesidues: 1-549 «MIN- A; Resperimental source: strain Bristol N2; clone T10B11 A; Experimental source: strain Bristol N2; clone T10B11 A; Genetice CESP: T10B11.2 A; Map position: 116/2; 109/3; 159/1; 187/3; 229/3; 353/1; 398/2; 434/1; 467/3 |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Out<br>Ber<br>Mat                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ery Match<br>st Local Similarity<br>tches 111; Conserv                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Query Match 28.3%; Score 486.5; DB 2; Length 549;<br>Best Local Similarity 34.6%; Pred. No. 1.4e-34;<br>Matches 111; Conservative 66; Mismatches 113; Indels 31; Gaps 6;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 3 8 8 8 8 8 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1 TATALLY TINE  1 14 PKNIIIFINE  1 TLYEINIDKY  1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| 8 6 8 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 237 RQSKQQLBEB<br>394 MKPQG<br>297 DGSSDLILIR<br>11           437 DGTLDLALVP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 237 ROSKQLEEEQKALYGLEAAEDVEEMQVVCGKFLAINATNMSCACRESPRGLSPAAHLG 296 394 MKPQGNDKYDYHWHAEFTHVICCVIPTVTPFTPYGLAPFTGIG 436 297 DGSSDLILIRKCSRFNFLRFL 317   :     : :  : :: : 437 DGTLDLALVPRISRFHNMQFM 457                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |

| hypothetical protein F18ES.160 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: 105162 R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew submitted to the Protein Sequence Database, August 1998 A;Reference number: Z15400 A;Reference number: Z15400 A;Residues: 1-1240 <bev> A;Residues: 1-1240 <bev 117="" 178="" 1:="" 206="" 237="" 2:="" 375="" 3:="" 4="" 416="" 449="" 474="" 503="" 5<="" a;3:="" a;rep="" a;reperimental="" bac="" c;genetics:="" clone="" columbia;="" cultivar="" f18e5="" position:="" source:="" th=""><th>QY 62 LYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAG 121  155 AKNLDVGSYDGILSVGGDGFHEVINGLGERDDYLEAFKLPVCMIPGG 202  QY 122 STDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD 181   </th></bev></bev></bev></bev></bev></bev>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | QY 62 LYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAG 121  155 AKNLDVGSYDGILSVGGDGFHEVINGLGERDDYLEAFKLPVCMIPGG 202  QY 122 STDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD 181                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
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| e 365.5; DB 2; Length 1240;<br>. No. 1.6e-23;<br>ismatches 115; Indels 73; Gaps 11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Db 298 SDRTEIKHMYEKSKNLAPMSESSDSDKTVSTSPESHLLTFEINDLSIFCAGLLPYIAPDA 357  Qy 279 SCACRRSPRGLSPAAHLGDGSSDLILI 305  Db 358 KMFPAASNDDGLIDVVIV 375                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| HLLVFINPEGGGGGRRIYERKVAPLFTLASITTDIIGNKFYVNYVSTRLVFVNYVERGGGGGGRRIYERKVAPLFEDADVQLEIGETKYQLH YELNIDKYDGIVCVGGDGMFSEVLHGLIGRTQ-RSAGVDQNHPRAVLN :::                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | RESULT 4 S51396 hypothetical protein YLR260w - yeast (Saccharomyces cerevisiae) N.Alternate names: hypothetical protein L8479.7 C.Species: Saccharomyces cerevisiae C.Date: 05-May-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004 C.Accesion: S51398 R.Miler, N. Submitted to the EMBL Data Library, November 1994 A.Description: The sequence of S. cerevisiae cosmid 8479. A.Reference number: S51395 A.Accession: S51398 A.Accession: S51398 A.Accession: S51398 A.Accession: MA A.Residues: 1-687 - MIL> A.Residues: 1-687 - MIL> A.Gene: SGD:LCB5; MIPS:YLR260w A.Gene: SGD:LCB5; MISM:Matches 126; Indels 107; Gaps 12; Best Local Similarity 22.6%; Pred. No. 3.9e-11; Batches 84; Conservative 55; Mismatches 126; Indels 107; Gaps 12; |
| cical protein SPAC4A8.07c - fission yeast (Schas: Schizosaccharomyces pombe si. Schizosaccharomyces pombe sion: T38776 n. J.; Churcher, C.M.; Barrell, B.G.; Rajandz dt ot the EMBL Data Library, August 1997 sion: T38776 si preliminary; translated from GB/EMBL/DDBJ tes: 1-458 «SKE> references: UNIPROT:014159; EMBL:298762; PIDN references: UNIPROT:014159; EMBL:298762; PIDN resion: 1 and 1 and 1 and 2 a |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| CAMETY MACTON LIAINING 23.2%; DE 2; DEGLA 458;  BEST LOCAL SIMILARITY 23.2%; Pred. NO. 7.66-12,  MATCHES 76; CONSERVATIVE 51; Mismatches 120; Indels 80; Gaps 10;  QY 2 KHLLVFINPFGGKGGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKET 61  DD 106 RRFIVFINPHGGKGAKHIWESEAEPVFSSAHSICEVVLTRRKDHAKSI 154                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ALPSDGTMDNV 602                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

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A;Cross-references: UNIPROT:Q92AQ5; GB:AL592022; PIDN:CAC97095.1; PID:g16414366; GSPDB:C
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein YOR171c - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein O3615
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Abace: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67059
R;Bordonne, R.; Camasses, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarassov, I.A.; Winsc Winsce to the Protein Sequence Database, July 1996
A;Reference number: S67032
A;Accession: S67059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Wolecule type: DNA
KRebidues 1.-624 ABOR>
A;Cross-references: UNIRROT:Q12246; EMBL:Z75078; NID:g1420415; PID:g1420417; GSPDB:GN000
A;Experimental source: strain S288C
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                                                                                                                                                                                                                                                                                                                                                                   LYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|: : | | :: | | :: | | :: | TINDFARALHVPRDVIKATKIIAAGOSVAMDIGKA--NDT---YFINIGGGGRITELTYD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 VPŠRLKTMĽGQLAYYLKG-----LKAT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 LYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STDCVCYSTVGTSDAETSALHIVVGDSLAMDV---SSVHHNSTLLRYSVSLLGYGFYGDI 178
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                                                                                                                                                                                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                         || || || || || KHARVIYNP----TSGREIIKKOLADVLS-----ILEQAGYVTSAHATTAEPGDAKHA
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                                                                                                                                                                                                                                                         2 KHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKET
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                                                                                                                                            Length 310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 10.6%; Score 181.5; DB 2; Similarity 25.2%; Pred. No. 9.1e-08; 62; Conservative 43; Mismatches 96;
                                                                                                                                         DB 2;
                                                                                                                                                                                              Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                      1.6e-08
                                                                                                                                         10.8%; Score 185.5; 23.0%; Pred. No. 1.66
                                                                                                                                                                                              46;
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220 FSLIIVKKVNLAEFIRLV 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: SGD:LCB4; MIPS:YOR171c
A,Cross-references: SGD:S0005697
A;Map position: 15R
                                                                                                                                                                                                 73; Conservative
                                                                                                                                                                 Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                      62
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AGIG65

Hypothetical protein homolog lin1865 [imported] - Listeria innocua (strain Clip11262)

C; Species interia innocua
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C; Accession: AGIG65

R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H. D.; Jones, L.M.; Karst, U.
Science 294, 494-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Tiele: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AG1665
A; Residues: 1-310 cGLA>
                                                                                                                              Cispecies: Caenorhabditis elegans
Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipate: 15-Oct-1990 #sequence 1990
Airestus: 1990
Airestus: preliminary; translated from GB/EMBL/DBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LGYGFYGDIIKDSEK-KRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 SIGWGLMADIDIDSEKWRKSLGHHRFTVMGFIRSCNLRSYKGRLTYRPYK-----PKGFH 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ LEAAEDVE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDL--ILIRKC-SRFNFLRFL- 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | |: |: |: |: | :: | :: | ETVVIEDNFUNIYAVTLSHIAADGP--FAPSAKLEDNRIHLSYILWKDIGTRVNIAKYLL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                      hypothetical protein C34C6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 Y-EINIDKYDGIVCVGGDGMFSEVLHGLIGRIQRSAGVDQNHPRAVLVPSSLRIGIIPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGNGLLCSVLSKYGTKMNEKS----VMERALEIATSPTAKAESVALYSVKTDNOSYASFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.8%; Score 219.5; DB 2; 24.7%; Pred. No. 2.9e-11; iive 56; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:C34C6.5
A;Map position: 2
A;Introns: 82/1; 126/1; 158/3; 276/1; 311/3; 427/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 24.7 1es 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -IRHTNQQD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 AIEHETHLD 422
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A;Molecule type: DNA *
Msesidues 1.-36 cGLA-
A;Kesidues 1.-36 cGLA-
A;Cross-references: UNIRROT:0927T6; GB:AL592022; PIDN:CAC97928.1; PID:g16415238; GSPDB:G:A;Experimental source: strain Clip11262
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Dateselvon: Alfa28
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mack, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: proposed A;Status: proposed A;Status: proposed A;Status: proposed A;Status: proposed A;Residues: proposed A;Residues: 1-309 cGLA> A;Residues: proposed A;Residues: prop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein lin0768 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                       14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 DCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK--D 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 VITEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRIQRSAGVDQNHPRAVLV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATN----MSCA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
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                                                                                                                                                                                                                                                                                                                                                                                                                  120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AKÓAAEAGÝEV-----VIAAGGDGTVNEVVNGLMQVEKRP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 130; DB 2; Length 309; 23.0%; Pred. No. 0.0012; artive 36; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                     Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                              91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 RITEITYA-----VKEŚMKSKW-GRLAYLFŚGL-----
                                                                                                                                                                                                                                                                                                                                 7.6%; Score 131; DB 2;
18.9%; Pred. No. 0.00095;
tive 55; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-----PPAQLNSGMFELLILKKVS 230
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                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 18.9%
Matches 62; Conservative
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Best Local Similarity
preliminary
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                                                                                                                                                                                                                                                    A;Gene: lin2702
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                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                             C;Genetics:
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                                                                                                                                                                                                                                                                         Argunate to the protein lmo1753 [imported] - Listeria monocytogenes (strain EGD-e)
C; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C; Accession: A11293
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C; Accession: A11293
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Residues: 1-310 cGLA>
A; Resi
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All 169
All 169
All 169
All 169
Conserved hypothetical protein lin2702 [imported] - Listeria innocua (strain Clip11262)
Cispecies: Listeria ainocua
All 169
Cispecies: Listeria ainocua
Cispecies: Listeria ainocua
Cispecies: Maitournam, A.; Mahand,
Alfitle: Comparative genomics of Listeria species:
A; Reference number: AB1077; MUID:21537279; PMID:11679669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATWMSCACRRSPRGLSPAAHLGDGS 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 LYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAG 121
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Matches 71; Conservative
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C;Accession: F69795

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C; Bron, S.; Brunsthi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krodh, S.; Kumano, M.; Kurita, R.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell, Y.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sekowska, A.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seronakeuchi, M.; Tamakoshi, A.; Tamaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Altthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Reference number: A69580; MUD:98044033; PMID:9384377

A;Residues: 1-303 «KUN»
A;Residues: 1-303 «KUN»
A;Residues: 1-303 «KUN»
A;Residues: 1-303 «KUN»
A;Reperimental source: strain 168
C;Genetics:
A;Genetics:
A;Genetics:
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hypothetical protein BH1953 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                           Species: Bacillus subtilis
Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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                                                                                                                         150 VEOKTKFGSVAYFLEGLKAF
                                                                          182 SEKKRWLGLARYDFSGLKTF
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C;Accession: A83894
R;Takami, H.; Nakasome, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83894
A;Accession: A83894
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <STO>
A;Gross-references: UNIPROT:Q9XBH4; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB056
C;Genetics:
A;Genetics:
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                                                   A;Cross-references: UNIPROT:Q97QZ6; GB:AB005672; PIDN:AAK75160.1; PID:g14972520; GSPDB:G
A;Experimental source: strain TIGR4
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 VCYSTVGTSDAE-----TSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGD 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 VCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TNIQITVDGKELFFS-----GVWLVA-----VANSPNYGGGIR----ICPEAS 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 IIK---DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LENKAKEYFEYVETKITEKALDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 VFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKETLYEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3%; Score 125.5; DB 2; 21.2%; Pred. No. 0.0027;
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D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Reference number: AB1077; MUID:21837279; PMID:11679669
A;Accession: AB1394
A;Accession: AB1394
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-306 <GLA>
A;Cross-references: UNIPROT:Q8Y497; GB:NC_003210; PIDN:CAD00635.1; PID:g16412045; GSPDB:C
A;Experimental source: strain EGD-e
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: 1mo2557
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Cipace: 27.Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipace: 27.Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipaces: 27.Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipaces: 27.Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipaces: Arith; Discorder Cipace 
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                                                                                                                                                                                                                                                                        64 EINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGST 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEKKRWLGLARYDFSGLKTF----LSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----FKIE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ APDAKID 214
              59 KETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGII 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK--D 181
                                                                                                        ---SGIDERD----YIP---KLGII 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEV-ITEHANQAKETLY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 WAAEQGFEAVIAMGGDGTLNETINGL-----AIHEKRP------DFGFIPLGTV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.2%; Score 123.5; DB 2; Length 309;
19.9%; Pred. No. 0.0044;
tive 47; Mismatches 113; Indels 101;
                                                                                                        47 THFABEASREQYDAVVVFGGDGTVNEVI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 IKDSEKKRWLGLARYDFSGLKTFLSHHCY 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 VEOKTKFGSVAYFLEGLKAFNRNELLH----
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DGYLHIIILTKLGLLDAANMIPQLIR 240
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83 DTPPKLGVLPVGTTNDYARALNFAKDPLEALRIJAKQETIRVDIGKANETEFFINNAAGG 142
                                                                                                                                                                                                                                                                          50 VITEHANOAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRIQRSAGVDQNHPRAVLV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -VSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRD 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 RKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLA--INATN----MS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KLSPVYVEIAYND----EIFKGKILLFFVNKSNSVGGME 208
                                                                                                                                                                                                                                                                                                                                                                                                               110 PSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYS--- 166
                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                     2 KHLLVFINPFGGKGQGKRI------YERKVAPLFTLASITTDIIGNKFYVNYVE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 KITEITYA-----VKESMKSKW-GRLAYLFSGL------TVLP----
                                                                94; Indels 124;
                                                                                                                                                                                                                                                                                                                                          ----AKQAAEAGFEV-----VIAAGGDGTVNEVVNGL-----
7.0%; Score 121; DB 2; Length 306; 18.5%; Pred. No. 0.0072; tive 51; Mismatches 94; Indels 1
                                                                                                                                                                                   | :: || || : || || 3 KKAMIIYNPAAGKNKFRKLLPDAEKILTEANFEVTLVPSTPAPKSTTFI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 CACRRSPRGLSPAAHLGDGSSDLILIRKCS 309
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-UNITS-bits -START=1 -END=-1 -MATRIX-biosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLCCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                   7; Search time 3134.86 Seconds (without alignments) 3958.373 Million cell updates/sec
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Xgapop 10.0, Xgapext
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|-------------------|-------------------|--------------------|--------------------|-----|--------------------|-----|--------------------|------|--------------------|-------------------|--------------------|--------------------|--------------------|-----|------|------|--------------------|------|------|--------------------|------|------|-------------|---------------|-------------|------------|----------|---------------|-------|---------------|--------------|-------|---------------|--------------|
| BP224560          | 100               |                    | 531                | 129 | 363                | 329 | 537                | 0052 | 9631               | 903               | 397                | 194                | 345                | 399 | 355  | 230  | 980                | 416  | 552  | CF535441           | 151  | 902  | 995         | 980           | 586         | 3902       | BU428926 | 132           | 541   | 115           | 368          | 004   | 558           | 3156         |
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## ALIGNMENTS

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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
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Yoneda,Y., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="unnamed protein product; DA59H18.2 (NOVEL PROTEIN SIMILAR TO HUMAN, MOUSE, YEAST, WORM AND PLANT (PREDICTED) SPOTEINS) (FRAGENT) homolog [Homo sapiens] (SPTR|O9UGE5, evidence: FASTY, 86.5%ID, 100%length, match=945)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Brybistal and Chemical Research (RIKEN), Laboratory for denome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Stanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL.http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FANTOM DB:A630056D11"
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                                                                                                                                                                                                            The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
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                                                                                                                                                                                                                                                                        Nature 409, 685-690 (2001)
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COMMENT

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                                                                                                                                                  CCGAAGCACTTGCTGGTATTCATCATCATCCTTTCGGAGGAAAGGTCAGGGCAAGCGCATC
                                                                                                                                                                                                                                                               GlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAla
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           Length:
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/tissue type="heart"
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                                                                                                                                                                                                                                                                                              Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Laginte; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="unnamed protein product; DA59H18.2 (NOVEL PROTEIN SIMILAR TO HUMAN, MOUSE, YEAST, WORM AND PLANT (PREDICTED) PROTEINS) (FRAGMENT) homolog [Homo sapiens] (SPTR|O9UGES, evidence: FASTY, 86.5%ID, 100%length, match=945)
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Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Obno, M., Obsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y. Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProLysHisLeuLeuValPheIleAsnProPheGlyGlyLysGlyGlnGlyLysArgIle
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/strain="C57BL/6J"
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                                                                                                                                                                                   1339 GACCTCATCCTTATCCGGAAGTGCTCCAGGTTCAACTTCCTGAGATTCCTCATCCGGCAC 1398
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 4248)
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281 AlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSer
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                          Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clond distribution: MGC clone distribution information and through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12140 row: c column: 18
High quality sequence stop: 665.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 6418742 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502281
5', mRNA sequence.
BM479389
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                                                                               HisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrValGlySerPro
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E. 1 (bases 1 to 1059)

E. 1 (bases 1 to 1059)

NIH-MCC http://mgc.nci.nih.gov/.

I. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:

http://image.llnl.gov

location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5803668"
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/tissue_type="lymphoma, cell line"
/tisb.pogt="DH108 (phage-resistant)"
/clone_lib="NIH MGC 99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
FCoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xhois site susing the following 5' adaptor:
GCCACGAG(G): Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ054406 1029 bp mRNA linear EST 29-MAR-2002 AGENCOURT 6771237 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5803668 S', mRNA Sequence.
BQ054406 GI:19813746
                                                                                                                                                                                                    687
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                                            ValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSerCysAlaCysArgArgSer
                                                                                                                                                                                                                                                                                                                                                     ArgLysCysSerArgPheAsnPheLeuArgPheLeuIleArgHisThrAsn-GlnGlnAs
                 CGGTGGTTGGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTCCCCACCAC
                                                                                                         ArgLysProCysArgAlaGlyCysPheValCysArgGlnSerLysGlnGlnLeuGluGlu
                                                                                                                         GluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspValGluGluTrpGlnVal
                                                                                                                                                                                                                                                748 CCCANGGGGCTCTCNCCCGCTGCCCACTTGNGAGACGGGTCTTCTGACCTCATCCTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

LOCUS DEFINITION

RESULT 5 CK000755

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1047 bp mRNA linear EST 29-MAR-2002
AGENCOURT_6769595 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5812382
5′, mRNA sequence.
                                                                                                                                                                                                                                                                               HisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAlaGlySer 122
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                                                                                                                                           96 TATGAGATTAACATAGACAAATACGACGCACGCATCGTCTGTGTCGCGGAGATGGTATGTTC 155
                                                                                                                                                                                                 | SerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAspGlnAsn 102
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1047)
                                                            CTGGAGGAGGAGCAGAAAGCACTGTATGGTTTGGAAGCTGCGGAGGACGTGGAGGAG
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                                     CGGCACGAGGCACCACTGTTCACCTTAGCCTCCATCACCACTGACATCATC-----
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Conteact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 ArgArgSerProArgGlyLeuSerProAlaAla 293
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NALL MAGC http://mgc.noi.nih.gov/.

NALL Moublished (1999)

Office of Caneer Genomies

NALLOAL Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

To Cofficer: Daniels S. Gerhard, Ph.D.

Office of Caneer Genomies

NALLOAL ST RANDAON Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Thesue Procurement: James Martin, University of Iowa

CDNA Library Preparation: M. Bento Soares, University of Iowa

CDNA Library Preparation: M. Bento Soares, University of Iowa

CDNA Library Preparation: M. Bento Soares, University of Iowa

CDNA Library Preparation: M. Bento Soares, University of Iowa

CDNA Library Preparation: M. Bento Soares, University of Iowa

CDNA Library Preparation: MCC clone distribution information can be

http://mage.llni.gov

Plate: NDAM1031 row: c Column: 20

High quality sequence stop: 656.

S Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

//Dressing Marker: Monton Sapiens"

//Dressing Marker: Monton Sapiens "

//Dressing Marker: Monton Sapiens "

//Dressing Marker: Monton Sapiens "

//Lone Library is oligo-dT primed and directionally clone and the notioned directionally into ByX-Asc. size fraction at 1% agarces

gel. First strand CDNA synthesis was primed with Cornectionally into ByX-Asc. vector. Average insert size

//Soquencing primers 5 (AAPTGCGCGACGACGACG) and 5 of ATTAACCCTCACTAAAGGGA)3.

Sequencing primers 3 'end: T7 promoter primer 5'd

('TATAACCCTCACTAAAGGGA)3.

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Library was constructed in the labrary"

Note: With Sapiens Marker Substance Monton Day Marker Substance Auguston Constructed in the Labrary "

Labrary"
                                                                                                                                                            CK000755 797 bp mRNA linear EST 26-NOV-2003
AGENCOURT 16363467 NIH MGC 221 Homo sapiens cDNA clone
IMAGE:30707875 5', mRNA sequence.
  CCGCCCGGACCCTCCAGGGGCCCTCTCCCCCGGGCTGGCCCAACTTGGGAAGACGGGGGTT 881
                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 797)
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                                       erSerAspLeuIleLeuIle-----ArgLysCysSer 309
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                  CITCGGACCTCTTTCTTCCTTTCGGGAAATGCTCC
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1283.00
92.62%
91.88%
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Homo sapiens
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source

FEATURES

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755

23

Pred. No.:

Score:

515 222 575

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dassa 1 to 758)

In (Dassa 1 to 758)

In Interpretatives of Health, Mammalian Gene Collection (MGC)

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:6835595"
/clone="IMAGE:6835595"
/tasue_rype="whole brain"
/dev stage="embryo 12.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NHH_BMAP_F10"
/clone_lib="NHH_BMAP_F10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB246749 17-8 bp mRNA linear BST 09-JUL-2003 UI-M-FIO-cdx-b-10-0-UI.rl NIH BMAP_FIO Mus musculus cDNA clone IMAGE:6835595 5', mRNA sequence.
                                                                                                                                                                                                                                                                                 281 laCysArgArgSerProArgGlyLeuSer---ProAlaAlaHisLeuGlyAsp---GlyS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTGTCGCCCGGAACCCCCCAGGGGCCTTCTCCCCCGGCTGCCCCAATTTGGGGAAAGGGTC 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                      AAGAAACGGTGGTTGGGTTTGCCAGATACGACTTTTCAGGTTTTAAAGACCTTTCCTCTCC
                                                                                                                                        HisHisCysTyrGlu-GlyThrValSerPheLeuProAlaGlnHisThrValGlySer-P
                                                                                                                                                                                                  roArgAspArgLysProCys-ArgAlaGlyCysPheVal-CysArgGlnSerLysGlnGl
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/organism="Mus musculus"
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Location/Qualifiers
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                        /clone="Invariation"
/clone="Invariation"
/tissue_type="lymphoma, cell line"
/lab host="DHIOB (phage-resistant)"
/clone lib="NHH MGC 99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/AnoI sites using the following 5: adaptor:
GGACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Thip://image.llnl.gov
Thip: LCM2062 row: 1 column: 15
High quality sequence stop: 535.
Location/Qualifiers
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Conservative:
Mismatches:
Indels:
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/mol_type="mRNA"
/db_xref="taxon:9606"
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primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with ECOR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACCAC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Drestlopping Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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BUU63738 1078 bp mRNA linear EST 02-APR-2002
AGENCOURT_6873251 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5925382
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM2096 row: p column: 23
High quality sequence stop: 640.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LysAlaLeuTyrGlyLeuGluAlaAlaGluAspValGluGluTrpGlnValValCysGly
tissue_type="Embryonic Stem cells"
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E. I (Bases 1 to 820)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Ordice of Cancer Genomics

Office of Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.inih.gov

Tissue Procurement: Irene Ginis and Mahendra Rao, NIA

CDNA Library Preparation: Yulan Piao and Minoru Mo

CDNA Library Preparation: Yulan Piao and Minoru Mo

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC c lone distribution information

can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: NDAMS121 row: K column: 18
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AGENCOURT 14552675 NIA Human H1 Embryonic Stem Cell cDNA Library (Long) Homo sapiens cDNA clone IMAGE:30426593 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     748 GGGGATCTCCCAGGGAATAAGGAAGCCCTGCCCGGGCCAGGGATGCCTTTGGTTTGCCAG 807
                MetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp
                                                                                             GlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAla
                                                                                                                                                                          GlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAla
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                                       388 CAGAACCACCCCGGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGAATCATTCCCGGA
                                                                                                                                                                                                     568 ACACTCCTTCGCTACTCCGTGTCCCTGCGGCTACGGCTTCTACGGGGACATCATCACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 sArgGlnSerLysGlnGlnLeuGluGluGlu-----GlnLysLysAla 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:30426593"
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Homo sapiens
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/Longe "Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; This is a long-transcript enriched cDNA library (Genome Res. 11: 153-1558 (2001). [PMID: 1154199] From WA01 cell line. Undifferentiated human BS cell line WA01/H1 was obtained from Wicell Research Institute, Inc., Madison, Wi, cultured according to their instructions, on MEF feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-1, OCT4, MEXI, UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4 DX1. NCAM, WSX1, FLT3, SSEA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRIZOl Reagent from Invitrogen. Protocol ref. Genome Res. 11: 153-1558 (2001). [PMID:11544199]) Double-stranded cDNAs were synthesized with an Oligo ddT) primer [Invitrogen: Synthesized with an Oligo ddT) primer [Invitrogen: Synthesized with an Oligo ddT) primer [Invitrogen: Gone-linker Li-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by centricon-100 column. Then, the cDNAs were amplified by column. Then, the cDNAs were amplified by were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were adgested with SalI and NotI enzymes and cloned into Sall/NotI site of pcMV-SPORTS plasmid vector. The average insert size is about 3.6kb."
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                                           clone lib="NIA Human H1 Embryonic Stem Cell cDNA Library [Long)"
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/cell line="WA01"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dases 1 to 584)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Contact: Yutaka Suzuki
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Feel, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yeuzukiélms, Letokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP310011 Sugano cDNA library, brain Homo sapiens cDNA clone NRR01274, mRNA sequence.
                                                                                                                                                                                                                                                                         206 CysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrValGlySerProArgAsp 225
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                                                                            243 GGGACTCGCTGGCCATGGATGTGTCCTCAGTCCACAACAGGACACTCCTTCGCTAC 302
                                                                                                                             SerValSerLeuLeuGlyTyrGlyPheTyrGlyAsp1leIleLysAspSerGluLysLys 185
                                                                                                                                                 303 TCCGTGTCCCTGCTGGGCTACGCTTCTACGGGGACATCATCAAGGACAGTGAGAAAAAA 362
                                                                                                                                                                                                  186 ArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThrPheLeuSerHisHis 205
                                                                                                                                                                                                                          CGGTGGTTGGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTCCCACCAC 422
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Conservative:
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Bukaryota, Metazoa, Primates, Catarrhini; Hominidae, Homo.
Mammalia; Euthoria; Primates, Catarrhini; Hominidae, Homo.

E 1 (bases 1 to 581)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizuki, Y., Yamashita, R., Shirota, Manai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Contact: Yutanone Res. 14 (9), 1711-1718 (2004)
Genome Res. 14 (9), 1711-1718 (2004)
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Email: ysuzukielms.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                            BP224560 BP224560 Sugano cDNA library, lymphocyte Daudi Homo sapiens cDNA clone DAT01067, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaValLeuValProSerSerLeuArgileGlyIleIleProAlaGlySerThrAspCys 125
                                                        LeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAspGlnAsnHisProArg 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 ValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAlaLeuHisIleValVal 145
   289 LeuSerProAlaAlaHisLeuGlyAspGlySerSerAspLeuIleLeuIleArgLysCys 308
                                                                                                                                                   492 CTCTCCCCGGCTGCCCACTTGGGAGACGGGTCTTCTGACCTCATCCTCATCCGGAAATGC 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="DAT01067"
/cell_type="lymphocyte"
/cell_tine="blaudi"
/clone line="Sugano cDNA library, lymphocyte Daudi"
/note="Burkitt's lymphoma"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BP224560.1 GI:52097465
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                                                                                                                                                                                                                                                                                                                                                                          267 CCCAGTAGCCTCCGGATTGGAATCATTCCGGCAGGGTCAACGGACTGCGTGTGTTACTCC 326
                                                                                                                                                                                                                                                                                                                                                                                                   387 GCCATGGATGTGTCCTCAGTCCACACAACAGCACTCTTCGCTACTCGTGTCCCTG 446
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 573)
Bonaldo, M. P., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                 50 ValileThrGluHisAlaAsnGlnAlaLysGluThrLeuTyrGluIleAsnIleAspLys
                                                                                                                                                                                                                                                                                                                      207 ATTGGGAGGACGCANAGGAGCGCCGGGGTCGACAGCAACCACCCCCGGGCTGTGCTGGTC
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112
          Length:
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Conservative:
Mismatches:
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Gaps:
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97044477
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            3.42e-96
965.50
93.69%
92.72%
56.23%
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                               Percent Similarity:
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E 1 (bases 1 to 584)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizuki, M., Yamashita, R., Shirota, M., Sagano, S., Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukishma.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP309990 Sugano cDNA library, brain Homo sapiens cDNA clone NRR01216, mRNA sequence.
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ThrLeuAlaSerIleThrThrAspIleIleGlyAsnLysPheTyrValAsnTyrValGlu
                                          ThrValGlyThrSerAspAlaGluThrSerAlaLeuHisIleValValGlyAspSerLeu
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/clone="NRR01216"
/tissue type="brain"
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          BP309990.1 GI:52238965
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Homo sapiens
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BP309990
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09-SEP-2003 clone

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Laurantain memoral metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (Bases I to 541)

El (Bases I to 541)

El (Bases I to 541)

I.i.Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
I.i.Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

AL Nat. Batcechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine
Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenbergeregeron.com
Insert Length: 541 Std Error: 0.00.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 16-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="GRN_ES"
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from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
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                                   197
                                                                       511
392 CACAACAGCACACTCCTTCGCTACTCCGTGTCNCTGCTGGGCTACGGCTTCTACGGGGAC 451
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                                                    CN296311 541 bp mRNA linear EST 16
17000532199536 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
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Matches:
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/organism="Homo sapiens"
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Best Local Similarity:
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           Contact: Soares, MB
Condinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@ulowa.edu
Tissue Procurement: Louis Staudt
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Library preparation: Distribution information can be found at
http://genome.ulowa.edu/distribution/humanfl.html
                                                                                                                                                                                                                                                                                                                         /mol Evpe="many" orgin:
/mol Evpe="many" orgin:
/db Xref="taxon:9606"
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(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 GCCAAGGAGACTCTGTATGAGATTAACATAGACAAATACGACGGCGACGGCATCGTCTGTGTCGGC 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 LysArglleTyrGluArgLysValAlaProLeuPheThrLeuAlaSerIleThrThrAsp 37
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gallus cDNA clone ChEST669il0 5', mRNA
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Busianinae; Gallus.

1 (bases 1 to 725)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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243
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                                                                                                          205 HiscystytGluGlyThrValSerPheLeuProAlaGlnHisThrValGlySerProArg
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TACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCATCAAGGACAGTGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                     Department of Biomolecular Sciences University of Manchester Institute of (UMIST) PO Box 88, Manchester, M60 10D, UK Tel: 01612008930 Fax: 01612360409 Email: Simon.Hubbard@umist.ac.uk. Location/Qualifiers
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603756937F1 CSEQCHN04 Gallus
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-631-958-2 1717 1 PKHLLVFINPFGGKGGGKRI......KCSRFNFLRFLIRHTNQQDQ 326 Title: Perfect score: Sequence:

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1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|           | Description           | Ostct0 homo sapien | เพนธ   | _          | Q6nx59 homo sapien |        |        | Q7pra8 anopheles g | drosophila |        |        |        |        |        |        |        |        |        |        |        |        | anophe | oryza  | Q7xn57 oryza sativ | Q94hy9 oryza sativ | Q7xcs9 oryza sativ | Q9vyy8 drosophila | Q9vzw0 drosophila |        | Q86kf9 dictyosteli | Q9nra0 homo sapien | Q6ayb2 rattus norv |
|-----------|-----------------------|--------------------|--------|------------|--------------------|--------|--------|--------------------|------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------------------|--------------------|-------------------|-------------------|--------|--------------------|--------------------|--------------------|
| SUMMARIES | QI<br>QI              | CEK1 HUMAN         | Q62PKS | CEK1 MOUSE | Q6NX59             | QGGMF3 | Q6GLV1 | Q7PRA8             | 095815     | Q9VNA6 | Q9LU45 | Q6USK2 | Q9TZI1 | Оенент | Q6UZF6 | Q8L7L1 | 065419 | Q949C3 | Q9FHL3 | Q9LRB0 | Q8H350 | Q7QIP4 | Q84S01 | Q7XN57             | Q94HY9             | Q7XCS9             | Q9VYY8            | OMZV6Q            | Q6ZP59 | Q86KF9             | SPH2_HUMAN         | Q6AYB2             |
|           | DB                    | -                  | 7      | н          | ~                  | ~      | 7      | ~                  | ~          | ~      | ~      | 7      | ~      | ~      | N      | ~      | 7      | ~      | ~      | ~      | ~      | ~      | ~      | ~                  | ~                  | ~                  | ~                 | ~                 | ~      | ~                  | -                  | 7                  |
|           | Query<br>Match Length | 537                | 409    | 531        | 339                | 485    | 572    | 410                | 487        | 687    | 533    | 608    | 549    | 700    | 532    | 485    | 1240   | 286    | 732    | 763    | 480    | 685    | 446    | 748                | 757                | 757                | 641               | 661               | 280    | 624                | 654                | 616                |
| d         | Query<br>Match        | 95.5               | 87.6   | 87.6       | 75.4               | 66.4   | 65.1   | 36.1               | 35.7       | 35.7   | 29.3   | 29.0   | 28.3   | 26.5   | 25.4   | 22.7   | 21.3   | 18.7   | 18.1   | 18.1   | 17.9   | 17.5   | 17.5   | 17.0               | 16.7               | 16.7               | 16.4              | 15.6              | 15.2   | 14.2               | 14.2               | 13.7               |
|           | Score                 | 1640.5             | 1503.5 | 1503.5     | 1295               | 1140   | 1117.5 | 620.5              | 613        | 613    | 502.5  | 498.5  | 486.5  | 455.5  | 436    | 389    | 365.5  | 321.5  | 311.5  | 311.5  | 307.5  | 301    | 300    | 292                | 287.5              | 287.5              | 282               | 268               | 261    | 244.5              | 243                | 236                |
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|            | авһЪуа довв  | homo sapien | homo sapien  | homo sapien | homo sapien | mus musculu  | mus musculu | mus musculu  | schizosacch  | mus musculu  | debaryomyce  | macaca fasc  | saccharomyc |
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| 09jia7     | Q74ze3       | Q9nya1      | Q96hv8       | Q96gk1      | Q8n632      | Q91zn3       | Q8ci15      | 088886       | 014159       | 088885       | Q6bwi4       | Q9n0a5       | 006147      |
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## ALIGNMENTS

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| PRT; 537 AA.  uence update)  otation update)  (Acylsphingosine kinase) (hCERK) ( Craniata; Vertebrata; Euteleostomi;                                                                                                                                                                                                                                                                                                                                         | Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TaxID=9606;  [1]  SEQUENCE FROM N.A., AND CHARACTERIZATION.  TISSUE=Leukemia;  MEDLINE=22075121; Pubmed=11956206; DOI=10.1074/jbc.M201535200;  Sugiura M., Kono K., Liu H., Shimizugawa T., Minekura H., Splegel  Kohama T.;  Ecramide kinase, a novel lipid kinase. Molecular cloning and  functional characterization.";  J. Biol. Chem. 277:23294-23300(2002).                    | р.м.<br>А.К.,                                                                                                                                                                                                                                                                                                                                                                                      | Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beaaley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Evans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C. Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Hollmes S., Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Macclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T., Phillips S.H., Plumb R.W., Rameay H., Rameey Y., Rogers L., Ross M.T. Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Scott C.E., Sealley S., Smith M.L., Steward C.A., Sulston J.E., Swann R.M., Walliams L., Williams D., Williams D., Williams S.A., Williams S.A., Williams S.A., Williams D.L., Williams S.A., Williams S.A., Williams J., Shimizu N. Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shimizu N. Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shimizu N.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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| kinase)<br>ta; Eut                                                                                                                                                                                                                                                                                                                                                                                                                                           | . M20153<br>ura H.,<br>cloning                                                                                                                                                                                                                                                                                                                                                                                                                        | ases<br>31,<br>Bea<br>abba                                                                                                                                                                                                                                                                                                                                                                         | asle<br>rges<br>en Y<br>onno<br>onno<br>El<br>A.A<br>B M.<br>Sing                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Mccorti<br>Orti<br>11im<br>11im<br>11im<br>Ch M<br>Ch M<br>Ch M<br>Ch M<br>Ch M<br>Ch M<br>Ch M<br>Ch M                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| kin kin ata;                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ijdae<br>jbc.<br>neku                                                                                                                                                                                                                                                                                                                                                                                                                                 | latab<br>9900<br>''.' B                                                                                                                                                                                                                                                                                                                                                                            | , Be<br>Ch<br>RR.M.<br>R.M.<br>R.H.<br>Fith<br>Eith                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Phi<br>Phi<br>Will<br>Will<br>Rog                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 1.<br>e)<br>osine                                                                                                                                                                                                                                                                                                                                                                                                                                            | Catarrhini; Hominidae; Homo. TERIZATION. 206; DOI=10.1074/jbc.M201535 himizugawa T., Minekura H., d kinase. Molecular cloning (2002).                                                                                                                                                                                                                                                                                                                 | )BJ ¢                                                                                                                                                                                                                                                                                                                                                                                              | KK.N. K.D. N.P. V. Constitution                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | S.P. S., S., S., S., S., S., S., S., S., Willm., S., S., I.N., Willm., S., I.W., S., I |
| 537 AA<br>pdate)<br>update<br>phingo:                                                                                                                                                                                                                                                                                                                                                                                                                        | N                                                                                                                                                                                                                                                                                                                                                                                                                                                     | nk/DE:10.1                                                                                                                                                                                                                                                                                                                                                                                         | Buc<br>Buc<br>Llier<br>Clier<br>Dur<br>Dur<br>V.'                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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| D; PRT; 537 AA.;; Created) Last sequence update) Last annotation update) 7.1.138) (Acylsphingosi; AA1646;                                                                                                                                                                                                                                                                                                                                                    | rrhir<br>ZATIC<br>DOI=<br>zugav<br>nase.                                                                                                                                                                                                                                                                                                                                                                                                              | enBar<br>DOI:<br>Bro                                                                                                                                                                                                                                                                                                                                                                               | A.M. CO.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | A., Me<br>H., Fee<br>H., Smë<br>J.A.,<br>nitel                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| PRT;<br>uence<br>otati<br>(Acy                                                                                                                                                                                                                                                                                                                                                                                                                               | ria; Primates; Catarrh ;; (A., AND CHARACTERIZAT ;; pubmed=11956206; DO OK., Liu H., Shimizug se, a novel lipid kinas zectarization."; 277:23294-23300(2002).                                                                                                                                                                                                                                                                                         | 3L/Ge<br>208;<br>J.E.,                                                                                                                                                                                                                                                                                                                                                                             | K.F. C., C., C., C., C., C., C., C., C., C.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | A.V., A.V., Saay P.C.D., Ard C.C.M. Ilian                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| 1<br>ted)<br>sequann<br>138)<br>46;                                                                                                                                                                                                                                                                                                                                                                                                                          | eB; (<br>ARAC:<br>1956;<br>., Sl<br>., Sl<br>lipic                                                                                                                                                                                                                                                                                                                                                                                                    | B.",<br>BEMI<br>05912<br>fins                                                                                   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                                                                                                                                                                                                                                                                                                                                  | urra)<br>rce /<br>Rame<br>nce (<br>J.W.<br>J.M.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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| ARD;<br>iE5;<br>Created);<br>Last sec<br>7.1.138)<br>KIAA1646;<br>Chordata;                                                                                                                                                                                                                                                                                                                                                                                  | Primates; AND CHARA bMed=1195 Liu H., novel lip ization." 3294-2330                                                                                                                                                                                                                                                                                                                                                                                   | nase: o the coll:                                                                                                                                                                                                                                                                                                                                                                                  | Bangaran Ban | McM<br>McM<br>Pear<br>'W',<br>'Sk',<br>Sk',<br>Sk',<br>Sk',                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| STANDARD;<br>Q9UGE5;<br>1. 42, Cr<br>1. 44, La<br>(EC 2.7.<br>'TMS=KIAA<br>uman).                                                                                                                                                                                                                                                                                                                                                                            | , ANI<br>Pubm<br>Pubm<br>Pubm<br>Pubm<br>Pubm<br>Pubm<br>Pubm<br>Pubm                                                                                                                                                                                                                                                                                                                                                                                 | d kin<br>2) to<br>PubM<br>R.,                                                                                                                                                                                                                                                                                                                                                                      | S.B.,<br>On G.E.,<br>W.Y.,<br>W.Y.,<br>W.Y.,<br>W.Y.,<br>W.Y.,<br>C.C.,<br>C.C.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | S., R., R.K. Gon Gon Gon Trd                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| STA<br>(B3; Q9<br>(Rel.<br>(Rel.<br>(Rel.<br>nase (E.<br>1K4).                                                                                                                                                                                                                                                                                                                                                                                               | eria<br>6;<br>N.A.<br>21;<br>no K<br>no K<br>se,                                                                                                                                                                                                                                                                                                                                                                                                      | N.A.<br>11pi<br>12pi<br>1200<br>-200<br>N.A.<br>K. L.                                                                                                                                                                                                                                                                                                                                              | key<br>bley<br>bley<br>bley<br>bley<br>ckre<br>ckre<br>Go,<br>Go,<br>Go,<br>Go,<br>Go,<br>Go,<br>Go,<br>Go,<br>Go,<br>Go,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | aren<br>vitt<br>Plu<br>hra Spra<br>Spra<br>1 M.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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                                                                                                                                                                                                                                                                                                                                  | MCL<br>MCL<br>S.H.<br>S.H.<br>Wal<br>Wal                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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| UMAN<br>; Q9<br>-200<br>-200<br>-200<br>de k<br>4)<br>4)<br>apie                                                                                                                                                                                                                                                                                                                                                                                             | axID;<br>CCE FI<br>CCE FI<br>E=22(<br>E=22(<br>T:;<br>ide ]                                                                                                                                                                                                                                                                                                                                                                                           | CE F<br>ldho<br>rch<br>ted<br>CE F<br>E=20                                                                                                                                                                                                                                                                                                                                                         | ey C. P., C. P., C. P., C. P., C. P., C. P., C. P.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | C.N. C.N. C.N. C.N. ms L C.E. C.E. T. ms L                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| LT 1 HUMAN CEKL HUMAN CORTO, 09BYB3; Q9UGE5; 10-OCT-2003 (Rel. 42, Created) 10-OCT-2004 (Rel. 42, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) kinase 4) (LK4). Name=CERK; Synonyme=KIAA1646; Homo sapiens (Human). Character (Human). Character (Human). Character (Created)  Annel (Human).  Character (Created)  Annel (Human).  Character (Created)  Cortain (Human).  Character (Created)  Cortain (Human).  Character (Created) | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TaxID=9606;  [1]  SEQUENCE FROM N.A., AND CHARACTERIZATION.  TISSUE-Leukemia;  MEDLINE=22075121; PubMed=11956206; DOI=10.1074/jbc.M201535200;  MODLINE-22075121; PubMed=11956206; Molecular H., Spie Kohama T.;  "Ceramide kinase, a novel lipid kinase. Molecular cloning and "Lunctional characterization.";  "Lunctional characterization.";  "Biol. Chem. 277:23294-23300(2002). | [2] SEQUENCE FROM N.A. Van Veldhoven P.P.; "A search for lipid kinases."; "A search for lipid kinases."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. [3] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031; Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M., Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., | Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P Bird C.P., Birdey S.E., Bridgeman A.M., Buck D., Burgess J., Burtill W.D., Burton J., Carder C., Carter N.P., Chen Y. Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conrory D., Corby N.E., Coville G.J., Cox A.V., Davis J., Daw Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellingt Evans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A., Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Marcyn 1.0 McClay 1.0 McClay 1.0 McClay 1.0 McClay 2.0  |
| <b>□</b> 1                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Mam<br>NCB<br>SEQ<br>TIS<br>MED<br>Sug<br>Koh<br>Koh<br>Hun<br>fun<br>J.                                                                                                                                                                                                                                                                                                                                                                              | (2)<br>SEQ<br>Van<br>"A<br>"A<br>SUb<br>(3)<br>SEQ<br>MED<br>MED<br>Oun                                         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| RESU<br>CEKI<br>ID<br>DT<br>DT<br>DT<br>OD<br>OS                                                                                                                                                                                                                                                                                                                                                                                                             | R R R R R R R R R R R R R R R R R R R                                                                                                                                                                                                                                                                                                                                                                                                                 | R R R R R R R R R R R R R R R R R R R                                                                           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Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
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Khan A.S., Lane L., Tilahun Y., Wright H.;
"The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hirosawa M., Nagase T., Murahashi Y., Kikuno R., Ohara O.;
"Identification of novel transcribed sequences on human chromosome 22
"Identification of novel transcribed sequences on human chromosome 22
"I bun Rese B.1-9(2001).

- 1- FUNCTION: Catalyzes specifically the phosphorylation of ceramide to form ceramide 1-phosphate. Acts efficiently on natural and analog ceramide 1-phosphate. Acts efficiently on natural and analog ceramides (G6, C8, C16 ceramides, and C8-dihydroceramide), to a lesser extent on C2-ceramide and C6-dihydroceramide, but not on other lipids, such as various sphingosines.

- CATALYTIC ACTIVITY: ATP + ceramide = ADP + ceramide 1-phosphate.
- COPACTOR: Calcium and magnesium.
- COPACTOR: Calcium and magnesium.
- SIBJELLULAR LOCATION: Cytoplasmic and membrane-associated.
- SIBJELLULAR LOCATION: Cytoplasmic and membrane-associated.
- I SUBCELLANBOUS: Optimal pH is 6.0-7.5.
- MISCELLANBOUS: Optimal pH is 6.0-7.5.
- SIMILARITY: Contains 1 DAGK domain.
- CAUTION: Ref.3 sequence differs from that shown due to erroneous gene model prediction. An additional exon may exist between amino acid positions 168 and 169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ457828; CAD29884.1; -..
EMBL; AL095766; CAB62977.1; ALT SEQ.
EMBL; AL095766; CAB62977.1; ALT SEQ.
EMBL; AL18316, -; NOT ANNOTATED_CDS.
EMBL; AB051433; BAB3316.1; -.
Genew; HGNC:19256; CERK.
GO; GO:0000299; C:integral to membrane of membrane fraction; IDA.
GO; GO:0004685; F:calcium/calmodulin-dependent protein kinase. ..; IDA.
GO; GO:0000287; F:caramide kinase activity; IDA.
GO; GO:000672; P:ceramide metabolism; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21156230; PubMed=11258795;
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InterPro; IPR001849; PH.
InterPro; IPR001036; PH. related.
Pfam; PF00781; DAGK cat; I.
ProDom; PD005043; DAGKc; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB079066; BAC01154.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 57-537 FROM N.A.
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SMART; SM00233; PH; 1.
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Calcium; Kinase; Magnesium; Transferase.

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240
                                                                                                                                          239 GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 298
                                                                                                                                                                                                                                                                                                                                                                                          241 QQLEEBQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 300
                                                                                                                                                                                       61 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
                                                                                                                                                                                                         121 GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180
                                                                                                                                                                                                                                                                                                                                                359 QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 418
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                                                                                                                   1 PKHLLVFINPFGGKGGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
                                                                                                                                                                                                                                                                                                                          181 DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK
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Saga Y., Nagase T., Ohara O., Koga H.;

"Prediction of the coding sequences of mouse homologues of KIAA gene:
III. the complete nucleotide sequences of 500 mouse KIAA-homologous
cDNAs identified by screening of terminal sequences of cDNA clones
randomly sampled from size-fractionated libraries.";
DNA Res. 10:167-180(2003).

EMBL; AK129416; BAC98256.1; -.

GO; GO:0004134; Fidiacylglycerol kinase activity; IEA.

GO; GO:0001205; P:protein kinase C activation; IEA.

InterPro; IPR001206; DAGKC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Gaps
                                                                                 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                 DB 1; Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.6%; Score 1503.5; DB 2; Length
86.8%; Pred. No. 6e-123;
tive 19; Mismatches 13; Indels
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER 1 1
SEQUENCE 409 AA; 45697 MW; 810E815B37E26808 CRC64;
                3DBFC0ED8D679F7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                     ö
                                              Score 1640.5; DB 1
Pred. No. 8.7e-135;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLILIRKCSRFNFLRFLIRHTNQQDQ 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DILLIRKCSRFNFLRFLIRHTNQQDQ 444
 DAGKC
              59977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKIAA1646 protein (Fragment).
                                              95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00781; DAGK cat; 1.
ProDom; PD005043; DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 283; Conservative
                                                                                 Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD005043; DAGKC
SMART; SM00046; DAGKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Embryonic tail;
132 2
537 AA;
                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=mKIAA1646;
                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
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Q6ZPK5;
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RC MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA OAZAZAKI Y. FULUND M., Kasukawa T., Adachi J., Bonc H., Kordo S.,

RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Hadarelli R., Hilli D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hilli D.P., Bult C., Hume D.A., Quackenbush J.,

RA Balla E., Dragani T.A., Fletcher C.F., Fortset A., Frazer K.S.,

RA Balla E., Dragani T.A., Fletcher C.F., Fortset A., Guush J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis.E.D.,

RA Acana A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numara K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sultain R., Jahlai R., Pontius J.U., Oli D., Ramachandran S.,

Randelin A., Schneider C., Sample C.A., Sactou M., Sahmada K.,

RA Wilming L.G., Wynahaw-Boris A., Yanagisawa M., Yang L.,

RA Milming L.G., Wynahaw-Boris A., Yanagisawa M., Yang I.,

RA Milming L.G., Wynahaw-Boris A., Yanagisawa M., Yang L.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakzume N., Sato K.,

RA Hara A., Hashizume W., Imotani K., Itahi Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Wasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
                                                                                                                    GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180
                                    DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK
                                                                                                                                                                                                       177 DSEKKRWMGLVRYDFSGLKTFLSHQYYEGTLSFLPAQHTVGSPRDNKPCRAGCFVCRQSK
                                                                                                                                                                                                                                                                 QOLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS
                                                                                                                                                                                                                                                                                     237 QQLEEEEKKALYGLENAEEVEEWQYTCGKFLAINATNWSCACPRSPGGLSPFAHLGDGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22075121; PubMed=11956206; DOI=10.1074/jbc.M201535200;
Sugiura M., Kono K., Liu H., Shimizugawa T., Minekura H., Spiegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ceramide Kinase (EC 2.7.1.138) (Acylsphingosine kinase) (MCERK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Ceramide kinase, a novel lipid kinase. Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                 DLILIRKCSRFNFLRFLIRHTNQQDQ 326
                                                                                                                                                                                                                                                                                                                                                                                          297 DLILIRKCSRFNFLRFLIRHTNQEDQ 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 277:23294-23300(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                functional characterization."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEK1 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Cerk;
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                                                                                                 121
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MDD; MGI:2386052; Cerk.
GO; GO:000299; C:integral to membrane of membrane fraction; ISS.
GO; GO:0004685; F:calcium/calmodulin-dependent protein kinase. .; ISS.
GO; GO:0001729; F:caramide kinase activity; ISS.
GO; GO:000287; F:magnesium ion binding; ISS.
GO; GO:000672; F:ceramide metabolism; ISS.
Interpro; IPRO11206; DAGKC.
Interpro; IPRO11036; PH related.
Probom; PPO0781; DAGK cat; 1.
Probom; PPO05043; DAGK cat; 1.
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                                                                                 --- FUNCTION: Catalyzes specifically the phosphorylation of ceramide to form ceramide 1-phosphate. Acts efficiently on natural and analog ceramides (G6, C8, C16 ceramides, and C8-dhydroceramide), to a lesser extent on C2-ceramide and C6-dhydroceramide, but not on other lipids, such as various sphingosines (By similarity).
--- COFACTIVITY: ATP + ceramide = ADP + ceramide 1-phosphate.
--- COFACTION: C3Loium and magnesium (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated (By
                                                                                                                                                                                                                                                                                                                               similarity).
-!- TISSUE SPECIFICITY: High level expression in heart, brain and testis; low expression in spleen, liver and lung; not detected in skeletal muscle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: Highly expressed at 7 dpc and decreases
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D -> Y (in Ref. 2; BAC34908).
31FEC534C348AAOA CRC64;
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86.8%; Pred. No. 8.4e-123;
tive 19; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rapidly thereafter. SIMILARITY: Contains 1 DAGKc domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calcium; Kinase; Magnesium; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB079067; BAC01155.1; -. EMBL; AK042077; BAC31157.1; -. EMBL; AK052269; BAC34908.1; -.
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CONFLICT
SEQUENCE
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Matches 28
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D6GMF3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MFSEVLHGLIGRIQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 MFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEBEQKKALYGLBAAEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC067255; AMH67255.1; GO:0004143; F:diacylglycerol kinase activity; IEA. GO; GO:0007205; P:protein kinase C activation; IEA. InterPro; IPR001206; DAGKC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AA; 37780 MW; A4C2ACDFF2E6F3D0 CRC64;
                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.4%; Score 1295; DB 2; I 100.0%; Pred. No. 8.4e-105; ive 0; Mismatches 0;
                                                                                                                      339 AA
419 DLILIRKCSRFNFLRFLIRHTNOEDO 444
                                                                                                                                                                      Created)
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Peripheral Nervous System;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Peripheral Nervous System;
                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD005043; DAGKc; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 246; Conservative
                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 TNQQDQ 326
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                             CERK protein.
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                                                                                                                      Q6NX59
                                                                      RESULT 4
                                                                                             Q6NX59
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MEDINE=2238825). PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDINE=2238825). PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buercw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Joederg B. Buercw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Joddin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                 estiopus Lagvis (Alitram Ciawa 1.19).
Eukaryota; Metazoa; Chorcata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Magner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO74110; AAH74110.1; -
GO; GO:0004143; F:diacylglycerol kinase activity; IEA.
GO; GO:0007205; P:proctein kinase C activation; IEA.
InterPro; IPR001206; DAGKc.
Pfam; PF00781; DAGK_cat; 1.
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                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                           485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58; Mismatches
                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 62.4%;
Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus.
241 TNQQDQ 246
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Matches 204; Conserv
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                                                                                                                                                                                                                                                                                                                                       MGC81777 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                           Name=MGC81777;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae;
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SEQUENCE
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A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A patchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B comnetein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prenge C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Mallek J.A., Glubs R.A., Glubs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Rachay J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Nones S.J., Marra M.A.;

"Marra M.A.,

"Marra M.A., Schelke U., Smailus D.E., Schnerch A., Schein J.E.,

"Marra M.A.,

"Marra 
                                                                                                                                                                                                                                                                        445
                                                                                                266 GSTDCICYATVGINDPETSALHIILGDCQPLDVCSVHNKRTFLKYSVSLLGYGFYGDVLK 325
                                                                                                                                                      181 DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK 240
                                                                                                                                                                          326 GIEKORWIGPARYDVSGCKIFLITHCYEGSVSFQPAKWVIGSPRDQIPCTSGCYICRQSS 385
                                                                                                                                                                                                                                241 QQLEEEQKKALYGLE-AAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGS 299
61 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA

206 NLYEVNLEKYDGVVCVGGDGIFSEVLHGLIGRVQKGSDVDHNNPNAHLSQCNIRIGIIPA
                                                                                                                                                                                                                                                      386 KQLEEQQKTQVFGSEHRGKQDDDWTTIKGRFWAINAVSMSCACPRTFKGLSPAAHLADGS
                                                                          GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                572 AA
                                                                                                                                                                                                                                                                                                            300 SDLILIRKCSRFNFLRFLIRHTNOODO 326
                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGC84197 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=MGC84197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 GSTDCICYATVGINDPETSALHIILGDCQPLDVCSVHYKRTFLKYSVSLLGYGFYGDVLK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 GSEKORWLGPARYDVSGFKTFLTHHCYEGSVSPQPAKWVLGSPRDQTTCTSGCY1CRQSS 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK
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Name=ENSANGS0000000355;
Anopheles gambiae str. PEST.
ENKaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL; AAABO1008859; EAA07556.2; --
GO; GO:00041205; P:protein kinase activity; IEA.
GO; GO:0007205; P:protein kinase C activation; IEA.
InterPro; IPR001206; DAGKC.
                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                         DB 2; Length 572;
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                                                                                                                                                                                                                                                Query Match 65.1%; Score 1117.5; DB 2; Length Best Local Similarity 62.0%; Pred. No. 5.6e-89; Matches 202; Conservative 54; Mismatches 59; Indels
                               IEA.
                                                                                                                                                                                   572 AA; 64899 MW; E3D22DB2C93B5B77 CRC64;
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EMBL, BC074350, AAH74350.1; -.
60; G0:0004143; Fidacylglycerol kinase activity; IE
G0; G0:0007205; P:protein kinase C activation; IEA.
InterPro; IPR001206; DAGKC.
Fam; PF00781; DAGKC.
ProDom; PD005043; DAGKC;
PRODOM; S000046; DAGKC;
III
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 DLILIRKCSRFNFLRFLIRHTNQQDQ 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||:|||||| :||| |||||: :||
446 DLILVRKCSRLDFLRHLIRHTSNKDQ 471
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01-MAR-2004 (TrEMBLrel. 26, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last anno
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ProDom; PD005043; DAGKc; 1.
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REDLINGE-20196606, PubMed=10731132, DOI=10.1126/Science.287.5461.2185; RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Ranastides P.G., Scherer S.E., 11 P.M., Hoskins R.A., Galle R.F., Ranastides P.G., Medical M.D., Zhang O., Chen L.X., Bardon R.C., Rogers Y.H., Blazels R.G., Hell G., Nelson C.R., Gabor G.L., RA Man K.H., Doyle C., Baxeer E.G., Hell G., Nelson C.R., Gabor G.L., RA Man K.H., Doyle C., Baxeer E.G., Hell G., Nelson C.R., Gabor G.L., Ranastides P.G., Baxeer E.G., Hell G., Nelson C.R., Gabor G.L., Ranastides P.C., Baxeer E.G., Hell G., Nelson C.R., Gabor G.L., Ranastides P.C., Baxeer B.D., Bandara D., Bolchan W.R., Bouck J., Broketein P., Brottier P., Rockova D., Bocchan W.R., Bouck J., Broketein P., Brottier P., Rank Burtis R.C., Busam D.A., Buller H., Cadle W. E., Churies P., Ranger R.A., Changer S., Dahlke C., Davenport L.B., Davies P., Ranger R.A., Changer S., Downes M., Durbin K.J., Evangalista C.C., Ferraz C., Ferraz C., Gabrielian A.B., Gargy N.S., Gelbart W.M., Gasser K., Gong P., Gorrell J.H., Guz Y., Gulan P., Harris M., Gong P., Gorrell J.H., Guz Y., Gulan P., Harris M., Gong P., Gorrell J.H., Guz Y., Gulan P., Harris M., Hookind Y., Rosiner D., Houston K.A., Howland T.J., Wei M.H., Ibeyam C., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Kantel B.L., Kodira C.D., Kraft C., Kravitz S., Rulp D., Lai Z., Ran H., Kalush P., Karlor C., Morris J., Mosheefi A., Monte S.M., Murphy B., Murphy, L., Muzyup D.M., Nelson D.L., Ranactol M., Murphy B., Wurphy, L., Warsup D.M., Murphy B., Murphy, L., Muzyup D.M., Nelson D.K., Ranactol W., Murphy B., Wurphy, L., Warsup M., Stone R., Shur R., Monte S.M., Murphy B.N., Nelson D.K., Mang Z., Mang Z.Y., Wasserman D.A., Wainstook M., Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao O.A., Ye J., Rhang Z.K., Mondager, Worley K.C., Wu D., Yang S., Yao O.A., Ye J., Rhang Z.K., Monger B.M., Kubi 288 PRPRPGNIRLPTGSISSMRNLGNDQWKVVRGNFFMICGANITCACARSPNGISRYSHLGD 347 -----EWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGD 297 

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15; 386 224 -----EWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGD 297 PRPRPGNLRLPTGSISSMRNLGNDQWKVVRGNFFMICGANITCACARSPNGISRYSHLGD 547 DRK-PCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACR 283 128 YSTVGTSDAETSALHIVVGDSLAMDVSSV-----HHNSTL---LRYSVSLLGYGFYGDII 180 KDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQ-----HT-----VGSPR SEKILCRANCKICUS----KVGWNSASTTLNPCPEKTRWCRTKGRFLSIGAAVMSNRNE PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE TLYEI ---NIDKYDGIVCVGGDGMFSEVLHG-LIGRIQ------RSAG----387 SESEKYRWMGPKRYDYVGTKIFLKHRSYEAEVMFEEAESENSKASLHTRSKTWPFRNTTR Gaps Similarity to unknown protein.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis. SEQUENCE FROM N.A. BODILNE=20181125; PubMed=10718197; Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H., Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 5. X. Se features of the regions of 3,076,755 bp covered by sixty P1 and 97; Length 533; Indels

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WCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387 YGFYGDVISESEKYRWMGPKRYDYVGTKIFLKHRSYEAEVMFEEAESENSKASLHTRSKT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VGSPRDRK-PCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINA 275
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01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-MAY-2003 (TrEWBLrel. 24, Last annotation update)
Hypothetical protein T10B11.2.
Name=T10B11.2; ORFNames=T10B11.2;
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                           Arabidopais thallana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnollophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.0%; Score 498.5; DB 2; Length 608; 33.6%; Pred. No. 9e-35; ive 48; Mismatches 112; Indels 105,
                                                                                                                                                                                                                                                                                                                                MEDLINE=22959668; PubMed=14563678; DOI=10.1101/gad.1140503; Liang H., Yao N., Song J.T., Luo S., Lu H., Greenberg J.T.; "Ceramides modulate programmed cell death in plants."; Genes Dev. 17:2636-2641(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TLYEI ---NIDKYDGIVCVGGDGMFSEVLHG-LIGRTQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      608 AA; 68462 MW; 65EB9353692D9CA6 CRC64;
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                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AY36252; AAQ6294.1; --
GO, GO:0004143; F:diacylglycerol kinase activity; I
GO, GO:0007205; P:protein Kinase C activation; IEA.
InterPro, IPRO1206; DagKc.
Pfam; PF00781; DAGK_cat; 1.
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                           608 AA
                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress)
                                                                       Created)
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                                                                  05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00781; DAGK cat; 1
ProDom; PD005043; DAGKc; 1
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                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                       Ceramide kinase.
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117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 MK-----POGNDKYDYHWHA----EFTHVICCVIPTVTPF-----TPYGLAPFTGIG 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 IPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 IIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDR-KPCRAGCFVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 ROSKQOLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TLYBINIDKY---DGIVCVGGDGMFSEVLHGLIGRIQRSAGVDQNHPRAVLVPSSLRIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
                                                                       investigating biology. The C. elegans: a platform for science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                   "The sequence of C. elegans cosmid T10B11.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson K.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE95737555534EEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.3%; Score 486.5; DB 2; Best Local Similarity 34.6%; Pred. No. 8.9e-34; Matches 111; Conservative 66; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                700 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2004) to the EMBL/GenB
EMBL; AF098993; AAC67466.1; -
PIR, T33517, T33517.
Wormbage; WBGene00020398; T10B11.2.
Wormbep; T10B11.2; CE18241.
InterPro; IPR001206; DAGKC.
PYGN: PF00781; DAGK_cat; 1.
Hypothetical protein.
SEQUENCE 549 AA; 62425 MW; DE9573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6H6H1;
05-JUL-2004 (TrEMBLrel. 27, Created)
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DGTLDLALVPRISRFHNMQFM 457
                                             MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormBase Consortium;
                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Bristol N2;
                       STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                Minx P., Kemp K.;
"The sequence of (
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A STRAIN-Bristol N2
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Similarity
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                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                             230 TLASLSDKDLKKFDGVIAVNTINACLSLFDIKHHNYKMSARPENTLSYDPQSAASGHKSM 289
                                                                                                                                                                                                                                                                                                                                                                                                                                  77 -----HGLIGRTQRSAGVD--- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 LIFYCFIINNMKCQEHRNNDLSNSELTGDDANAISGSSNTPDDHEPLLSTTRSTGLDISS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R---OSKOOLBEEOKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAA 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
                                                                                                                                                                                                                                                                                                                                                                                          TLYEI ---NIDKYDGI VCV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 VVGDSLAMDVSSV-----HHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDF
                                                                                                                                                                                                                                                                                                                            55; Mismatches 114; Indels 147; Gaps
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Putative ceramide kinase.
Putative ceramide kinase.
Name=P0519E06.23; Synonyms=OJ1003 B06.39;
Oryza sativa (japonica cultivar-group).
Shakaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                      DB 2; Length 700;
                                                                                                                   Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2,
                                                                                                                                                                                  Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AP005006; BAD25578.1;
EMBL, AP04676; BAD25337.1;
                                                                                                                                                  Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                              IEA.
                                                                                                                                                                                                                                                                                  700 AA; 77961 MW; FBB2C2A3DF31C75D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Ceramide kinase-like protein.
                                                                                                                                                                                                                            GO; GO:0004143; F:diacylglycerol kinase activity; I
GO; GO:0007205; P:protein kinase C activation; IEA.
InterPro; IPR001206; DAGKC.
                                                                                                                                                                                                                                                                                                      26.5%; Score 455.5; DB 2 29.8%; Pred. No. 6.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLGDGSSDLILIRKCSRFNFLRFLIRHTNQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD005043; DAGKc; 1
                                                                                                                                                                                                                                                                                                                          134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                         SEQUENCE FROM N.A.
                                                                                      NCBI_TaxID=39947;
                                                                                                                                          clone: P0519E06,"
                                                                                                                                                                                                                                                                                 SEQUENCE
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Q6UZF6;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 LLKECELQGFDGVVCVGGDGSASEVAHALLLRAQKNAGMETDR---ILTPVRAQLPLGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 IKDSEKKRWLG-LARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 QSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGD
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SEQUENCE FROM N.A.
SIGNATION STATION STATION STATION STATION M., Miranda M.,
Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Kim C., Lin J., Thoslogis A., Sati M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRIQRSAGVDQNHPRAVLVP--SSLRIGII
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                      causes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.4%; Score 436; DB 2; Length 53 31.3%; Pred. No. 2.2e-29; tive 63; Mismatches 121; Indels
                                                                                                                                                                                                                                                                      gene,
                                                                                                                                                         PubMed=14681825;
PubMed=14681825;
Tuson M., MarEng, G., Gonzalez-Duarte R.;
Tuson M., MarEng, G., Gonzalez-Duarte R.;
"Mutation of CERKJ, a novel human ceramide kinase gene autosomal recessive retinitis pigmentosa (RP26).";
Am. J. Hum. Genet. 74:128-138(2004).
EMBL, AV357073; AAR13670.1; -
GO; GO:0004143; F:diacylglycerol kinase activity; IEA.
GO; GO:0007205; P:proctein kinase C activation; IEA.
InterPro: IPR001206; DAGKC.
EMBL, PF00781; DAGK_cat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532 AA; 59602 MW; C73E590F7C25EED1 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485 AA
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A Shinn P. (Thon H.) Cheuk R., Kim C.J., Bowser L., Carninci P.,
A Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
A Shinn P., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A.,
A Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
A Mauyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
Embl. Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
Embl. AY128394; AAM91597.1; -.
B EMBL; AY128394; AAM91597.1; -.
B EMBL; BYOO6621; AAM91597.1; -.
B CO; GO:0007205; Piprotein kinase C activation; IEA.
B ProDom; PD005043; DAGKc.
B ProDom; PD005043; DAGKc.
B ProDom; PD005043; DAGKc.
B SMART; SM00046; DAGKc.
B SMART; SM00046; DAGKc.
B SWART; SM00046; DAGKc.
B SEQUENCE 485 AA; 53698 MW; 3FFE99FA6DACED5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 IVRSMDVSKYDGIVCVSGDGILVEVVNGLLER-----EDWKTAIKLP----IGWVPA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSTDCVCYS---TVGTSDAETSA-LHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQ--HTVGSPRDRKPCRAGCF 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || :|| || :|| || :| || :| DIDIESEKFRWMGSARFDIYGLQRIICLRQYHGRILFVPAPGFESYGQ-----RASCS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 VCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRG----L 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKHLLVPINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                                                                                                                                           Length 485;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
22.7%; Score 389; DB 2; Length 48;
Best Local Similarity 30.9%; Pred. No. 2.6e-25;
Matches 102; Conservative 69; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 SPAAHLGDGSSDLILIRKCSRFNFLRFLIR 319
[2]
SEQUENCE FROM N.A.
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1654 bp mRNA linear PRI 25-MAY-2004 Homo sapiens bK29F11.1 full length open reading frame (ORF) cDNA clone (CDNA clone C22ORF:pGEM.bK29F11.1).
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Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see http://www.sanger.ac.uk/HGP/Chr22/.
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CRA56404.1 GI:47678338
GDNA, chromosome 22; ORF.
Homo sapiens (human)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammaalia; Putheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1654)
Collins,J.E., Wright,C.L., Edwards,C.A., Davis,M.P., Grinham,J.A.,Golo-6.C.G., Goward,M.E., Aguado,B., Mallya,M., Mokrab,Y.,
Direct Submission
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AX457006 Sequence
AR541900 Sequence
AR541900 Sequence
BD102675 Ceramide
BD10343468 Novel gen
AR51434 Homo sapi
AX224383 Sequence
CQ730476 Sequence
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CR386590 Gallus ga
BC0741360 Xenopus 1
BC074110 Xenopus 1
AX457005 Sequence
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- 2005 Compugen Ltd.
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Van Veldhoven, P.P.
Direct Submission
Submitted (18-APR-2002) Van Veldhoven P.P., Farmakologie,
K.U.Leuven, Herestraat, B-3000 Leuven, BELGIUM
Location/Qualifiers
j. .2042 CGACTCTTTGCACGAGGAATTGAAGAGAATCCGAAGCCAGACTCACACGCTGA PRI gene) HSA457828 2042 bp mRNA linear Homo sapiens mRNA for putative lipid kinase (LK4 g AJ457828 AJ457828 I GI:20269072 lipid kinase; LK4 gene. Homo sapiens (human) GAGAAGAAACGGTGGTTGGGTCTTGCCAGATACGA /organism="Homo sapiens" Chordata; Primates; Van Veldhoven, P.P. A search for lipid kinases Unpublished Homo sapiens Eukaryota, Metazoa; Mammalia; Eutheria;

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.larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0;
/mol_type="mRNA"
/db_xref="taxon.9606"
/chromosome="22"
/map="22413"
1. 2042
11. 2042
71. .1684
/gene="LK4"
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| 616 TATGAGATTAACATAGACAAATACGACGGCATCGTCTGTGTCGGCGGAGATGGTATGTTC 675 601 AGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGCGCCGGGGTCGACCAGAAC 660                                | 661 CACCCCGGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGAATCCTTCCCGCAGGGTCA 720 [                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 721 ACGGACTGCGTGTTACTCCACCGTGGGCACCAGCGACGAGAAACCTCGGCGCTGCAT 780 | 781 ATCGTTGTTGGGGACTCGCTGGCCATGGATGTCTCCTCAGTCCACCACAACAGCACACTC 840 | 841 CTTCGCTACTCCGTGTCCTGGGCTACGGCTTCTACGGGGACATCATCAAGGACGT 900<br>                                                                                                          | 901 GAGAAGAAACCTTGGCTGTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTC 960<br>                                                                                                                                                                        | 961 TCCCACCACTGCTATGAAGGGACAGTGTCCTTCCTCCCTGCACAACACACGGGGGATCT 1020 1036 TCCCACCACCACTGCTATGAAGGACAGTGTCCTTCCTCCCTGCACAACAACACGGTGGGATCT 1095 | 1021 CCAAGGATAGGAAGCCCTGCCGGCAGGATGCTTTGTTTGCAGCCAAAGCAAGC                                                                                                          | 1081 CTGGAGGAGCAGAAAGCACTGTATGGTTTGGAAGCGGGAGGACGTGGAGGAG 1140<br> | 1141 TGGCAAGTCGTCTGTGGGAAGTTTCTGGCCATCAATGCCACAACATGTCCTGTGCTTGT 1200 | 1201 GCCGGAGCCCCAGGGGCCTCTCCCCGGCTGCCCACTTGGGAGACGGGTCTTCTGACCTC 1260 | AICCICAICCGGAAAIGCICCAGGIICAAIIIIICIGAGAIITICICAICAGGACACCCAAC 132<br> | CAGCAGACCAGTTTGACTTCACTTTTGTTGAAGTTTATCGGGTCAAGAAATTCCAGTTT 1<br> |                                                                     | GGGCACATTTGCAGCAGCCACCCTCCTGCTGCTGCACCGTCTCCAACAGCTCCTGGAAC 1       | TGCGACGGGGAGTCCTGCACAGCCCTGCCATCGAGGTCAGAGTCCACTGCCAGCTGG<br>         | 1561 CGACTCTTTGCACGAGAATTCAAGAATCCGAAGCCAGACTCACACGGTGA 1614<br>    | SULT 4<br>:541900                                                    |
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| SOURCE Homo sapiens (human) ORGANISM Homo sapiens Electropical Solutions (Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. | Regulation Patent: Westent: We | urce 1                                                            | CDS 761689 /note="unnamed protein product" /codon start=1            | /procein_ia=(LAD3255.1"<br>/db_xref="G1:21715796"<br>/translation="MGATGAAEPLQSVLWVKQQRCAVSLEPARALLRWRRSPGPGAGA<br>/pgAAGSVPVPSEIIAVDEFIPUHGKHQGSRWQXMERPYRFYPTWYRARPRWKWAQV | 1 FROEDEQUELINGQ TERROLLOSTE AND VERT CONSOGNATI ZERVAFUL ILL ASITTDI I VTEHANQAKETLYENINDKYDGI VCVGGGGGRESEVLHGLIGRIQRAGVD QNHPRAVLVPSSLRIGI I PAGSTDCVCX STVGTSDAETSALHI VVGGSLAMDVSSVHH NGTLLRYSVSVLGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG |                                                                                                                                                | ORIGIN  Query Match 100.0%; Score 1614; DB 6; Length 4413; Best Local Similarity 100.0%; Pred, No. 0; Marches 1614; Canservative 0, Mismarches 0, Indels 0, Cans 0. | TGGGGGGAACGGGGGGGGGGGAACCGTGCAATCCGTGCTGTGGGTGAAGCAGCAGGG 60       | TIGGECCETERAGECCEGCGCGCGCGCTCTCTCTCTCTCTGTGCGCGCGCGC                  | GGAGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                | CARGADACAGACGTTCACGGGDAACATCAAGGCAGTGGDAAATGGCAGAAATGGAAAAG 24         | 30                                                                | 301 CAGGTGACTTTCTGGTGTCCAGAGGAGCAGCTGTGTGTCATGTGGCTGCAGCCCTGCGG 360 | 361 GAGATGCTGGAGAAGCTGACGACCAAAGCATTTACTGGTATTTATCAACCCGTTT 420<br> | 421 GGAGGAAAAGGACAAGGGAAGAATATATGAAAGAAAGTGGCACCACTGTTCACCTTA 480<br> | Qy 481 GCCTCCATCACCACTGACATCATACTGAACATGCTAATCAGGCCAAGGAGACTCTG 540 | 541 TATGAGATTAACATAGACAAATACGACGGCATCGTCTGTGTCGGCGGAGATGGTATGTTC 600 |

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1264 ATCCTCATCCGGAAATGCTCCAGGTTCAATTTTCTGAGATTTCTCATCAGGCACACCAAC 2523
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                           CTGGAGGAGGAGAAGAAAGCACTGTATGGTTTGGAAGCTGCGGAGGACGTGGAGAG
                                                                                                                                                                                 2104 GAGAAGAAACGGTGGTTGGGTCTTGCCAGATACGACTTTTTCAGGTTTAAGACCTTCCTC
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Homo saplens cerk mRNA for ceramide kinase, complete cds.
AB079066
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                                                                                                                    1 (bases 1 to 4432)
TangyYrT., Zhou,P., Goodrich,R., Liu,C., Asundi,V., Ren,F.,
Zhang,Yr., Zhoo,C.A., Yang,Y., Xue,A.J., Wehrman,T., Wang,J.-R.
Wang,D. and Drmanac,R.T.
Nucleic acids and polypeptides
Patent: 18 6743619-8 148 01-JUN-2004;
Location/Qualifiers
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AR541900
Sequence 148 from patent US 6743619.
AR541900.1 GI:53933980
                                                                                                                                                                                                                        1. .4432
/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 99.9%;
Matches 1613; Conservative
                                                                                                     Unclassified.
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   Ceramide Kinase, a Novel Lipid Kinase. MOLECULAR CLONING AND FUNCTIONAL CHARACTERIZATION
J. Biol. Chem. 277 (26), 23294-23300 (2002)
                                                                                       Sugira,M., Kono,K., Shimizugawa,T., Minekura,H., Spiegel,S.
Kohama,T.
                                                                                                                 Direct Submission
Direct Submission
Submitted (29-JAN-2002) Masako Sugiura, Sankyo Co., Ltd.,
Pharmacology and Molecular Biology Research Laboratories;
Hiromachi 1-chome, Shinagawa-ku, Tokyo 140-8710, Japan
(B-mall:maugiura@shina.sankyo.co.jp, Tel:81-3-3492-3131,
Fax:81-3-5436-68565)
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/db_xref="taxon:9606"
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E 2 (bases 1 to 4171)
S Chara,O., Nagase,T. and Kikuno,R.
S Direct Submission
AL Submitted (22-NOV-2000) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913, Fax:81-438-52-3913,

Location/Qualifiers
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Identification of novel transcribed sequences on human chromosome.
22 by expressed sequence tag mapping
DNA Res. 8 (1), 1-9 (2001)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Homo saplens mRNA for KIAA1646 protein, partial cds.
AB051433
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larity 100.0%; Pred. No. 2.4e-313;
Conservative 0; Mismatches 0;
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Homo sapiens
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| Oy         1488 CAGCTCCTGGAACTGCGACGGGGGGGCCTGCCTTCGAGGTCAGGTCCA 1547           Db         1321 CAGCTCCTGGAACTGCGGGGGGGGGGCCTGCCTGCCATCGAGGTCCAGGTCCA 1380           Oy         1548 CTGCCGGTGGTCTTTGCACGGGGAATTGAAGAATCGAAGCCACACTCACA 1607           Db         1381 CTGCCAGCTGGTTCGACTCTTTGCACGGGAATTGAAGAATCGAAGCCACACTCACA 1607           Oy         1608 CAGCTGA 1614           Db         1441 CAGCTGA 1614           Db         1441 CAGCTGA 1647 | MACRO   MACR | Db 421 GAACATGCTAATCAGGCCAAGGAGACTCTGTATGAGATTAACATAGACAAATACGACGGC 480 |

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Pred. No. 1.4e-312;
0; Mismatches 0;
                                                                /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                /gene="CERK"
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/db_xref="GI-45595583"
/db_xref="LocusID:64781"
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Rlausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Jordan, H., Moore, T., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Youchman, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
I (base, 1722)
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,

Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth

Peatherstone, Malachi Griffith, Obj Griffith, Ran Guin, Nancy Liao,

Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,

Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,

Parvaneh Saeedi, JR Santcos, Angelique Schnerch, Ursula Skalska,

Duane Smailus, Jeff Stott, Maranda Tsai, George Yang, Jacquie

Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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         bcu67255
Homo sapiens ceramide kinase, mRNA (cDNA clone IMAGE:6185601),
complete cds.
                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/tissue_type="Peripheral Nervous System, dorsal root
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Email: cgapbs-r@mail.nih.gov
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 /organism="Homo sapiens"
 /mol\_type="unassigned DNA"
 /db\_xref="taxon:9606"

Corporation (NY) (US) Location/Qualifiers

03-FEB-2004

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Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                             126;
6; Length 1459;
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Score 1209.8; DB 6;
Pred. No. 3.7e-260;
0; Mismatches 2;
Query Match
Best Local Similarity 91.3%;
Matches 1347; Conservative
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   Hiromachi 1-chome, Shinagawa-ku, Tokyo 140-8710, Japan (E-mail:meugiuza6ahina.sankyo.co.jp, Tel:81-3-3492-3131, Fax:81-3-5456-655)
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Pred. No. 4.8e-240;
0; Mismatches 300;
                                                                                                                                                                                            /product="ceramide kinases"
/protein_id="BAC01155.1"
/db_xref="GI:21624342"
                                                                           musculus"
                                                           1. .2830 /organism="Mus musculus" /mol type="mRNA" /db xref="taxon:10090" /db 27810
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                          GGACAGTGTCCTTCCTCCTGCACACACACGGTGGGATCTCCAAGGGATAGGAAGCCCT
                                                                           GCCGGCCAGGATGCTTTGTTTGCAGGCAAGCAAGCAGCAGCTGGAGGAGGAGCAGAAGA
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J. Biol. Chem. 277 (26), 23294-23300 (2002)
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Sugiura,M., Kono,K., Shimizugawa,T., Minekura,H., Spiegel,S.
Kohama,T.
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Submitted (29-JAN-2002) Masako Sugiura, Sankyo Co., Ltd.,
Pharmacology and Molecular Biology Research Laboratories;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus cerk mRNA for ceramide kinases, complete cds.
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Length 979;
                                                                                 Kossida, S. and Encinas, J.
Regulation of human sphingosine kinase-like protein
Patent: WO 0228906-A 111-APR-2002;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                        55.9%; Score 903; DB 6; I 96.6%; Pred. No. 1.9e-191;
                                                                                                                                                           /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                0; Mismatches
 AX456998.1 GI:21715789
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Homo sapiens
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Prediction of the coding sequences of mouse homologues of KIAA gene: III. the complete nucleotide sequences of 500 mouse of KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries DNA Res. 10 (4), 167-180 (2003)
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Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.

Direct Submission

Submitted (23-JUL-2003) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7

Kazusa, kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)

The CREATE program supported by Japan science and technology

corporation; cDNA full insert sequencing: Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
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IIITEHANQAKETLYEINTDSYDGIVCVGGDGMFSEVLHGVIGRTQQSAGIDPNHPRA
VLVPSTLRIGIIPAGSTDCVCYSTVGTNDAETSALHIIIGBSLAIDVSSVHYHNTLLR
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/note="CDS is predicted by in silico analysis. Start codon
is not identified.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                    GGAGGAGTGGCAACTCTGGGAAGTTTCTGGCCATCAATGCCAAAAAAAGTGCCTG
                          GGAGGAGTGGCAAGTCTCTGGGGAAGTTTCTGGCCATCAATGCCACAAACATGTCCTG
                                                                                                                 TGCTTGTCGCCCGGAGCCCCCAGGGGCCTCTCCCCGGCTGCCCACTTGGGAGACGGGTCTTC
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/product="mKIAA1646 protein"
/protein_id="BAC98226.1"
/db_xref="GI:37360496"
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mol_type="mRNA"
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| clone="mph01246"
| tissue_type="embryonic tail"
| note="vector:modified pBC Si
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Mus musculus mRNA for mKIAA1646 px AK129416.1

AK129416.1 GI:37360495

FLI CDNA.

Mus musculus (house mouse)

Mus musculus
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Db 1131 TCATTTGTAGATGTTTATCGGGTGAAGAGTTTTACATTTACATCAAGAGAC 1190

Qy 1402 GAGGACAGCGACCTCAAGGAGGGGAAGAGCGCTTTGGGCACATTTGCAGCAGCCA 1461

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Qy 1522 AGCCTGCAATTGAATAGCTACATCACTGCTCGTTCACGAGGAATT 1310

Qy 1582 GAAGGAAA 1589

Db 1371 GAGGAAAA 1378
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Search completed: September 5, 2005, 23:41:46 Job time: 7343.65 secs

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us-10-631-958-9.rng

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September 5, 2005, 15:04:18; Search time 929.933 Seconds (without alignments) 10274.357 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description                   | Abl40828 Human sph | Adj96598 Human lip | Abx70921 Novel hum | Adp55247 Human PRO | Ada 05679 Human NOV | Aba96945 Human cer | Adn62844 Human NOV | Aaa50510 Human sph | Aad14426 Human sph | Acc70838 Human Sph | Ads10370 Human the | Aas77728 DNA encod | Abl40822 Human sph | Aas77730 DNA encod | Aas77731 DNA encod | Aac76031 Human ORF | Abq99499 Human cod | Ads11669 Human the | Aac76592 Human ORF | Abl40827 Human sph |
|-----------|-------------------------------|--------------------|--------------------|--------------------|--------------------|---------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ū                             | ABL40828           | ADJ96598           | ABX70921           | ADP55247           | ADA05679            | ABA96945           | ADN62844           | AAA50510           | AAD14426           | ACC70838           | ADS10370           | AAS77728           | ABL40822           | AAS77730           | AAS77731           | AAC76031           | ABQ99499           | ADS11669           | AAC76592           | ABL40827           |
|           | DB                            | y                  | 12                 | 80                 | 13                 | 80                  | 9                  | 12                 | m                  | ហ                  | 8                  | 13                 | Ŋ                  | 9                  | വ                  | Ŋ                  | ᠬ                  | 9                  | 13                 | m                  | 9                  |
|           | *<br>Query<br>Match Length DB | 4413               | 4429               | 4432               | 4445               | 1740                | 4463               | 1740               | 4231               | 1840               | 3975               | 4702               | 2241               | 979                | 2186               | 1570               | 753                | 817                | 817                | 547                | 550                |
|           | %<br>Query<br>Match           | 100.0              | 100.0              | 99.9               | 99.9               | 8.66                | 99.6               | 98.3               | 89.7               | 9.68               | 77.5               | 63.0               | 57.7               | 55.9               | 46.7               | 46.6               | 37.1               | 35.3               | 35.3               | 33.9               | 29.4               |
|           | Score                         | 1614               | 1614               | 1612.4             | 1612.4             | 1610.8              | 1607.6             | 1586.2             | 1448.2             | 1446.4             | 1251               | 1017.6             | 931                | 903                | 753.8              | 752.4              | 598.8              | 569                | 569                | 547                | 475                |
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                                                      The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g. asthma), autoimmune diseases (e.g rheumatoid arthritis) and central and peripheral nervous system disorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein encoding cDNA
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protein polypeptide or allergy, an autoimmune disorder.
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                                                                                                                                                                                                                                                                                                                                                                               Hundan; gene; ss; nervous system disorder; peripheral neuropathy; huntington's disease; amyotrophic lateral sclerosis; haemophilia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound; ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke; fibrosis; reperfusion injury; infection; allergic rhinitis; asthma; coagulation disorder; cancer; tumour; inflammatory disease; septic shock; differentiation; stem cell growth factor; haematopolesis; chemokinetic; haemostatic; antinflammatory; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptide useful for treating neurodegenerative diseases, myeloid or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.
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                                                   CAGCAGGACCAGTTTGACTTCACTTTTGTTGAAGTTTATCGCGTCAAGAAATTCCAGTTT
                                                                 CAGCAGGACCAGTTTGACTTTTGTTGAAGTTTATCGCGTCAAGAATTCCAGTTT
                                                                                            GGGCACATTTGCAGCCACCCCTCCTGCTGCTGCACCGTCTCCAACAGCTCCTGGAAC
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Wang D,
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T, Wang J,
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                                                                                                                                                                                                                                                                                                                                                             human cDNA sequence #146.
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Wehrman
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thuman polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. Parkinson's disease, continuous rheumatoid arthritis, insulin-dependent diabetes mellitus); myeloid or lymphoid cell disorders (e.g. anaemia and thrombocytopaenia); wounds, ulcers, burns; bone disorders (e.g. osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head trauma); lung or liver fibrosis; reperfusion injury in various tissues; cancer and tumours; and inflatmatory diseases (e.g. septic shock, Crohn's disease, anaphylaxis). The protein may be used to inhibit the growth, infection or function of infections agents such as bacteria, fungi, infection or function of infections agents such as bacteria, fungi, viruses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have cycles of rhythms. The protein may also have cycles of rhythms. The protein may also have cycles of the invention are useful for expressing recombinant protein for analysis. The present sequence represents a novel for analysis. The present sequence represents a novel for analysis, and man continuous this sequence of the invention, this sequence represents and thrombolysic, and this sequence of the invention, this sequence represents and processing the protein for analysis. The present sequence represents and processing the protein for analysis, this sequence represents and processing than a control of the invention are useful.
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The present invention describes an isolated PRO nucleic acid (1). Also described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptides; (5) a chimeric molecule comprising the cisolated PRO polypeptide; (5) a chimeric molecule comprising the composition of matter comprising a polypeptide of (4); an agonist or composition of matter comprising a polypeptide of (4); an agonist of the polypeptide or an antibody that binds to the composition of matter of (7); (9) a method of treating an immune related disease in a matter of (7); (9) a method of treating an immune related disease in a comprising a container, a label on the container and a composition of mammal; (10) a method for determining the presence of a PRO polypeptide or in a sample suspected of having the polypeptide; (11) a method of identifying a compound that inhibits or cit in mammal; (12) a method of stimulating the immune response in a mammal. The container have antialleragic, antianaemic, antialiabetic, antianaemic, antianaemic, antithyroid, CNS, dermatological, gastrointestinal, antishmatic, antithyroid, CNS, dermatological, gastrointestinal, container and expected or immunostimulant, immunosuppressive, muscular, container and the encoded polypeptide, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid container and mand the encoded polypeptides, compositions, kits and method or immunostimulant, immunostim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.
                                                                                          human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiasthmatic; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antityroid; CNS; dermatological; gastrointestinal; heemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
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stimulating an immune response. The present sequence represents a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams PM;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 1223; 3009pp; English.
                                                  Human PRO cDNA sequence SEQ ID NO:1223
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Best Local Similarity 99.9%;
Matches 1613; Conservative C
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ADP55247 standard; cDNA; 4445

ADP55247;

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| 124 ATGGGGGGGGGGGGGGGGGTGCGCTGCTGGTGGTGGAAGCGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

2001US-0330142P.
2001US-0330309P.
2001US-0331266P.
2001US-0345629P.
2001US-0345629P.
2001US-0345657F.
2002US-0373260P.
2002US-0373260P.
2002US-0373260P.
2002US-0373464P.
2002US-037384F.
2002US-037384F.
2002US-037384F.
2002US-037384F. 2002US-0381042P. 2002US-0381642P. 2002US-0383656P. 2002US-0383831P. 2002US-00262511 01-NOV-2001; 17-APR-2002; 19-APR-2002; 19-APR-2002; 29-MAY-2002; 19-APR-2002; 19-APR-2002; 16-MAY-2002;

## (CURA-) CURAGEN CORP.

og; Dipippo VA; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

## 2003-381626/36.

P-PSDB; ADA05680

obesity, New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing pharmacogenomics

## Claim 20; Page 134; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising a polypeptide containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for streaming for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (11) a method of cor preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a corputation and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a corputation and antilipaemic activities, and can be used in gene therapy. The colypeptide is useful in manufacturing a medicament for treating a colypeptide and an believe associated with a human disease. The polypeptide cold activities and can be used in gene therapy. The cold and antilibration associated with a human disease. The polypeptide cold activities and can be used in gene the activity of the polypeptide cold and antilibration of activities. acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoletic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and

| ខូខូ   | $\ensuremath{\text{c}}$ pharmacogenomics. The present sequence encodes a human NOVX protein $\ensuremath{\text{c}}$ the present invention. | from           |
|--------|--------------------------------------------------------------------------------------------------------------------------------------------|----------------|
| ¥8     | A Sequence 1740 BP; 389 A; 476 C; 530 G; 345 T; 0 U; 0 Other;                                                                              |                |
| ÕάΣ    | ; DB 8                                                                                                                                     | ,0             |
| ò      | 1 ATGGGGCGACGGGGGGGGGGGGGCGCTGCAATCCGTGCT                                                                                                  | 09             |
| g      | 76                                                                                                                                         | -              |
| දු දු  | TGGGCGTGAGCCTGGAGCCGGGGGGTCTGCTGCGGTGGTGGCGGAGCCGGGGGCCCGGGGGCCCGGGGGGCCCGGGGGG                                                            | 120            |
| ò      | 121                                                                                                                                        | 18             |
| g      | 196 GGAGCCGGCCCCCCGGTGCTGATCTCTGTGCCTGTATCTGAGATCATCGCTGTT                                                                                 | r 255          |
| දු පු  | y 181 GAGGAAACAGACGTTCACGGGAAACATCAAGGCAGTGGAAAATGGCAGAAAAGG                                                                               | 315            |
| ò      | 241 CCTTACGCTTTTACAGTTCACTGTGTAAAGAGAGAGGACGACGACCCCC                                                                                      | 3 300          |
| g      | 316 CCTTACGCTTTTACAGTTCACTGTGTAAAGAGAGCACGACGACGACCGCTGGAAGTGGCG                                                                           | <br>G 375      |
| à      | 30                                                                                                                                         | 36             |
| d<br>d | 376                                                                                                                                        | 3 435          |
| පු පු  | 7 361 GAGATGCTGGAGAAGCTGCGTCCAGACCAAAGCATTTACTGGTATTTATCAACCCGTTT                                                                          | r 420          |
| È      | 421 GGAGGAAAAGGACAAGGCAAGCGGATATATGAAAAAAAGTGGCACCACTGTTCACCTTA                                                                            | 8              |
| g      | 496                                                                                                                                        | 555            |
| ò      | 48                                                                                                                                         | 54             |
| g      | 556 GCCTCCATCACCACTGACATCGTTACTGAACATGCTAATCAGGCCAAGGAGT                                                                                   | 3 615          |
| දු දු  | 541 TATGAGATTAACATAGACAAATACGACGGCATCGTCTCTGTCTCGGCGGAGATGGTATGTT                                                                          | C 600<br>C 675 |
| ò      | 601                                                                                                                                        | 99             |
| g      | 676 AGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGCGCCGGGGTCGACAGAAC                                                                            | 735            |
| ò      | 661                                                                                                                                        | 720            |
| 쉱      | 736                                                                                                                                        | 795            |
| ò      | 721 ACGGACTGCGTGTTACTCCACCGTGGGCACCAGCGACAGAAACCTCGGCGCTGCAT                                                                               | 78             |
| 셤      | 196                                                                                                                                        | r 855          |
| ò      | y 781 ATCGTTGGGGACTCGCTGGCCATGGATGTCTCCTCAGTCCACACACA                                                                                      | 840            |
| g      | 856                                                                                                                                        | 3 915          |
| Š      | y 841 CTTCGCTACTCCGTGCCCTGCTGGGCTACGGCTTCTACGGGGCACATCATCAAGGACAGT                                                                         | 006 1          |
| g      | 916                                                                                                                                        | 375            |
| 8      | 06                                                                                                                                         | 960            |
| Ор     | 916                                                                                                                                        | 1035           |

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Kohama

Kono K,

2002-179513/23

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Human ceramide kinase gene and the enzyme encoded by it for screening substances as drugs for neurological, inflammatory and other disorders
                                                                                                                                                                                                              Claim 5; Page 46-53; 61pp; Japanese
11-JUN-2001; 2001WO-JP004889
                            14-JUN-2000; 2000JP-00178039
                                                        (SANY ) SANKYO CO LTD
                                                                                                                                    P-PSDB; AAM49115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, ceramide kinase, hCBRK1; drug screening; gene therapy; neurological disease; inflammation; human immunodeficiency virus; HIV infection; type 2 diabetes; obesity; sepsis; arteriosclerosis; cancer; neuropyrotective; antiinflammatory; anti-HIV; antidiabetic; anorectic; antibacterial; antiseptic; antiarteriosclerotic; cytostatic;
                                                                             CTGGAGGAGGAGCAGAAAGCACTGTATGGTTTGGAAGCTGCGGAGGACGTGGAGGAG
                                                                                                                                        CTGGAGGAGGAGCAGAAAAACACTGTATGGTTTGGAAGCTGCGGAGGACGTGGAGGAG
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124. 1737
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This sequence represents CDNA encoding a human ceramide kinase designated hCERKI. The invention relates to hCERKI, nucleic acids encoding it, expression vectors and host cells containing hCERKI nucleic acids, the recombinant production of hCERKI and antibodies specific for hCERKI. The invention also encompasses methods of isolating hCERKI from samples, the use of hCERKI in drug screening, and the use of hCERKI nucleic acid sequences in gene therapy. hCERKI mediates the ATP-dependent 1 phosphorylation of ceramides and can be used to screen for therapeutic and preventive agents for a wide range of disorders. Such disorders in the neurological disease, inflammation, human immunodeficiency virus
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                                                                                                                                                                                                                   (HIV) infection, type 2 diabetes, obesity, sepsis, arteriosclerosis and
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Pred. No. 0;
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Best Local Similarity
Matches 1610; Conserv
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TATGAGATTAACATAGACAAATACGACGGCATCGTCTGTGTCGGCGGAGATGGTATGTTC 723
                                          ACGGACTGCGTGTTACTCCACCGTGGGCACCAGCGACGCAGAAACCTCGGCGCTGCAT
                                                                                CTTCGCTACTCCGGGTGCCCTGCTGGGGCTTCTACGGGGACATCATCAAGGACAGT
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de; gene; human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X; wasting disorder.
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20010S-0328044P.
20010S-0328024P.
20010S-0328044P.
20010S-0328044P.
20010S-0328044P.
20010S-032914P.
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2002US-0381037P.
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BDINGER S R.
ELLERMAN K.
MALYANKAR U M
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MILLET I.
PEYMAN J A.
KEKUDA R.
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CATTERTON E
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ZERHUSEN E
ANDERSON I
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MILLER C H
RASTELLI
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                                                 DNA
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05-0CT-2001; 2
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19-APR-2002;
19-APR-2002;
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17-MAY-2002;
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EI E.
GUO X.
                                                 Human NOV9a
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(KERU/)
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GGAGCCGGCGCCCCCGGTGCTGATGCCTGTGTCTGTATCTGAGATCATCGCCGTT 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated NoVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NoVX polypeptides. For example, NoVX polypeptides and activity of NoVX polypeptides. For example, NoVX polypeptides and polymucleotides may be used to treat disorders associated with decreased expression or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NoVX polypeptides by binding with the cells own genes and preventing their expression. NoVX polymetroleotides and complementary sequences may also be used as DNA probbes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of cretorative therapy. NoVX polypeptides may also be used as INA probes and antagonists of the expression and activity of NoVX. The cretorative therapy. NoVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators anti-NoVX polypeptide antibodies, agonists and antagonists may be used in this way to prevent, clasmostic agents for detecting the presence of NoVX in samples. NoVX polypeptides and polymucleotide may also be used as diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, and the various dyslipidaemias, metabolic disorders, and the various dyslipidaemias, metabolic disorders, and the various dyslipidaemias, metabolic creamers, and the various dyslipidaemias, metabolic chancer metabolic syndrome X and contents and polymedial and polymedial and antipolic disorders, and the various dyslipidaemias, metabolic contents and antiparts and antiparts and antiparts and the presence of NoVX in samples.

Content and disorders, and the various dyslipidaemias, metabolic contents and antiparts and 
                                                                                                                                                                                                                                                                                                                                   Dipippo VA;
                                                                                                                                                                                                                                                         Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides and nucleic acids, useful for preventing, I treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              They may also be used as antibacterial agents. The present sequence represents DNA encoding a human NOVX protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 39; 395pp; English.
                                                                                                           AGEE M L.
BERGHS C.
DIPIPPO V A.
EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                  PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
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     STONE D J.
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(SHEN/)
(SHEN/)
(SHIM/)
(ILGAC/)
(AGEE/)
(BERG/)
(BIPI/)
(GANG/)
(SPAD/)
     STON/)
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1274 1019 1079 1199 1259 615 599 719 779 839 899 974 674 629 794 854 914 734 GTGGCAAGTCGTCTGTGGGAAGTTTCTGGCCATCAATGCCACAAAACATGTCCTGTGCTTG GTGGCAAGTCGTCTGTGGGAAGTTTCTGGCCATCAATGCCACAAACATGTCCTGTGCCTTG TCGCCGGAGCCCCAGGGGCCTCTCCCCGGCTGCCCACTTGGGAGACGGGTCTTCTGACCT 780 TATCGTTGGGGACTCGCTGGCCATGGATGTCTCCTCAGTCCACCACACAGCACACT 915 CCTTCGCTACTCCGTGTCCCTGCTGGGCTACGGGTTCTACGGGGACATCATCAAGGACAG 1080 GCTGGAGGAGGAGCAGAAGAAGAAGACTGTATGGTTTGGAAGCTGCGGAGGACGTGGAGGA CAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGGGCGCCGGGGTCGACCAGAA CAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGGAGCCCGGGGTCGACCAGAA CCACCCCCGGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGAATCATTCCCGCAGGGTC CCACCCCGGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGAATCATTCCCGCAGGGTC 720 AACGGACTGCGTGTGTTACTCCACCGTGGGCACCAGCGACGCAGAAACCTCGGCGCTGCA CCTTCGCTACTCCGTGTCCCTGGTGGCTACGGCTTCTACGGGGACATCATCAAGGACAG 900 TGAGAAGAAACGGTGGTTTGGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCT 975 TGAGAAGAACGGTGGTTGGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCT TATGAGATTAACATAGACAAATACGACGGCATCGTCTGTGTCGCGGGGGAT-GGTATGTT 1155 ( 1215 ( 1200 1140 셤 g ò 셤 ò ઠે 135 120 195 121 GGAGCCGGCCCCCCGGCGCGGATGCCTGCTCTGTGCCTGTATCTGAGATCATCGCCGTT 180 9 ATGGGGGCAACGGGGCGCGGAGCCGCTGCAATCCGTGCTGTGGGTGAAGCAGCAGCGC 1 ATGGGGGCGACGGGGCGGCGGCGCCCTGCAATCCGTGCTGTGGGTGAAGCAGCAGCGC TGCGCCGTGAGCCTGGAGCCCCGCGCGCGCTTCTGCTGCGCTGGTGGCGGGGCCCCGGGGGCCC TECCECCETEAGCCTGGAGCCCGCGCGCGCTCTGCTGCTGCTGGTGGTGGCGGAACCCCGGGGCCC Gaps DB 12; Length 1740; 3; Indels 98.3%; Sco... 99.7%; Pred. No. v, ... 0; Mismatches Best Local Similarity 99.7 Matches 1610; Conservative 92 61

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human sphingosine kinase A, B and C polynucleotides and polypeptides useful in e.g. chromosome and gene mapping, and detecting inflammation or disease associated with abnormal levels of sphingosine kinase expression.
                                                                                                                               TCGCCGGAGCCCCAGGGGCCTCCCCCGGCTGCCCACTTGGGAGGACGGGTCTTCTGACCT
                                                  CCAGCAGGACCAGTTTGACTTCACTTTTGAAGTTTATCGCGTCAAGAAATTCCAGTT
                                                                   CCAGCAGGACCAGTTTGACTTCACTTTTGTTGAAGTTTATCGCGTCAAGAAATTCCAGTT
                                                                                    TACGTCGAAGCACATGGAGGATGAGGACAGCGACCTCAAGGAGGGGGGAAGAGCGCTT
                                                                                                                     TGGGCACATTTGCAGCAGCCACCCCTCCTGCTGCTGCACCGTCTCCAACAGCTCCTGGAA
                                                                                                                                                       CTGCGACGGGGGCCTGCACAGCCCTGCCATCGAGGTCAGAGTCCACTGCCAGCTGGT
                                                                                                                                                                                                    TCGACTCTTTGCACGAGGAATTGAAGAGAATCCGAAGCCAGACTCACACAGCTGA 1614
                                                                                                                                                                                                                                                                                                                       Sphingosine kinase C; SKC; human; drug screening; infection; antiinflammatory; antiallergic; anticancer; inflammation; allergy; cancer; therapy; diagnosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 7; 81pp; English.
                                                                                                                                                                                                                                                                                                         Human sphingosine kinase C cDNA.
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The polymucleotides may be used as hybridization probes, in the construction of PCR primers for chromosome and gene mapping, in the recombinant production of SKA, SKB and SKC, and in the generation of SKA, SKB and SKC, and in the generation of antisense DNA or RNA. They can be used to detect inflammation or disease associated with abnormal levels of SK expression, or to detect differences in gene sequence between normal and carrier or affected individuals. Host calls expressing SK can be used in drug screening. Human SK specific antibodies, inhibitors, ligands or their analogues are useful as bioactive agents to treat inflammation or disease including viral, bacterial or fungal infections, allegic responses, mechanical injury associated with trauma, hereditary diseases, lymphoma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281
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                                                                                                                                                                                                                                                                                                                                                                                carcinoma, and other conditions with activate the genes of kidney, lung heart, lymphoid or tissues of the nervous system
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The present invention relates to sphingosine kinase (SphK) polypeptides and nucleic acids encoding them. SphK is useful for treating a SphK-associated disorder especially cancers such as leukaemia, lymphoma, ovarian, breast, lung, colon, testicular, stomach and skin, atherosclerosis, restenosis or ischaemia and cell proliferative disease or disorder associated with vascular diseases. SphK gene is used in gene therapy and antisense-therapy. Sphingolipids serving as signalling molecules, have recently emerged as regulators of cell growth, diverse cell phenotypes and cell death. Activation of SphK by tumour necrosis factor (TNF) alpha inhibits apoptosis in human endothelial cells. The present sequence is human sphingosine kinase
                                                                                                                                                                                                                                                                                              An isolated Sphingosine kinase polypeptide useful for treating a SphK-
associated disorder especially cancer, restenosis or ischemia in a human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TACGCTTTTACAGTTCACTGTGTAAAGAGAGCACGACGGCACCGCTGGAAGTGGGCGCAG
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|TCCATCACCACTGACATCATCGGAACAATTCTATGTTAACTATGTAGAAGTAATTACT
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Best Local Similarity 97.8%;
Matches 1490; Conservative 0
                                                                            14-FEB-2000; 2000US-0182360P.
22-MAR-2000; 2000US-0191261P.
                                       14-FEB-2001; 2001WO-US004789
                                                                                                                                   (CURA-) CURAGEN CORP. (GETH ) GENENTECH INC
                                                                                                                                                                                                                                    WPI; 2001-514770/56.
P-PSDB; AAE07884.
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109. :1524
/product= "Human sphingosine kinase (SphK) protein #2"
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  CAGGCAAAGCAAGCAGCTGGAGGAGGAGCAGAAGAAAGCACTGTATGGTTTGGAAGC
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                 ACGCAGAGGGGCCGGGGTCGACCAGAACCACCCCCGGGCTGTGCTGGTCCCCAGTAGC
                             ACGCAGAGAGCGCCGGGGTCGACCAGAACCACCCCCGGGCTGTGCTGGTCCCCAGTAGC
                                                                                           ACCAGCGACGCAGAAACCTCGGCGCTGCATATCGTTGGGGGACTCGCTGGCCATGGAT
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The present sequence is the coding sequence for human sphingosine kinase 4 (SPHK4). The kinase can be used for the diagnosis and treatment of sphingosine related disorders. The kinase can also be potentially used for controlling toxicity of platelet transfusion and as a platelet
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et transfusion; platelet stabiliser; gene; ds
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                                                                                                                                         Human Sphingosine kinase 4 coding sequence
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                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .1251
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P-PSDB; ABR56301.
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Best Local Similarity 81.4%;
Matches 1261; Conservative 0
                                                                                                                                                                                                                                                                                     2004-668857/65.
                                                                                                                                                                                                            (NUVE-) NUVELO INC
                                                                                                                                                                                                                                                                                    WPI; 2004-668857/
P-PSDB; ADS11054.
                                                                                       WO2004080148-A2
                                                            Homo sapiens
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                                          GTTGTTGGGGACTCGCTGGCCATGGATGTGTCCTCAGTCCACCACAACAGCACACTCCTT
                                                                                                        GTTGTTGGGGACTCGCTGGCCATGGATGTGTCCTCAGTCCACCACAACAGCACACTCCTT
                                                                                                                                                  CGCTACTCCGTGTCCCTGCTGGCTACGGCTTCTACGGGGACATCAAGGACAGTGAG
                                                                                                                                                                     CGCTACTCCCTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCATCAAGGACAGTGAG
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1513

259

1453

4702; 75;

Length

Score 1017.6; DB 13; Lengt Pred. No. 1e-253; 0; Mismatches 214; Indels

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TCACCACTGACATCATCGTTACTGAACATGCTAATCAGGCCAAGGAGACTCTGTATGAGA

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The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoletic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic DNA of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhou P;
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antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for diagnosing disorders, e.g.
                                    inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
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Weng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide, useful in preparing a composition treating inflammatory, neurodegenerative or stem cell aplastic anemia or cancer for promoting wound healing.
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Xue
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Wang J, Ghosh M,
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                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2002; 2002US-0416186P.
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Chen R, Zhao QA,
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in sent disease states involving (II). (II) is useful in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging complypatide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging involving aberrant protein expression of biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and anino acid sequences. AAS6419-AAS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coding sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 CGGATGCCTGCTGTGCCTGTATCTGAGATCATCGCCGTTGAGGAAACAGACGTTCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
2894 TCTTTGCACGAGGAATTGAAGAGAATCCGAAGCCAGACTCACACAGGTGA 2943
                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 931; DB 5; Length 2241;
Pred. No. 2.4e-231;
0; Mismatches 5; Indels 309;
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                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #13532.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                    BP.
                                                                                                                      standard; cDNA; 2241
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23-AUG-2000; 2000US-00649167.
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Matches 1273; Conservative
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TTAACAT -----AGACAAATACGACGCCATCGTCTGTGGCGCGGAGATG-
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 central or peripheral nervous system
                                                               The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g. asthma), autoimmune diseases (e.g. rheumatoid arthritis) and central and peripheral nervous system discorders (e.g. reakinson's disease). The present sequence represents the human sphingosine kinase-like protein
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No. 3.2e-224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequences of the invention. Note: The sequence data for this
                     TGCTTGTCGCCGGAGGCCCCAGGGCCTCTCCCCGGCTGCCCACTTGGGAGACGAGCTCTTC
                                                                                                                                           TGACCTCATCCTCATCCGGAAATGCTCCAGGTTCAATTTTTCTGAGATTTCTCATCAGGCA
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GGAGGAGTGGCAAGTCGTCTGTGGGAAGTTTCTGGCCATCAATGCCAAACAAGTGTCCTG
                                                                      TGCTTGTCGCCGGAGCCCCAGGGGCCTCTCCCCGGCTGCCCACTTGGGAGAGACGGGTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding novel human diagnostic protein #13534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 13534; 103pp; English
                                                                                                                                                                                                                  CACCAACCAGCAGGACCAG 1332
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23-AUG-2000; 2000US-00649167.
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patent did not appear in the printed specification, but was obtained electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                         Length 2186;
                                                                                                                           Sequence 2186 BP; 455 A; 637 C; 669 G; 425 T; 0 U; 0 Other;
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                                                                                                                                                                                      Query Match
46.7%; Score 753.8; DB 5;
Best Local Similarity 99.7%; Pred. No. 2.9e-185;
Matches 755; Conservative 0; Mismatches 2;
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
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| 6 67.8 4.2 1857 4 US-09-970-516-3 Sequence 6 67.8 4.2 2380 4 US-09-970-67-30448 Sequence 6 67.8 4.2 2380 4 US-09-817-676A-11 Sequence 8 61.2 3.8 2698 4 US-09-817-676A-11 Sequence 51.2 3.2 1155 4 US-09-970-516-1 Sequence 51.2 3.2 1155 4 US-09-970-516-1 Sequence 51.2 3.2 11783 4 US-09-949-016-1155 Sequence 6 2 US-09-949-016-1155 Sequence 7 US-08-075-034A-1 Sequence 7 US-08-075-034B-1 US-08-075-034B-1 US-08-075-034B-1 US-08-075-034B-1 US-08-075-034B-1 US-08-075-034B-1 US-08-075-034B-1 US-08-075-034B-1 US-08-075-035-034B-1 US-08-075-035-035-035-035-035-035-035-035-035-03                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 4             | O     | 4.3                 | 498    | 4  | -09-893-737-5       |                   |
| 6 67.8 4.2 2380 4 US-09-817-676A-13 Sequence 65.6 4.1 901 4 US-09-270-767-30448 Sequence 61.2 3.8 15.2 3.2 12658 4 US-09-270-767-30448 Sequence 51.2 3.2 1265 4 US-09-970-516-1 Sequence 51.2 3.2 1265 4 US-09-970-516-1 Sequence 22.4 12.8 3.1 1875 4 US-09-989-1 Sequence 23.4 1875 4 US-09-989-97-1 Sequence 23.4 1875 4 US-09-989-91-1 Sequence 49.2 3.0 1149 4 US-09-68-1-21A-399 Sequence 44.2 2.7 1533 4 US-09-25-990 Sequence 44.2 2.7 1533 4 US-09-25-991A-1179 Sequence 43.4 2.7 1050 4 US-09-949-016-17554 Sequence 43.4 2.7 1050 4 US-09-25-991A-1179 Sequence 44.2 2.7 3619 3 US-09-25-991A-12 Sequence 5 US-08-25-991A-12 Sequence 5 US-08-25-991A-1 | S             | 67.8  | •                   | 1857   | 4  | -60-                | 3, 1              |
| 65.6 4.1 901 4 US-09-270-767-30448 Sequence 51.2 3.8 2698 4 US-09-877-678-11 Sequence 51.2 3.8 2698 4 US-09-870-516-11 Sequence 51.2 3.2 1205 4 US-09-970-516-11 Sequence 51.2 3.2 1205 4 US-09-970-516-11 Sequence 49.8 3.1 1875 4 US-09-949-016-1155 Sequence 49.8 3.1 1875 4 US-09-949-016-1155 Sequence 49.2 3.0 1611 4 US-09-248-796A-1756 Sequence 44.2 2.7 7218 1 US-09-270-516-5 Sequence 77 7218 1 US-09-270-516-5 Sequence 43.4 2.7 7218 1 US-09-270-516-5 Sequence 43.4 2.7 7218 1 US-09-252-991A-1179 Sequence 43.4 2.7 3071 4 US-09-252-991A-1179 Sequence 43.4 2.7 3071 4 US-09-949-016-17554 Sequence 43.4 2.7 3619 3 US-09-949-016-17554 Sequence 43.4 2.7 3619 3 US-09-949-016-17554 Sequence 74.8 2.7 3619 3 US-09-949-016-17554 Sequence 74.8 2.7 3619 3 US-09-949-016-1298 Sequence 74.8 2.7 3619 3 US-09-949-016-1298 Sequence 74.8 2.6 115963 4 US-09-949-016-1298 Sequence 74.8 2.6 115963 4 US-09-949-016-1298 Sequence 74.8 2.6 2.6 115963 4 US-09-949-016-1298 Sequence 74.8 2.7 3619 3 US-09-949-016-1298 Sequence 74.8 2.6 2.6 115963 4 US-09-949-016-1298 Sequence 74.8 2.7 3619 3 US-09-949-016-1298 Sequence 74.8 2.8 2.6 115963 4 US-09-949-016-1298 Sequence 74.8 2.8 2.6 115963 4 US-09-949-016-1298 Sequence 74.8 2.5 2.6 115963 4 US-09-949-016-1298 Sequence 74.8 2.5 2.6 115963 4 US-09-949-016-1298 Sequence 74.8 2.5 2.6 115963 5 US-09-949-016-1298 Sequence 74.8 2.5 2.6 11596 Sequence 74.8 2.5 2.6 115963 5 US-09-949-016-1298 Sequence 74.8 | 9             | 7.    | •                   | 2380   | 4  |                     | 13,               |
| 61.2 3.8 2698 4 US-09-817-676A-11 Sequence 51.2 3.2 1155 4 US-09-970-516-1 Sequence 51.2 3.2 1155 4 US-09-970-516-1 Sequence 51.2 3.2 1783 4 US-09-949-016-1155 Sequence 49.8 3.1 666 2 US-09-949-016-1155 Sequence 49.2 3.0 1611 4 US-09-248-796A-1756 Sequence 49.2 3.0 1611 4 US-09-248-796A-1756 Sequence 44.2 2.7 7218 1 US-09-276-516-5 Sequence 43.4 2.7 7218 1 US-09-25-991A-1179 Sequence 43.4 2.7 7218 1 US-09-25-991A-1179 Sequence 43.4 2.7 7014 4 US-09-949-016-5812 Sequence 43.4 2.7 7014 4 US-09-949-016-5812 Sequence 43.2 7 3619 3 US-09-949-016-1754 Sequence 43.2 7 3619 3 US-09-949-016-1754 Sequence 43.4 2.7 3619 3 US-09-949-016-1754 Sequence 44.2 2.6 115963 4 US-09-949-016-12298 Sequence 54.2 2.6 115963 4 US-09-949-016-12298 Sequence 56.2 2.6 115963 4 US-09-912-891-3 Sequence 56.2 2.6 115963 5 US-09-912-912-912-912-912-912-912-912-912-91                | 7             | 'n.   | 4.1                 | 901    | 4  | -09-270-767-3044    | 304               |
| 9 51.2 3.2 1155 4 US-09-970-516-1 Sequence 51.2 3.2 1205 4 US-09-959-897-1 Sequence 51.2 3.2 1205 4 US-09-959-897-1 Sequence 51.2 3.2 1205 4 US-09-959-897-1 Sequence 79.8 3.1 1875 4 US-09-614-218-399 Sequence 5 48.4 3.0 1149 4 US-09-614-218-399 Sequence 6 48.4 2 2.7 1533 4 US-09-570-516-5 Sequence 6 43.4 2 2.7 1533 4 US-09-252-9918-1269 Sequence 73.8 2.7 1050 4 US-09-252-9918-1179 Sequence 73.9 13.0 13.0 13.0 13.0 13.2 14.2 2.7 1050 4 US-09-252-9918-1179 Sequence 73.1 13.0 13.0 13.0 13.0 13.0 13.0 13.0 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 80            | ä     | 3.8                 | 2698   | 4  | -09-817-676A-1      | Ξ,                |
| 15.2 3.2 1205 4 US-09-959-897-1 Sequence 49.8 3.1 1875 4 US-09-949-016-1155 Sequence 49.8 3.1 1875 4 US-09-949-016-1155 Sequence 49.8 3.1 1875 4 US-09-614-221A-399 Sequence 49.2 3.0 1611 4 US-09-614-221A-399 Sequence 44.2 3.0 1611 4 US-09-970-516-5 Sequence 6 44.2 3.0 1611 4 US-09-970-516-5 Sequence 7 43.8 2.7 1533 4 US-09-970-516-5 Sequence 7 43.8 2.7 7218 1 US-08-232-463-14 Sequence 43.4 2.7 1050 4 US-09-252-991A-1179 Sequence 43.4 2.7 3071 4 US-09-949-016-17554 Sequence 43.2 2.6 430 4 US-09-949-016-17554 Sequence 43.4 2.7 36519 4 US-09-949-016-17554 Sequence 7 42.2 2.6 115963 4 US-09-949-016-12298 Sequence 7 42.2 2.6 115963 4 US-09-949-016-12298 Sequence 5 41.2 2.6 115963 4 US-09-949-016-12298 Sequence 6 41.2 2.6 115963 4 US-09-949-016-12298 Sequence 7 40.8 2.5 115963 4 US-09-912-540-9500 Sequence 8 2.5 1164 4  | 0             | ä     | 3.2                 | 1155   | 4  | US-09-970-516-1     | 1,                |
| 1 51.2 3.2 1783 4 US-09-949-016-1155 Sequence 49.6 3.1 666 2 US-095-016-1155 Sequence 49.6 3.1 666 2 US-09-645-014A-1 Sequence 49.6 3.1 1875 4 US-09-248-796A-1756 Sequence 5.4 49.2 3.0 1611 4 US-09-248-796A-1756 Sequence 44.2 2.7 7218 1 US-09-205-258-90 Sequence 7.4 3.8 2.7 7218 1 US-09-252-991A-1179 Sequence 43.4 2.7 1050 4 US-09-252-991A-1179 Sequence 43.4 2.7 1050 4 US-09-252-991A-1179 Sequence 43.2 2.7 3071 4 US-09-949-016-15812 Sequence 43.2 2.7 3619 3 US-09-949-016-17554 Sequence 42.8 2.7 3619 3 US-09-949-016-1298 Sequence 42.8 2.7 3619 3 US-09-949-016-1298 Sequence 5.4 1.2 2.6 115963 4 US-09-949-016-1298 Sequence 5.4 1.2 2.6 115963 3 US-09-128-891-1 Sequence 5.4 1.2 2.6 1318 3 US-09-128-891-1 Sequence 40.8 2.5 114 4 US-09-902-540-9500 Sequence 5.4 1.2 2.6 2014 4 US-09-912-891-1 Sequence 5.4 1.2 2.6 2014 4 US-09-912-891-3 Sequence 5.4 1.2 2.6 2014 2 US-09-2012-891-3 Sequence 5.4 1.2 2.6 2014 2 US-09-2012-2014 2 US-09-2012-2012 2 US-09-2012-2012 2 US-09-2012-2012 2 US-09-2012-2012 2 US-09-2012-2012 2 US | 70            | ä     | 3.2                 | 1205   | 4  | -60-                | 'n                |
| 49.8 3.1 666 2 US-08-875-034A-1 Sequence 49.6 3.1 1875 4 US-09-614-221A-399 Sequence 49.6 3.1 1875 4 US-09-614-221A-399 Sequence 5 48.4 3.0 1149 4 US-09-570-516-5 Sequence 44.2 2.7 1533 4 US-09-252-89-90 Sequence 8 43.4 2.7 1551 1 US-08-252-991A-1179 Sequence 43 2.7 1050 4 US-09-252-991A-1179 Sequence 43 2.7 1050 4 US-09-252-991A-1179 Sequence 43 2.7 1050 4 US-09-949-016-1754 Sequence 43 2.7 5619 3 US-09-949-016-1754 Sequence 43 2.7 3619 3 US-09-949-016-1754 Sequence 43 2.7 3619 3 US-09-949-016-1754 Sequence 43 2.7 3619 3 US-09-949-016-12298 Sequence 5 US-08-23-137-2 2.6 115563 4 US-09-621-976-656 Sequence 5 US-08-23-137-2 Sequence 5  | 11            | ä     | 3.2                 | 1783   | 4  | 15                  | 115               |
| 49.6 3.1 1875 4 US-09-614-221A-399 Sequence 49.2 3.0 1611 4 US-09-248-796A-1756 Sequence 48.4 2.0 1611 4 US-09-248-796A-1756 Sequence 44.2 2.7 1533 4 US-09-205-258-90 Sequence 7 43.8 2.7 1218 1 US-08-222-991A-1269 Sequence 43.4 2.7 1050 4 US-09-252-991A-1179 Sequence 43.2 2.7 1050 4 US-09-252-991A-1179 Sequence 43.2 2.7 3071 4 US-09-949-016-5812 Sequence 43.2 2.7 36519 3 US-09-949-016-17554 Sequence 43.4 2.7 36519 3 US-08-932-137-2 Sequence 44.2 2.6 115963 4 US-09-949-016-12298 Sequence 5 41.2 2.6 115963 4 US-09-949-016-12298 Sequence 5 41.2 2.6 115963 4 US-09-125-891-1 Sequence 5 41.2 2.6 104 4 US-09-125-891-1 Sequence 5 40.8 2.5 104 4 US-09-9500 Sequence 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 12            | φ.    | 3.1                 | 999    | 7  | US-08-875-034A-1    | 1, A              |
| 49.2 3.0 1611 4 US-09-248-796A-1756 Sequence 44.2 3.0 1149 4 US-09-270-516-5 Sequence 44.2 3.0 1149 4 US-09-970-516-5 Sequence 44.2 3.0 1149 4 US-09-970-516-5 Sequence 7 43.8 2.7 7218 1 US-08-232-463-14 Sequence 43.4 2.7 7218 1 US-09-252-991A-1179 Sequence 43.4 2.7 3071 4 US-09-252-991A-1179 Sequence 43 2.7 3071 4 US-09-949-016-17554 Sequence 14.2 2.6 430 4 US-09-949-016-17554 Sequence 4 42.2 2.6 115963 4 US-09-949-016-12298 Sequence 5 41.2 2.6 115963 4 US-09-122-991-1 Sequence 5 41.2 2.6 266 3 US-09-125-891-3 Sequence 7 40.8 2.5 114 4 US-09-912-540-9500 Sequence 5 6 266 5 266 5 Sequence 7 0.8 2.5 114 4 US-09-912-540-9500 Sequence 7 0.8 2.5 114 4 US-09-912-540-9500 Sequence 7 0.8 2.5 2.6 266 5 3 US-09-252-9500 Sequence 7 0.8 2.5 2.6 266 5 3 US-09-125-891-3 Sequence 7 0.8 2.5 2.6 266 5 3 US-09-125-891-3 Sequence 8 0.8 2.5 2.6 266 5 3 US-09-252-9500 Sequence 8 0.8 2.5 2.6 266 5 3 US-09-202-540-9500 Sequence 8 0.8 2.5 26 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266 5 266  | 13            | 49.6  | 3.1                 | 1875   | 4  | US-09-614-221A-399  | 399               |
| 5         48.4         3.0         1149         4         US-09-970-516-5         Sequence           6         44.2         2.7         1531         4         US-09-205-288-90         Sequence           8         43.4         2.7         1050         4         US-09-252-991A-1149         Sequence           9         43.4         2.7         1050         4         US-09-252-991A-1179         Sequence           1         43         2.7         1071         4         US-09-949-016-1812         Sequence           2         42.8         2.7         3619         3         US-09-949-016-1754         Sequence           2         42.8         2.7         3619         3         US-09-949-016-1754         Sequence           3         42.2         2.6         115963         4         US-09-949-016-1754         Sequence           4         42.2         2.6         115963         4         US-09-949-016-1754         Sequence           5         41.2         2.6         1318         3         US-09-949-016-12298         Sequence           4         42.2         2.6         115963         4         US-09-949-016-12298         Sequence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 14            | 49.2  | 3.0                 | 1611   | 4  | -09-248-796A-17     | 1756              |
| 6 44.2 2.7 1533 4 US-09-205-258-90<br>43.8 2.7 7218 1 US-08-232-463-14<br>43.4 2.7 1050 4 US-09-252-991A-1179<br>0 43 2.7 62908 4 US-09-949-016-5812<br>2 42.8 2.7 36519 3 US-09-949-016-1754<br>42.2 2.6 115963 4 US-09-949-016-1754<br>42.2 2.6 115963 4 US-09-949-016-12298<br>5 41.2 2.6 115963 4 US-09-949-016-12298<br>6 41.2 2.6 1318 3 US-09-125-891-1<br>40.8 2.5 1014 4 US-09-9502-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 15            | 48.4  | ω.                  | 1149   | 4  | US-09-970-516-5     | 5, A              |
| 7 43.8 2.7 7218 1 US-08-232-463-14<br>8 43.4 2.7 1050 4 US-09-252-991A-1269<br>9 43.4 2.7 1308 4 US-09-252-991A-1179<br>0 43 2.7 3071 4 US-09-949-016-5812<br>1 43 2.7 62908 4 US-09-949-016-17554<br>2 42.8 2.7 36519 3 US-09-923-137-2<br>3 42.2 2.6 115963 4 US-09-621-976-16656<br>4 42.2 2.6 115963 4 US-09-949-016-12298<br>5 41.2 2.6 21596 3 US-09-912-891-3<br>40.8 2.5 1014 4 US-09-022-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 16            | 4.    |                     | 1533   | 4  | US-09-205-258-90    | Sequence 90, Appl |
| 8 43.4 2.7 1050 4 US-09-252-991A-11269<br>9 43.4 2.7 1308 4 US-09-252-991A-1179<br>1 43 2.7 3071 4 US-09-949-016-1754<br>2 42.8 2.7 36519 3 US-09-949-016-1754<br>3 42.2 2.6 430 4 US-09-949-016-1656<br>4 42.2 2.6 115963 4 US-09-621-976-16656<br>5 41.2 2.6 115963 4 US-09-949-016-12298<br>6 41.2 2.6 2636 3 US-09-125-891-1<br>7 40.8 2.5 1014 4 US-09-902-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 17            | 6.1   |                     | 7218   | -  | -89-                | 14,               |
| 9 43.4 2.7 1308 4 US-09-252-991A-1179 0 43 2.7 3071 4 US-09-949-016-5812 1 42.8 2.7 36519 3 US-09-949-016-17554 2 42.2 2.6 430 4 US-09-621-976-16656 4 42.2 2.6 115963 4 US-09-949-016-12298 5 41.2 2.6 115963 4 US-09-949-016-12298 6 41.2 2.6 2346 3 US-09-125-891-3 7 40.8 2.5 1014 4 US-09-9502-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 18            | ന     | 2.7                 | 1050   | 4  | -09-252-991A-126    | 126               |
| 1 43 2.7 3071 4 US-09-949-016-5812<br>2 42.8 2.7 62908 4 US-09-949-016-17554<br>2 42.2 2.6 430 4 US-09-621-376-16656<br>4 42.2 2.6 115963 4 US-09-621-976-16656<br>4 42.2 2.6 115963 4 US-09-949-016-12298<br>5 41.2 2.6 115963 4 US-09-949-016-12298<br>6 41.2 2.6 236 3 US-09-125-891-3<br>7 40.8 2.5 1014 4 US-09-902-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 19            | ω.    | 2.7                 | 1308   | 4  | US-09-252-991A-1179 | 1179,             |
| 1 43 2.7 62908 4 US-09-949-016-17554 2 42.8 2.7 36519 3 US-08-923-137-2 3 42.2 2.6 430 4 US-09-621-976-16656 4 42.2 2.6 115963 4 US-09-949-016-12298 5 41.2 2.6 1318 3 US-09-15-891-1 6 41.2 2.6 2636 3 US-09-125-891-3 7 40.8 2.5 1014 4 US-09-902-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 20            | 43    | 2.7                 | 3071   | 4  | US-09-949-016-5812  | 581               |
| 2 42.8 2.7 36519 3 US-08-923-137-2<br>3 42.2 2.6 1430 4 US-09-621-976-16656<br>42.2 2.6 115963 4 US-09-949-016-12298<br>5 41.2 2.6 1318 3 US-09-125-891-1<br>6 41.2 2.6 2318 3 US-09-125-891-3<br>7 40.8 2.5 1014 4 US-08-9502-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 21            | 43    | 2.7                 | 62908  | 4  | -09-949-016-1755    | Sequence 17554, A |
| 3 42.2 2.6 430 4 US-09-621-976-16656<br>4 42.2 2.6 115963 4 US-09-949-016-12298<br>5 41.2 2.6 1318 3 US-09-125-891-1<br>6 41.2 2.6 2346 4 US-09-125-891-3<br>7 40.8 2.5 1014 4 US-09-902-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 22            | ς.    | 2.7                 | 36519  | m  | US-08-923-137-2     |                   |
| 4 42.2 2.6 115963 4 US-09-949-016-12298<br>5 41.2 2.6 1318 3 US-09-125-891-1<br>6 41.2 2.6 2636 3 US-09-125-891-3<br>7 40.8 2.5 1014 4 US-09-902-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 23            | 42.2  | 5.6                 | 430    | 4  | -60-                | 16                |
| 5 41.2 2.6 1318 3 US-09-125-891-1<br>6 41.2 2.6 2636 3 US-09-125-891-3<br>7 40.8 2.5 1014 4 US-09-902-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 24            | 42.2  | 5.6                 | 115963 | 4  |                     | 12                |
| 6 41.2 2.6 2636 3 US-09-125-891-3<br>7 40.8 2.5 1014 4 US-09-902-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 25            |       | 5.6                 | 1318   | m  | US-09-125-891-1     | H,                |
| .8 2.5 1014 4 US-09-902-540-9500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 56            |       | 5.6                 | 2636   | m  | US-09-125-891-3     | 3, App            |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 27            | 40.8  | 2.5                 | 1014   | 4  | -09-902-            | 95                |

| Sequence 1080, Ap Sequence 12420, A Sequence 12794, A Sequence 16589, A Sequence 16580, A Sequence 1963, Ap Sequence 1110, Ap Sequence 1070, Ap Sequence 6976, Ap Sequence 12677, A Sequence 1277, A Sequence 1277, A Sequence 1575, A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | i Length 4432; Indels 0; Gaps 0; Trergegreadecaecaecaecaecaecaecaecaecaecaecaecaecae |
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| US-09-902-540-1080<br>US-09-949-016-12420<br>US-09-949-016-16589<br>US-09-949-016-16589<br>US-09-949-016-16580<br>US-09-902-540-2472<br>US-09-902-540-1963<br>US-09-902-540-1110<br>US-09-902-540-1110<br>US-09-252-991A-7070<br>US-09-252-991A-7070<br>US-09-252-991A-8213<br>US-09-252-991A-8213<br>US-09-252-991A-8213<br>US-09-252-991A-8213<br>US-09-949-016-4013<br>US-09-902-31B-11<br>US-09-949-016-15755<br>US-09-949-016-15755                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ALIGNWENTS 74528 9el Nucleic Acids and e8 09/774,528 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Score 1612.4; DB 4                                                                   |
| 2.5 14101<br>8 2.5 112507<br>8 2.5 112507<br>6 2.5 112508<br>6 2.5 112508<br>6 2.5 1027<br>6 2.5 1027<br>6 2.5 1027<br>7 2.5 1027<br>8 2.5 1020<br>8 2.5 1020<br>8 2.5 1020<br>9 3 5 6 7 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | : Tom YY. Tom Ping Ping Ping Ping Ping Ping Ping Ping                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | rn m                                                                                 |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | RESULT 1 US-09-774-528-148 Sequence 148, Appli Patent No. 6743619 GENERAL INFORMATION APPLICANT: Tang, APPLICANT: Goodri APPLICANT: Goodri APPLICANT: Glao, APPLICANT: Abundi APPLICANT: Abundi APPLICANT: Abundi APPLICANT: Abundi APPLICANT: Ren, F APPLICANT: Ren, F APPLICANT: Rang, APPLICANT: Wang, APPLICANT: APPLICATIO CURRENT FILING DAT, CURRENT FILING DAT, SOCTWARRE: PL PL PL SCOTWARRE: PL PL SCOTWARRE: PL PL SCOTWARRE: PL PL SCOTWARRE: PL SCOTWARR | Query Match<br>Best Local 9<br>Matches 1611<br>Qy 1204<br>Qy 61<br>Db 1264<br>Qy 121 |

| Qy         1261 ATCCTCATCCGGAAATGCTCCAGGTTCAATTTTCTGAGATTTCTCATCAGGCACACCAAC 1320           Db         2464 ATCCTCATCCGGAAATGCTCCAGGTTCAATTTTCTGAGATTTCTCATCAGGCACACCAAC 2523           Qy         1321 CAGCAGGACCAGTTTGACTTCACTTTTGTTGAAGTTTATCGCGTCAAGAATTCCAGTTT 1380           Db         2524 CAGCAGGACCAGTTTGACTTCACTTTTGTTGAAGTTTATCGCGTCAAGAATTCCAGTTT 1380           Qy         1381 ACGTCGAAGCACAGTTGACACTTTGTTGAAGTTTATCGCGTCAAGAATTCCAGTTT 1440           Db         2584 ACGTCGAAGCACATGAGGACAGCAGCACCTCCAAGGAGGGGGAAAATTCCAGTTT 1440           Db         2584 ACGTCGAAGCACATGAGGACAGCAGCCTCCAAGGAGGGGGAAAATTCCAGTTT 1440           Db         2584 ACGTCGAAGCACATGAGGACAGCAGCCTCCAAGGAGGGGGAAAATTCCAGTTT 1440           Db         2644 ACGTCGAAGCACATGAGGACAGCACCCCTCCTGCACCCGCTCCAAGAGAGAG | 0-767-15155/c  10. 6703491  1. NO. 6703491  1. INFORMATION: CANT: Homburger et al. CANT: Ho | 3 3 3 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                          |
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| 181   GAGGAAACGATCACGGGAAACATCAAGGCAGTGGAAAATGGCAGAAAATGGAAAAG   143   1384   GAGGAAACGATCACGGGAAACTCAAGGCAGTGGAAAATGGCAAAATGGAAAAG   1443   241   CCTTACGCTTTACAGTTCACTGTAAAGAGAGCACCACCGCACCGCTGGAAGTGGCCG   160   1444   CCTTACGCTTTTACAGTTCACTGTAAAGAGAGCACCACCACCACCACCACAGAGCCGCG   150   161                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | CTTCGCTACTCCCTGGCCTACGGCTTCTACGGGGGACATCATCACGACACGT 900 CTTCGCTACTCCCTGGCTGGCTTCTACGGGGGACATCATCAGGACAGT 900 CTTCGCTACTCCCTGTGCCTGGCTTCTACGGGGGACATCATCAGGACAGT 210 CTTCGCTACTCCTGGTTGGCTTGGGCTTCTACGGGGGGGACATCATCAGGTTCT 102 GAGAAGAAACGGTGGGTTGGCTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTC 216 GAGAAGAAACGGTGGGTTGGCTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTC 216 TCCCACCACTGCTATGGAGGACAGTGCCTTCCTCCTCCTGCACACACA |

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671 TGAGGACAGCGCTATCCATGTGATTCTGGGCCAGCATCGGGGATTGGATGTGCAGTG 612
                                       821 TCCACCACACACACACTCCTTCGCTACTCCGTGTCCCTGGGGCTACGGCTTCTACG 880
                                                                                                                                GGGACATCATCAAGGACAGTGAGAAAGAAACGGTGGTTGGGTCTTGCCAGATACGACTTTT 940
                                                                                                                                                                          551 GCGATGTGGCAGCCCAGAGCGAGAACTACCGCTGGATGGGACCGCGCCGCTACGAGTACA 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7126-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14306
LENGTH: 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             740 ACCAAGTGAAGGACATACTTCTGAGCCATGATCTGGGAGTATACGATGCGGTTTGCTGTG
                                                                                 611 reascaaresceasrecerscrearrerersceasureresceaseres
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                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-270-767-14306
Sequence 14306, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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; ORGANISM: Drosophila melanogaster
US-09-270-767-14306
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Sequence 3. Application US/09970516
Patent No. 6610534
APPLICANT: No. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REFERENCE: 4-316.7
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
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                         1157 GTGGCGTCAAGGCCTTCCTGAATAATCGCGGGCTATGACGCCGAACTG 1203
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4.2%; Score 67.8; DB 4; Length 1
Best Local Similarity 45.4%; Pred. No. 7.7e-08;
Matches 292; Conservative 0; Mismatches 342; Indels
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941 CAGGTTTAAAGACCTTCCTCTCCCACCACTGCTATGAAGGGACAGTG
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                                                                                                                                                           Sequence 59, Application US/09893737
Fatent No. 6822082
GENERAL INFORMATION:
APPLICANT: Presentl, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
FRICR APPLICATION NUMBER: US 60/215,446
FRICR APPLICATION NUMBER: US 60/215,446
FRICR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 329
SOFTWARE: FastSEQ for Windows Version 3.0
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4.3%;
Best Local Similarity 91.4%;
Matches 74; Conservative C
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ORGANISM: Homo sapiens
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US-09-893-737-59
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; OTHER INFORMATION:
US-09-970-516-3
                                                                                                                                           US-09-893-737-59/c
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NAME/KEY: CDS
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US-09-970-516-3
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30448
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Sequence 1, Application US/09970516
Patent No. 6610534
GENERAL INFORMATION:
TITLE OF INVENTION: Dolynucleotides encoding sphingosine kinases
FILE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE SEERRING: 4-316.7
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT APPLICATION NUMBER: 0201-10-04
NUMBER OF SLO ID NOS: 6
SOFTWARE: Patentin version 3.1
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ORGANISM: Homo sapiens
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LOCATION: (1).
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LENGTH: 1155
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US-09-970-516-1
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Sequence 11, Application US/09817676A

Sequence 11, Application US/09817676A

GENERAL INFORMATION:

APPLICANT: Spiegel, Sarah

APPLICANT: Kohama, Takafumi

TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,

TITLE OF INVENTION: Expression and Methods of Use Thereof

FILE REFERENCE: 00170/HG

CURRENT FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: US 60/194,318

PRIOR FILING DATE: 2000-04-03

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 11

LENGTH: 2698
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                               GAGGAGTGGCAAGTCTGTGGGAAGTTTCTGGCCATCAATGCCACAAACATGTCCTGT
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3.8%; Score 61.2; DB 4; Length 2698;
Best Local Similarity 53.3%; Pred. No. 5.5e-06;
Matches 129; Conservative 0; Mismatches 113; Indels 0
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NAME/KEY: CDS
LOCATION: (387)..(2237)
PUBLICATION INFORMATION:
TITLE: Molecular cloning and functional characterization
TITLE: novel mammalian sphingosine kinase type 2 isoform
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DATE: 2000-06-30
DATABASE ACCESSION NUMBER: AF245448
DATABASE ENTRY DATE: 2000-06-27
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VOLUME: 275
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Matches 131; Conservative
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New York
                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
; SEQ ID NO 1155
; LENGTH: 1783
; TYPE: DNA
; ORGANISM: Human
                                                                          US-09-949-016-1155
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 0.0/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-03

PRIOR FILING DATE: 2000-0-09

REGO ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 TACTGGTATTTATCAACCCGTTTGGAGAAAAGGACAAGGCAAGCGGATATATGAAAGAA 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.2%; Score 51.2; DB 4; Length 1205; 49.6%; Pred. No. 0.0018; ive 0; Mismatches 133; Indels 0
             322 GGGAGACCCCATCCAGAAGCCCC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGCGCCGGGGTCGACCAGAACC 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 49.6
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (33)..(1184)
; OTHER INFORMATION:
US-09-959-897-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-949-016-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1205
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                                                                                                                         398 TACTGGTATTTATCAACCCGTTTGGAGGAAAAGGACAAGGCAAGCGGATATATGAAAGAA 457
                                                                                                                                                                            386 recrecrecrearececececececesasesen 445
                                                                                                                                                                                                                                     458 AAGTGGCACCACTGTTCACCTTAGCCTCCATCACCACTGACATCGTTACTGAACATG 517
                                                                                                                                                                                                                                                                                                                                                                                                               566 rearereregadadeseregarentesegadeseregadeserearegadeseregaen 625
                                                                                                                                                                                                                                                                                            446 ACGIGCAGCCCCTITIGGCIGAGGCIGAATCICCTICACGCIGAIGCICACTGAGGGGC
                                                                                                                                                                                                                                                                                                                                                     518 CTAATCAGGCCAAGGAGACTCTGTATGAGATTAACATAGACAAATACGACGGCATCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           578 GTGTCGGCGGAGATGGTATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGA
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Score 51.2; DB 4; Length 1783;
Pred. No. 0.0022;
0; Mismatches 133; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bieseler, Barbara; Reinemer, Peter; Hain, APPLICANT: Rudiger; Mann, Karlheinz; Reif, Hans-Jorg; and APPLICANT: Thomaik, Jurgen Ernet TITLE OF INVENTION: DEOXYRIBONUCLEIC ACID CODING FOR TITLE OF INVENTION: GLUTATHIONE-S-TRANSPERASE AND ITS NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSEE: Sprung Kramer Schaefer & Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sprung Kramer Schaefer & Briscoe STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9895-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/875,034A FILING DATE: 16-JUL-1997 CLASSIPFCATION: 45 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/EP96/00068 FILING DATE: 10-JAN-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: DE 195 01 840.0 FILING DATE: 23-JAN-1995 ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           638 GGAGCGCCGGGTCGACCAGAACC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626 GGGAGACCGCCATCCAGAAGCCCC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08875034A, Patent No. 5968796, GENERAL INFORMATION:
   3.2%;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
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US-09-614-221A-399
i Sequence 399, Application US/09614221A
j Patent No. 6723837
j GENERAL INFORMATION:
j APPLICANT: Karunanandaa, Balasulojini
j APPLICANT: Karunanandaa, Balasulojini
j APPLICANT: Kishore, Ganesh M.
j TITLE OF INVENTION: WITH STROL SYNTHESIS AND OTHER MOLECULES ASSOCIATED
j TITLE OF INVENTION: WITH STROL SYNTHESIS AND METABOLISM
j TILE OF INVENTION: WITH STROL SYNTHESIS AND METABOLISM
j CURRENT FILING DATE: 10516.075
j CURRENT FILING DATE: 2000-07-12
j PRIOR APPLICATION NUMBER: US 60/142,981
j PRIOR PILING DATE: 1999-07-12
j NUMBER OF SEQ ID NOS: 626
j SEQ ID NOS: 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 GTGAGCCTGGAGCCCGCGCGGGGCTCTGCTGCGCTGGTGGCGGGAGCCCGGGGGCCCGGAGCC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGCCCCCGGCGGATGCCTGTTCTGTGTATCTGAGATCATCGCCGTTGAGGAA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 dacecececrearedadanacacececeaecrececeaaecrececaaecreceaecreared 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       578 GTGTCGCCGGAGATGCTATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGA 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49.8; DB 2; Length 6
Pred. No. 0.0031;
n. Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.1%; Score 49.8; DE
Best Local Similarity 53.3%; Pred. No. 0.003
Matches 105; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 ACAGACGTTCACGGGAA 203
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                                LENGTH: 666 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
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US-09-248-796A-1756

Sequence 1756, Application US/09248796A

Sequence 1756, Application US/09248796A

Sequence 1756, Application US/09248796A

Sequence 1756, Application US/09248796A

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

FRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER: OF SEQ ID NOS: 28208
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Sequence 5, Application US/09970516
Patent No. 6610534
GENERAL INFORMATION:
TATLE OF INVENTION: Induction of blood vessel formation through administration of TITLE OF INVENTION: Dolynucleotides encoding sphingosine kinases
TITLE REFERENCE: 4.31617
TITLE REFERENCE: 2001-10-04
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT PILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SSOFTWARE: PatentIn version 3.1
SSOFTWARE: PatentIn version 3.1
SSOFTWARE: PatentIn version 3.1
SSOFTWARE: PatentIn version 3.1
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552 TAAAATCTTACCAATATTACAAGCGGCTCGTGCTAATGTTACGTATTTTGAAACTAAATA 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612 TCATGGACACGCCACTGAGATTGCGCGTGAGCTAGATGATCAATGATTATGATATAATTGT 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 TATTTTGGTATTGATAAACCCGCATGGCGCCCAAGGACACGCCAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456 AAAAGTGGCACCACTGTTCACCTTAGCCTCCATCACCACTGACATCATCGTTACTGAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 TTTACTGGTATTTATCAACCCGTTTGGAGGAAAAGGACAAGGCAAGCGGATATATGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.0%; Score 49.2; DB 4; Length 1611; Best Local Similarity 51.4%; Pred. No. 0.007; Matches 114; Conservative 0; Mismatches 108; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 CTGTGTCGGCGGAGATGGTATGTTCAGCGAGGTGCTGCACGG 617
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                                                                                                                                                           926 GAGTGGATGCGTŤCAA 941
                                                                                                 638 GGAGCGCCGGGGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Candida albicans
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FEATURE:
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CTHER INFORMATION:
US-09-970-516-5
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Sequence Sequence Sequence

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5, 2005, 12:52:06; Search time 1173.31 Seconds (without alignments) 9008.663 Million cell.updates/sec
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(cgn2_6/ptodata/2/pubpna/PCT_NBW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/DS0_NBW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*
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(cgn2_6/ptodata/2/pubpna/US106_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd
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Maximum Match 100%
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Maximum DB
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Database

Sequence 8, Appli Sequence 4, Appli Sequence 5, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 21227, A Sequence 21226, A Sequence 3, Appli 
9 US-09-784-810A-5
22 US-10-876-281-5
10 US-09-96-86-1
119 US-10-631-988-1
110 US-01-115-635-247
110 US-09-96-96-8
110 US-10-36-345A-21228
110 US-10-36-343A-21226
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Sequence 13, Sequence 139,

US-09-893-737-59 US-09-893-737-59 US-09-970-516-3 US-09-817-676A-13 US-10-354-358-77 US-10-283-975A-515 US-10-283-975A-515 US-10-283-975A-515 US-10-737-450-139

ö 9 9 ATGGGGCGACGACGGCGGCGGAGCCGCTGCAATCCGTGTGTGGGTGAAGCAGCAGCGC 1 ATGGGGGCGGCGGCGGCGGCGCTGCTGCATCCGTGCTGTGGGTGAAGCAGCAGCAGCGC Gaps ö DB 10; Length 1614; Indels Sequence 9, Application US/09969896
; Publication No. US20030125533A1
GENERAL INFORMATION:
; APPLICANT: KOSSIGA, Sophia
; TITLE OF INVENTION: Regulation of human Sphingosine
; TITLE OF INVENTION: Kinase-Like Protein
; TILE REPRENCE: 004974.00594
; CURRENT APPLICATION WIMBER: US/09/969,896
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/238,005
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 9 100.0%; Score 1614; 100.0%; Pred. No. 0; ive 0; Mismatches Best Local Similarity 100. Matches 1614; Conservative TYPE: DNA ORGANISM: Homo sapiens 6-968-696-60-SD Query Match ò 셤

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Sequence 9, A Sequence 16, Sequence 16, Sequence 55, Sequence 148,

US-09-969-896-9 US-10-611-958-9 US-09-966-896-16 US-10-631-958-16 US-10-18-941-55 US-10-120-988-148 US-10-262-511-39

1614 4413 4413 4429 1740

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1614 1614 1614 1614 1612.4 1610.8

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Result

Sequence

Sequence 9, Appl

| 1141 TGGCAAGTCGTCTGGGGAAGTTTCTGGCCATCAATGCCACAAACATGTTCTTGTTTTTTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | RESULT 2   US-10-631-958-9   Sequence 5, Application US/10631958   Sequence 5, Application No. US2040.092580A1   Sequence 7, TITLE OF INVENTION: Kinase-Like Protein   FILE OF INVENTION: Kinase-Like Protein   FILE OF INVENTION NO. WINSER: US/09/56,896   September 5, 2001-10-60   September 5, 2001-10-60   September 5, 2001-10-60   September 6, 2001-10-60   September 6, 2001-10-60   September 7, 2001-60-60   September 7, 2001-60   Septe |
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US-10-120-988-148
                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
GENERAL INFORMATION
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NAME/KEY: CDS
LOCATION: (112
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                                                    ACGGACTGCGTGTTACTCCACCGTGGGCACCAGCGACGAAACCTCGGCCTGCAT
                                                            GAGAAGAAACGGTGGTTGGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTC
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; Sequence 148, Application US/10120988 ; Publication No. US20030219745A1

RESULT 6 US-10-120-988-148

1683 1743 1263 1323 1383 1503 1563 1623 1804 AGGGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGGCGCCGGGGTCGACCAGAAC 1863 ö 120 180 300 360 9 420 480 540 900 9 1444 CCTTACGCTTTTACAGTTCACTGTGTAAAGAGAGCACGGCACGGCACCGCTGGAAGTGGGCG 1624 GGAGGAAAAGGACAAGGCAAGCGATATATGAAAGAAAAGTGGCACCACTGTTCACCTTA 1684 GCCTCCATCACCACTGACATCATCGTTACTGAACATGCTAATCAGGCCAAGGAGACTCTG GCCTCCATCACCACTGACATCATCGTTACTGAACATGCTAATCAGGCCAAGGAGACTCTG TATGAGATTAACATAGACAAATACGACGGCATGGTCTGTGTGGCGGGGGAGATGGTATGTTC AGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGCGCCGGGGTCGACAGAAC GGAGCCGGCCCCCCGGCGCGATGCCTGCTCTCTGTATCTGAGATCATCGCCGTT CCTTACGCTTTTACAGTTCACTGTGTAAAGAGAGCACGGCACCGCTGGAAGTGGGCG CAGGTGACTTTCTGGTGTCCAGAGGAGCAGCTGTGTTGTCGCTGCTGCAGACCCTGCGG 361 GAGATGCTGGAGAAGCTGACGTCCAGACCAAAGCATTTACTGGTATTTATCAACCCGTTT 421 GGAGGAAAAGGACAAGGCAAAGATATATGAAAGAAAAAGTGGCACCACTGTTCACCTTA 1 ATGGGGGGGACGGGGGGGGGGCGCTGCAATCCGTGCTGTGGGTGAAGCAGCAGCAGC Gaps Length 4432; ö APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Riu, Chenghua
APPLICANT: Riu, Chenghua
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
TITLE OF INVENTION: No. US2003019745A1e1 Nucleic Acids and
TITLE OF INVENTION: No. US2003019745A1e1 Nucleic Acids and
TITLE OF INVENTION: NO. US20030404
FILE REFERENCE: 802CON
CURRENT FPLIATION NUMBER: US/10/120, 988
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/774,528
PRIOR PLING DATE: 2001-01-30
NUMBER OF SEC ID NOS: 4441
SEC ID NO 148
SEC ID NO 148 and 1; Indels DB 17; Query Match 99.9%; Score 1612.4; Best Local Similarity 99.9%; Pred. No. 0; Matches 1613; Conservative 0; Mismatches 601 g ઠ

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APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFRENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
FRIOR APPLICATION NUMBER: 60/326,483
FRIOR PELING DATE: 2001-10-09
FRIOR PELING DATE: 2002-04-19
FRIOR APPLICATION NUMBER: 60/327,917
FRIOR APPLICATION NUMBER: 60/327,917
FRIOR APPLICATION NUMBER: 60/327,917
FRIOR PELING DATE: 2002-05-16
FRIOR FILING DATE: 2002-05-16
FRIOR APPLICATION NUMBER: 60/381,629
FRIOR PELING DATE: 2002-05-16
FRIOR PELING DATE: 2002-06-16
FRIOR PELING DATE: 2002-06-16
FRIOR FILING DATE: 2002-04-19
FRIOR PELING DATE: 2002-04-19
FRIOR FILING DATE: 2001-10-06
FRIOR FILING DA
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99.9%; Pred. No. 0;
iive 0; Mismatches
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Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
Gorman, Linda
Zerhusen, Bryan D.
Anderson, David W.
                                                                                                             Guo, Xiaojia (Sasha)
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Catterton, Elina
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; LOCATION: (76)..(1686)
US-10-262-511-39
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   APPLICANT:
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2404 CGCCGGAGCCCCAGGGGCCTCTCCCCGGCTGCCACTTGGGAGACGGGTCTTCTGACCTC 2463
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61 receccercaseccreasecccecececercrecrecerrecrearescendesecence 120 9 1 ATGGGGGCGACGGGGGGGGGGGGCGCTGCAATCCGTGCTGTGGGTGAAGCAGCAGCGC Gaps DB 18; Length 1740; ö 셤 ò g ઠે

Sequence 39, Application US/10262511 Publication No. US20040038223A1 GENERAL INFORMATION: APPLICANT: Smithson, Glennda APPLICANT: Millet, Isabelle APPLICANT: Peyman, John A.

US-10-262-511-39

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| Oy 1201 CGCCGGAGCCCCAGGGCCTCTCCCCGGCTGCCCACTTG                                                                                                                                          | Qy 1261 ATCTCATCCGGAAATGCTCCAGGTTCAATTTCTGAGA 1336 ATCCTCATCCGGAAATGCTCCAGGTTCAATTTTCTGAGA | Qy 1321 CAGCAGACCAGTTTGACTTCACTTTGTTGAAGTTTAT Db 1396 CAGCAGACCAGTTTGACTTTGTTGTTGAAGTTTAT | 1381                                                                        | 1441 1516                                                         |                                                                     | DD 1636 CGACTCTTTGCACGAGAATTGAAGAATCCGAAGCCA                      | RESULT 8 US-10-315-597A-1 ; Sequence 1, Application US/10315597A | GENERAL INFORMATION: OSZUGJUEZZUBAI GENERAL INFORMATION: APPLICANT: Sugiura, Masako APPLICANT: Kono, Keita | ; APPLICANT: KODAMA; Takatum; ; TITLE OPF INVENTION: Ceranide Kinase and DNA Encodi; ; FILE REFERENCE: 02658CIP/HG ; CURRENT APPLICATION NUMBER: US/10/315,597A | FRIOR APPLICATION NUMBER: JP 2000-178039 ; PRIOR FILING DATE: 2000-06-14 ; NUMBER OF SEQ ID NOS: 4 | ; SEQ ID NO 1; LENGTH: 4463 ; LENGTH: 4463 ; TYPE: DWA             | COCATION: 3371                                                       | ; OTHER INFORMATION: US-10-315-597A-1 Query Match 99.6%; Score 1607.6; DB 1 | Best Local<br>Matches 16                                    | Dy 1 ATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG               |                                          | Db 184 TGGGCGTGAGCCTGGAGCCCGGGGGGGGTCTGCTGGGG                              | Db 244 GGAGCGGCGCCCCGGGGGGAATGCCTGCTCTGTGCCT  Qy 181 GAGGAAACAGACGTCAGGGAAAACATCAAGGCAGTGGA |   |
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| 121 GGAGCCGCCCCCGGCGGATGCCTGTTGTGCCTGTATCTGAGATCATCGCCGTT 180 10. CCACCTCCCCCCCGCGCAATGCCTGCTCTGTGCCTGTATCTGAGATCATCGCCGTT 180 10. CCACCTCCCCCCCCCTGTATATCTCTCTCTATATATCATATATCATATATAT | 93 GORGEGOGGEGECCGGGGGGGGGGGGGGGGGGGGGGGGGG                                                | CCTTACCTTTTACAGTTCACCGTTGAGGGCCGCGCGCGCG                                                  | CAGGTGACTTTCTGGTGTCCAGAGGAGCAGCTGTGTCACTTGTGGCTGCAGACCCTGCGGGGCAGACTGTGTGTG | 361 GAGATGCTGGAGATGCTCAGACCAAAGCATTTACTGGTATTTATCAACCGTTT 420<br> | 421 GGAGGAAAAGGACAAGGGGATATATGAAAGAAAAGTGGCACCACTGTTCACCTTA 480<br> | 481 GCCTCCATCACCACTGACATCATTACTGAACATGCTAATCAGGCCAAGGAGACTCTG 540 | 541 TATGAGATTAACATAGACAAGGGCATCGTCTGTCGGCGGAGATGGTATGTTC 600<br> | 601 AGCGAGGTGCTGCACGGTCTGATTGGGAGGCGCAGAGGGCGCCGGGGTCGACCAGAAC 660                                         | 661 CACCCCGGGGTGTGGTCCCCAGTAGCCTCCGGATTGGAATCATTCCCGCAGGGTCA 720<br>                                                                                            | 721 ACGACTGCGTGTTACTCCACCGTGGGCACCAGCGACGCAAACCTCGGCGCTGCAT 780<br>                                | 781 ATCGTIGTIGGGGACTCGCTGGCCATGGATGTCTCCAGTCCACCACAACAGCACACTC 840 | 841 CTTCGCTACTCCGTGTCCCTGCTGCGCTACGGCTTCTACGGGGACATCATCAAGGACAGT 900 | 901 GAGAAGAAACGGTGGTTGGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTC 960<br>    | TCCCACCACTGCTATGAAGGGACAGTGTCCTTCCTCCTGCACAACACACGGTGGGATCT | 1036 TCCCACCACTGCTATGAAGGGACAGTGTCCTCCTCCCTGCACAACACACAC | CCAAGGGATAGGAAGCCTGCCGGGCAGGATGCTTTGTTTG | 1081 CTGGAGGAGGAGCAGAAGAAAGCACTGTATGGTTTGGAAGCTGCGGAGGACGTGGAGGAG 1140<br> | 1141 TGGCAAGTCGTCTGTGGGAAGTTTCTGGCCATCAATGCCACAAACATGTCCTGTGCTTGT 1200<br>                  |   |
| જે તે                                                                                                                                                                                   | 8 8 8                                                                                      | 8 8                                                                                       | & g                                                                         | oy<br>Pb                                                          | \$ <b>8</b>                                                         | දු පු                                                             | 9<br>9                                                           | S S                                                                                                        | \$ 8                                                                                                                                                            | 8 G                                                                                                | දු පු                                                              | <i>ò</i> 8                                                           | ò a                                                                         | ö                                                           | 영 &                                                      | qa                                       | දු පු                                                                      | <i>&amp;</i> 8                                                                              | ! |

| Qy         1321         CAGCAGGACCAGTTTGACTTTGTTGAAGTTTATCGCGTCAAGAAATTCCAGTTT         1380           Db         1444         CAGCAGGACCAGTTTGACTTCACTTTTGTTGAAGTTTATCGCGTCAAGAAATTCCAGTTT         1503           Qy         1381         ACGTCGAAGCACTGAAGGACAGCGACCTCAAGGAGGGAAGAAGTTT         1440           Db         1504         ACGTCGAAGCACTCAAGGACACCTCCAAGGAGGAAGAAGCCTTT         1563           Qy         1441         ACGTCGAAGCACCTCCTCCTGCTGCTCCTCCAACAGCTTT         1563           Qy         1564         AGGCACATTTGCAGCACCCCTCCTGCTGCTGCTCCCAACAGCTCCTGGAAC         1623           Ph         1564         AGGCACATTTGCAGCACCCCCTCTGCTGCTGCTGCTCCCAACAGCTCTGGAAC         1623           Ph         1564         AGGCACATTTGCAGCACCCCCTCCTGCTGCTGCTGCTCCCAACAGCTCTGGAAC         1623           Ph         1564         AGGCACATTTGCAGCACACCCCTCTGCTGCTGCTGCTCCCAACAGCTCTGGAAC         1623           Ph         1624         TGCGACGGAGCTCTGCACACACCCCTCTGCTGCTGCTCCCACTGCAGGTTCTTGCAACACGCTGGTT         1680           Qy         1561         AGGATTTGCAGGAGAATTGAAGAATTGAAGAATTGAAGATCCAACACACAC | RESULT 9   US-09-784-810A-5   Sequence 5, Application US/09784810A   Sequence 5, Application US/09784810A   Sequence 5, Application US/09784810A   Sequence 5, Application US/09784810A   Sequence 5, Application US/0908203A1   Sequence 5, Application US/0908203A1   Sequence 5, Application Novels Parent Novels | 0y         244 TACGCTTTACAGTTCACTGTGTAAAGAGAGCACGCACGCA               |
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| 304 GAGGAAACAGACGTTCACGGGAAACATCAAGGCAGTGGAAAATGGCAGAAAATGGAAAAG 363 241 CCTTACGCTTTTACGTTCACTGTGTAAAGAGCACGCGCGCCCCTCGAAGTGGGGG 300 364 CCTTACGCTTTTACAGTTCACTGTGTAAAGAGAGCACGCCTGTGTGTTTTTTACAGTTCACTGTGTGAAGAGAGCACGCTGTGTGTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 14                                                                                                                                                                                                                                                                                                                   | CTGGAGGAGGAGGAGGACTGTATGGTTTTGAAGCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA |

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RESULT 10
US-10-876-281-5
Sequence 5, Application US/10876281
Publication No. US20050123942A1
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: NOWEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
FILE REPREMENCE: 1071-6-08
CURRENT APPLICATION NUMBER: US/10/876,281
CURRENT PILING DATE: 2004-06-24
PRIOR APPLICATION NUMBER: US/9/784,810
PRIOR APPLICATION NUMBER: 60/192,360
PRIOR PILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/191,261
PRIOR PILING DATE: 2000-03-14
PRIOR PILING DATE: 2000-03-14
PRIOR PILING DATE: 2000-03-14
PRIOR PILING DATE: 2000-03-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTING DATE: 2000-03-12
SEQ ID NO 5
LENGRITH: 1840
TACGCTTTTTACAGTTCACTGTGTAAAQAGAGCACGACGGCACCGCTGGAAGTGGGCGCAG
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; Pred. No. 0;
0; Mismatches
                                          1614
                                                        CCGAAGCCAGACTCACACAGCTGA 1524
                                          CCGAAGCCAGACTCACACAGCTGA
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Best Local Similarity 97.8%;
Matches 1490; Conservative
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US-10-876-281-5
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              APPLICANT: KOSSIGA, SOPHIA
TITLE OF INVENTION: Regulation of human Sphingosine;
TITLE OF INVENTION: Riase-Like Protein;
FILE REFERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2001-06
PRIOR FILING DATE: 2001-06-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
FRIOR OF THE                                                                                                                                                                                                                                                                                                                                                                                         tch 55.9%; Score 903; DB 10;
al Similarity 96.6%; Pred. No. 1.7e-268;
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RESULT 11 US-05-969-896-1 Sequence 1, Application US/0996986 ; Publication No. US20030125533A1

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901 TGACCTCATCCTCATCCGGAAATGCTCCAGGTTCAATTTTCTGAGATTTCTCATCAGGCA 960
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361 AGGTCAACGGACTGCGTGTTACTCCACCGTGGGCACCAGCGACGAGAAACCTCGGC
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APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Goodrich, Ryle
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Xnog, Yonghong J.
APPLICANT: Xnog, Yonghong J.
APPLICANT: Wehrman, Tom
APPLICANT: NOWEL NOWEL SOOPH SOO
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Publication No. US20040192800A1

GENERAL INFORMATION:

APPLICANT: Kossida, Sophia

TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Regulation of human Sphingosine
FILE REFERENCE: 004974.00594

CURRENT APPLICATION NUMBER: US/10/631,958

CURRENT FILING DATE: 2003-08-01

PRIOR APPLICATION NUMBER: US/09/969,896

PRIOR FILING DATE: 2001-10-04

PRIOR FILING DATE: 2001-10-04

PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: US 60/238,005

PRIOR FILING DATE: 2001-08-05

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 1

SEQ ID NO 1

LEMENT OF SECULO NO 10-06

SEQ ID NO 1

SEQ ID NO 1
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Pred. No. 1.7e-268;
0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-10-631-958-1
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Best Local Simil
Matches 946; (
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                                                                                           Length 817;
                                                                                                                         Indels
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GENERAL INFORMATION:
APPLICANT: Kossida, Sophia
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Kinase-Like Protein
FILE OF INVENTION: Kinase-Like Protein
FILE OF INVENTION: Kinase-Like Protein
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT FILING DATE: 2001-10-04
PRIOR PILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 550
                                                                            DB 19; Le..
. 4.4e-165;
0;
                                                                                         Query Match
35.3%; Score 569; DE
Best Local Similarity 100.0%; Pred. No. 4.4
Matches 569; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
FEATURE:
                            ; NAME/KEY: CDS
; LOCATION: (90)..(662)
US-10-115-635-247
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US-09-969-896-8
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                                                                                                                                                                                                                                                       136 TGCGCCGTGAGCCTGCGCGCGCGCGCTCTGCTGCCGCTGGTGGCGCGAGCCCGGGGCCC 195
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                                                                                                                                               76 ATGGGGGCGACGGGGCGCGCGGAGCCGCTGCAATCCGTGCTGTGGGTGAAGCAGCAGCGC
                                                                                                                                                                                                                    TGCGCCGTGAGCCTGGAGCCCGCGCGCTCTGCTGCGCTGGCGGAGCCCCGGGGCCC
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                                                                                                             1 ATGGGGGGGGGGGGGGGGGGGGCGGTGCTGCTGTGGGTGAAGCAGCAGCGCG
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                                                         Gaps
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US-10-631-958-8

i Sequence 8, Application US/10631958

publication No. US20040192580A1

GENERAL INFORMATION:
TILE OF INVENTION: Regulation of human Sphingosine
FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: US 60/236,005

PRIOR FILING DATE: 2001-10-06

PRIOR APPLICATION NUMBER: US 60/314,113

PRIOR FILING DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 16
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Best Local Similarity 100.0%; Pred. No. 4.8e-136;
Matches 475; Conservative 0; Mismatches 0;
29.4%; Score 475; DB 10; L
100.0%; Pred. No. 4.8e-136;
tive 0; Mismatches 0;
Query Match
Best Local Similarity 100.
Matches 475; Conservative
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| TGCGCCGTGAGCCTGGAGCCCGCGCGCGCTCTGCTGCGGCGCGCGGAGCCCGGGGCCC 195 | GGAGCCGCGCCCCCGGCGCGCGGATGCCTGCTGTATCTGAGATCATCGCCGTT 180 | GGAGCCGGCGCCCCCGGCGGATGCCTGCTCTGTGTTCTGAGATCATCGCCGTT 255 | GAGGAAACAGACGTTCACGGGAAACATCAAGGCAGTGGAAAATGGCAGAAAAAG 240 | GAGGAAACAGACGTTCACGGGAAACATCAAGGCAGTAGAAAATGGCAGAAAATGGAAAAAG<br>315 | CCTTACGCTTTTACAGTTCACTGTGTAAAGAGAGCACGACACCGCTGGAAGTGGGCG 300 | CCTTACGCTTTTACAGTTCACTGTGTGTAAAGAGACACGGCACCGCTGGAAGGGGGGGG | CAGGTGACTTTCTGGTGTCCAGAGGAGCAGCTGTGTCACTTGTGGCTGCAGACCCTGCGG 360 | CAGGTGACTTTCTGGTGTCCAGAGGAGCAGCTGTTCTTGTGGCTGCAGACCCTGCGG 435 | GAGATGCTGGAGAAGCTGACGGAGAAGCATTTACTGGTATTTATCAACCCGTTT 420 | GAGATGCTGGAGAAGCTGAGACCAGAACCAAAGCATTTACTGGTATTTATCAACCCGTTT 495 | GGAGGAAAAGGACAAGGCGATATATGAAAGAAAAGTGGCACCACTGTTCA 475 | GGAGGAAAAGGACAAGCGGATATATGAAAGAAAGTGGCACCACTGTTCA 550 |  |
|----------------------------------------------------------------|-----------------------------------------------------------|-----------------------------------------------------------|------------------------------------------------------------|----------------------------------------------------------------------|---------------------------------------------------------------|-------------------------------------------------------------|------------------------------------------------------------------|---------------------------------------------------------------|------------------------------------------------------------|------------------------------------------------------------------|--------------------------------------------------------|-------------------------------------------------------|--|
| 136 TG                                                         | 121 GG                                                    | 196 GG                                                    | 181 GA(                                                    | 256 GA(                                                              | 241 CC                                                        | 316 CC                                                      | 301 CA                                                           | 376 CA                                                        | 361 GA                                                     | 436 GA                                                           | 421 GG                                                 | 496 GG                                                |  |
| Dp<br>1                                                        | ò                                                         | 원<br>[                                                    | ò                                                          | 4G                                                                   | ò                                                             | 셤                                                           | ď                                                                | QQ                                                            | à                                                          | q <sub>Q</sub>                                                   | à                                                      | qq                                                    |  |

Search completed: September 5, 2005, 20:00:16 Job time: 1181.31 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 3, 2005, 03:56:01; Search time 17.8442 Seconds (without alignments) 1363.781 Million cell updates/sec Run on:

Title: ,US-10-631-958-2
Perfect score: 1717
Sequence: 1 PKHLLVFINPPGGKGQGKRI......KCSRFNFLRFLIRHTNQQDQ 326

Scoring table:

513545 seqs, 74649064 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:\*
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|        |       | die   |              |     | SUMMARIES            |                   |
|--------|-------|-------|--------------|-----|----------------------|-------------------|
| Result | Č     | Query |              | á   | ;                    |                   |
| 02     | score | Match | Match Length | a : | 1D                   | Description       |
| 1      | 613   | 35.7  | 687          | 4   | US-09-270-767-45874  | Sequence 45874, A |
| 8      | 999   | 33.0  | 359          | 4   | US-09-270-767-46720  | Sequence 46720, A |
| m      | 282   | 16.4  | 490          | 4   | US-10-053-510-19     |                   |
| 4      | 270.5 | 15.8  | 524          | 4   | US-10-053-510-20     | 20,               |
| 2      | 243   | 14.2  | 618          | 4   | US-09-970-516-4      | 4,                |
| 9      | 243   | 14.2  | 618          | 4   | US-09-817-676A-14    |                   |
| 7      | 236   | 13.7  | 617          | 4   | US-09-817-676A-12    |                   |
| æ      | 228   | 13.3  | 384          | 4   | US-09-949-016-7026   | Sequence 7026, Ap |
| 6      | 228   | 13.3  | 384          | 4   | US-09-796-487-3      |                   |
| 10     | 227.5 | 13.2  | 384          | 4   | US-09-970-516-2      | ς,                |
| 11     | 227.5 | 13.2  | 384          | 4   | US-09-959-897-2      | 7                 |
| 12     | 226   | 13.2  | 373          | 4   | US-09-796-487-5      | 5                 |
| 13     | 226   | 13.2  | 381          | 4   | US-09-796-487-1      | 1,                |
| 14     | 226   | 13.2  | 381          | 4   | US-09-796-487-4      | Sequence 4, Appli |
| 15     | 226   | 13.2  | 382          | 4   | US-09-970-516-6      | 9                 |
| 16     | 226   | 13.2  | 388          | 4   | US-09-817-676A-15    | 15                |
| 17     | 226   | 13.2  | 388          | 4   | US-09-796-487-2      | 7                 |
| 18     | 223.5 | 13.0  | 368          | 4   | US-10-053-510-21     | 2,                |
| 19     | 220.5 | 12.8  | 424          | 4   | US-09-796-487-8      | Sequence 8, Appli |
| 20     | 219.5 | 12.8  | 392          | 4   | US-09-796-487-6      | Ġ                 |
| 21     | 216   | 12.6  | 536          | 4   | US-09-248-796A-15859 | 158               |
| 22     | 193   | 11.2  | 204          | 4   | US-09-796-487-9      |                   |
| 23     | 181.5 | 10.6  | 403          | 4   | US-09-796-487-7      | 7,                |
| 24     | 172   | 10.0  | 299          | 4   | US-09-270-767-61405  |                   |
| 25     | 143   | 8.3   | 312          | 4   | US-09-949-016-9811   | 9811,             |
| 56     | 132   | 7.7   | 313          | 4   | US-09-107-532A-7154  | 7154,             |
| 27     | 131.5 | 7.7   | 372          | 4   | US-09-603-208A-264   | 264, 1            |

| Sequence 788, App | Sequence 3740, Ap  | Sequence 3121, Ap  | Sequence 373, App | Sequence 62339, A   | Sequence 5366, Ap   | Sequence 5133, Ap   | Sequence 6786, Ap   | Sequence 328, App | Sequence 1350, Ap  | Sequence 4774, Ap   | Sequence 3813, Ap   | Sequence 45, Appl | Sequence 37, Appl | Sequence 53, Appl | Sequence 29, Appl | Sequence 5598, Ap   | Sequence 3616, Ap   |
|-------------------|--------------------|--------------------|-------------------|---------------------|---------------------|---------------------|---------------------|-------------------|--------------------|---------------------|---------------------|-------------------|-------------------|-------------------|-------------------|---------------------|---------------------|
| US-09-205-258-788 | US-09-583-110-3740 | US-09-107-433-3121 | US-09-634-238-373 | US-09-270-767-62339 | US-09-134-000C-5366 | US-09-107-532A-5133 | US-09-107-532A-6786 | US-09-205-258-328 | US-09-710-279-1350 | US-09-134-001C-4774 | US-09-134-000C-3813 | US-09-959-897-45  | US-09-959-897-37  | US-09-959-897-53  | US-09-959-897-29  | US-09-107-532A-5598 | US-09-134-000C-3616 |
| 4                 | 4                  | 4                  | 4                 | 4                   | 4                   | 4                   | 4                   | 4                 | 4                  | ٣                   | 4                   | 4                 | 4                 | 4                 | 4                 | 4                   | 4                   |
| 119               | 294                | 315                | 283               | 160                 | 304                 | 303                 | 325                 | 293               | 316                | 324                 | 345                 | 63                | 64                | 65                | 64                | 323                 | 297                 |
| 7.5               | 7.3                | 7.3                | 6.9               | 8.9                 | 6.8                 | 6.4                 | 6.3                 | 6.3               | 6.2                | 6.2                 | 6.1                 | 6.1               | 5.9               | 5.4               | 5.3               | 5.2                 | 5.2                 |
| 129.5             | 125                | 125                | 118.5             | 117                 | 117                 | 110                 | 109                 | 108               | 106                | 106                 | 105                 | 104               | 102               | 92                | 90.5              | 89.5                | 83                  |
| œ ·               | δ.                 | စ္က                | 37                | 32                  | 33                  | 34                  | 32                  | 36                | 37                 | 88                  | 39                  | 40                | 11                | 42                | £3                | 44                  | 12                  |

## ALIGNMENTS

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43
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                   APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: 05/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46720
LENGTH: 359
                                                                                                                                                                                                                                                                                                                                                           SEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFL-----PAQHTVGSPRD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 VPSVCYANCQRCSFASSIQEQRSSLFIQEESKEA----ERNQQVETEDSHLAASEAALLR
                                                                                                                                                                                                                                                                                                                                          2 KHLLVFINPFGGKGGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKET
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Patent No. 6830881

GENERAL INFORMATION:

APPLICANT: Saba, Julie D.

APPLICANT: Fyrst, Henrik

TITLE OF INVENTION: SPHINGSINE-1-PHOSPHATE LYASE POLYPEPTIDES,

TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: 200116.402C2

CURRENT APPLICATION NUMBER: US/10/053,510

CURRENT FILING DATE: 2002-01-17

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PSSEC for Windows Version 4.0

SEQ ID NO 19
                                                                                                                                                                                                                                                                                                             80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 -RKPCRAGCFVC-----RQSKQQLEEEQKKALYGLEAAEDVE----
                                                                                                                                                                                                                                                                                   DB 4; Length 359;
                                                                                                                                                                                                                                                                              Query Match 33.0%; Score 566; DB 4; Length 35: Best Local Similarity 34.3%; Pred. No. 9e-55; Matches 124; Conservative 55; Mismatches 102; Indels
                          US-09-270-767-46720
; Sequence 46720, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
                                                                                                                                                                                                                                   ORGANISM: Drosophila melanogaster US-09-270-767-46720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-053-510-19
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US-10-053-510-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 ELPAESTAAGIRSSLPLNAGEF----HDLPEEEEGEAVLDGEQFADAISLDRSVYROHAD 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                             61 --TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGII
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                                                                                                                  Gaps
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APPLICANT: Saba, Julie D.
APPLICANT: SADA, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: PRETROBE OF USE THEREFOR
FILE REFERENCE: 200116.402C2
CURRENT FILING DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 21
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 20
LENGTH: 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 524;
16.4%; Score 282; DB 4; Length 490; 25.0%; Pred. No. 1.3e-22;
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                                                                                                            52; Mismatches 134;
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US-10-053-510-20
                                                              Best Local Similarity 25.09
Matches 104; Conservative
                                                         Similarity
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193 LVQGLSLSEWDGIVTVSGDGLLHEVLNGLLDR-----PDWEEAVKMP----VGILPC 240
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                                                                                                                                                                                                    144 PPRILILLVNPFGGRGLAWQWCKNHVLPMISEAGLSFNLIO-----TERQNHARE 192
                                                                                                                                                                                                                                                                    TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
                                                                                                                                                                                                                                                                                                                                                                    GSTDCVCYS-----TVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLG 171
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197 GLSLSEWEGIVIVSGDGLLYEVLNGLLDR------PDWEDAVRMP----IGVLPCGSG 244
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APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Kohama, Takafumi
TITLE OF INVENTION: Bxpression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 60/194,318
PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                        1 PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 243; DB 4; Length 618; 
; Pred. No. 4.6e-18; 
43; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%; Score 236; DB 4; Length 617; 29.7%; Pred. No. 2.8e-17; tive 40; Mismatches 84; Indels
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Sequence 7026, Application US/09949016

Sequence 7026, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09817676A Patent No. 6800470
                                                                       14.2%;
                                                               Query Match
Best Local Similarity 28.9*
Matches 67; Conservative
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SOFTWARE: Patentin Ver. 2.0
; ORGANISM: Homo sapiens
US-09-817-676A-14
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Best Local Similarity
Matches 66; Conserv
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Patent No. 6610534
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Dolynucleotides encoding sphingosine kinases
TITLE OF INVENTION with the polynucleotides encoding sphingosine kinases
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT APPLICATION NUMBER: US/09/970,516
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                               254 RMOSSRSCNTHIDMLNGPAPIYHSSAEYLPQEFADVISLETSINQSFRSRCDSWLSGGSR 313
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                                                                                                                       ----GLEAAE------DVEE-----WQVVCG 268
                                                                                                                                                                314 RSFYYSISESIYHSLADESEFAGLAAASLENRQONYGPASELPDLNEPLSEDQGWLVEEG 373
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Patent No. 6800470
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
APPLICANT: Soloron, Takafumi
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT APPLICATION NUMBER: US 60/194,318
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                 269 KFLAINA---TNMSCACRRSPRGLSPAAHLGDGSSDLILIRK-CSRFNFLRFL 317
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                      -----VCRQSKQQLEEE
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Matches 67; Conservative
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ORGANISM: Homo sapiens
                      RKPCRAGCF-
                                                                                                                     249 KALY----
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                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-970-516-4
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Gaps

32;

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Sequence 2, Application US/09970516

Sequence 2, Application US/09970516

Patent No. 6610534

GENERAL INFORMATION:
APPLICANT: No. 6610534artis AG

TITLE OF INVENTION: polynucleotides encoding sphingosine kinases

CURRENT APPLICATION NUMBER: US/09/970,516

CURRENT PILING DATE: 2001-10-04

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 --VVVQQGPVDAH-----LVPLE--EPVPSHWTMVPDEDFVLILALLHSHLGSEMFAAP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRIQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GSTDCVC-----YSTVGTSDAETSALHIVVGDSLA-MDVSSVHHNSTLLRYSVSLLG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 YGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRA 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
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                                                                                         human spingosine kinase-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.3%; Score 228; DB 4; Length 384; Best Local Similarity 25.9%; Pred. No. 1e-16; Matches 88; Conservative 53; Mismatches 137; Indels
     sequence Accession Number AAF73423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 RGLSPAAHLGDGSSDLILIRK-CSRFNFLRFLI-----RH 320
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                          PUBLICATION INFORMATION:
AUTHORS: Nava et al.
TITLE: Functional characterization of
JOURNAL: FEBS Lett.
                                                                                                                                                                                                                                                        DATABASE ACCESSION NUMBER: AAF73423
DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1)..(384)
                                                                                                                                                                                                                                                                                                                                                                   DATABASE ACCESSION NUMBER: AFF73423
DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1)..(384)
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                                                                                                                                                                                                       PAGES: 81-84
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                                                                                                                                                   VOLUME: 473
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Best Local
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OTHER INFORMATION: SEQ ID NO 3 is the peptide sequence of hSPHK1 in Fig. 3, corresponther INFORMATION: ading to amino acid residue 1 to 384 of Homo sapiens SPHK-1 of Ge
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASICEQ for Windows Version 4.0
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; Sequence 3, Application US/09796487
; Sequence 3, Application US/09796487
; Patent No. 6830916
; FATCHE NEPREMENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR FILING DATE: 2000-03-03
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 09/530,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 --VVVQQGPVDAH-----LVPLE--EPVPSHWTMVPDEDFVLILALLHSHLGSEMFAAP 276
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25.9%; Pred. No. 1e-16;
ive 53; Mismatches 137; Indels
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SOFWARE: Patentin version 3.1
SEQ ID NO 34
ENGTH: 384
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Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-7026
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 384
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                      TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRIQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
                                                                            GSTDCVC-----YSTVGTSDAETSALHIVVGDSLA-MDVSSVHHNSTLLRYSVSLLG 171
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14 PCRVLVLLINPRGGKGKALQLFRSHVQPLLABABI------SFTLMLTERRNHARE 62
                                                                                                                                                                                 YGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKP 228
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171 WGFIADVDLESEKYRRLGEMRFILGTFLRLAALRTYRGRLAYLPVGR-VGSKTPASP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: B11411, MAILELLAND.
APPLICANT: Richard, D'ANDREA J
APPLICANT: Richard, D'ANDREA J
APPLICANT: Jennifer, BAMBLE R
APPLICANT: Mathew, VADAS A
TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
FILE REFERENCE: PITSON=1
CURRENT APPLICATION NUMBER: US/09/959,897
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: PCT/AU00/00457
PRIOR APPLICATION NUMBER: AU PQ 0339
PRIOR FILING DATE: 1999-05-13
PRIOR PILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-16
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PALENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09959897
Patent No. 6730480
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PITSON, Stuart M
APPLICANT: Brian, WATTENBERG W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Conservative
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Best Local Similarity
Matches 64; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-796-487-5
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Sequence 5, Application US/09796487

Patent No. 6830916
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah

TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use FILE REFERENCE: 07320001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487

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LOCATION: (1)...(373)
OTHER INFORMATION: SEQ ID NO 5 is the peptide sequence of Mouse SPHKIa in Fig. 2, CC OTHER INFORMATION: SEQ ID NO 5 is the peptide sequence of Mouse SPHKIa in Fig. 2, CC OTHER INFORMATION: rresponding to amino acid residue 131 to 504 of SPHKIa of GenBank; OTHER INFORMATION: sequence Accession Number AAC61697.
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (132)..(504)
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OTHER INFORMATION: SEQ ID NO 1 is the peptide sequence of SPHK1a in Figure 1, corres
OTHER INFORMATION: ponding to amino acid residue 124 to 504 of SPHK1a of GenBank sec
OTHER INFORMATION: uence Accession Number AAC61697. SEQ ID NO 1 is equivalent to SEC
OTHER INFORMATION: ID NO 4 that is the amino acid sequence of mSPHK1a in Figure 3.
PUBLICATION INFORMATION:
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TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
FILE REFERENCE: 07320001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GSTDCVC-----YSTVGTSDAETSALHIVVGDSLA-MDVSSVHHNSTLLRYSVSLLG 171
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CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR FILING DATE: 2000-03-03
PRIOR PEPLICATION NUMBER: US 09/530,868
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/09796487; Patent No. 6830916
                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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; ORGANISM: Mus musculus
US-09-970-516-6
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Best Local Similarity
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US-09-970-516-6
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US-09-796-487-4
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NAME/KEY: MISC_FEATURE
LOCATION: (1)..(381)
OTHER INFORMATION: SEQ ID NO 4 is the peptide sequence of mSPHKla in Figure 3, correOTHER INFORMATION: SEQ ID NO 4 is the peptide sequence of SPHKla of GenBank seQTHER INFORMATION: SPONDING to amino acid residue 124 to 504 of SPHKla of GenBank seQTHER INFORMATION: quence Accession Number AF068748. SEQ ID NO 4 is equivalent to SEQTHER INFORMATION: Q ID NO 1 that is the amino acid sequence of SPHKla in Figure 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAREAL INFORMATION: Spiegel, Sarah
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use FILE REFERENCE: 0732001aa (2033957-0001)
CURRENT PAPLICATION NUMBER: 0/09/796,487
CURRENT FILING DATE: 2001-03-02
PRIOR PAPLICATION NUMBER: US 60/186,532
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR PILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PALENT NOS: 17
LENGTHARE: 18
TITLE: Molecular cloning and fuctional characterization of murine sphingosin
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13 PCRVLVLLNPQGGKGKALQLFQSRVQPFLEEAEITFKLI------LTERKNHARE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|| |: :|| || || |: :|| WGFVADVDLESEKYRRLGEIRFTVGTFFRLASLRIYQGQLAYLP----VGTVASKRP 222
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                      TITLE: kinase
JOURNAL: Journal of Biological Chemistry
VOLUME: 237
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                                                                                                                       DATE: 1998
DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124)..(504)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124)..(504)
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Patent No. 6830916
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DATE: 1998
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US-09-796-487-4
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PAGES: 237
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Best Local
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Sequence 6, Application US/09970516

Patent No. 6610534

GENERAL INFORMATION

APPLICATION OF 6610534

TITLE OF INVENTION: Induction of blood vessel formation through administration of

TITLE OF INVENTION: polynucleotides encoding sphingosine kinases

TITLE OF INVENTION UNDER: US/09/970,516

CURRENT APPLICATION NUMBER: US/09/970,516

CURRENT FILING DATE: 2001-10-04

NUMBER OP SEQ ID NOS: 6

SEQ ID NO 6
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                                                                                                                                                                                                                                                                          Length 381;
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DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDIES: (124)..(504)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC61697
DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124)..(504)
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Mouse sph Human sph Human sph Human sof

A human r

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New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous system disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g. asthma), autoimmune diseases (e.g. rheumatoid arthritis) and central and peripheral nervous system disorders (e.g. parkinson's disease). The present sequence represents the human sphingosine kinase-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human sphingosine kinase-like protein; intracellular signalling; cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma; autoimmune disease; rheumatoid arthritis; Parkinson's disease.
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            ABR82192
AAE07885
AAE02393
ABR82293
ABR82293
ABR82293
AAU09074
ABG31587
ADU09075
ADU09075
ADU09079
ABB00809
ABG3144
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N-PSDB; ABL40822
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(c) 1993 - 2005 Compugen Ltd.
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                                                                                                 3, 2005, 04:09:18
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Maximum Match 100%
Listing first 45 summaries
                                                                     sw model
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ABR56301
AAY96059
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ABB07856
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Gapop 10.0 , Gapext 0.5
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                                                                    OM protein - protein search, using
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length: 2000000000
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1717
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GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis, restenosis or ischaemia and cell proliferative disease or disorder associated with vascular diseases. SphK gene is used in gene therapy and antisense-therapy. Sphingolipids serving as signalling molecules, have recently emerged as regulators of cell growth, differentiation, diverse cell phenotypes and cell death. Activation of SphK by tumour necrosis factor (TNF)-alpha inhibits apoptosis in human endochelial cells. The present sequence is human sphingosine kinase
                                                                                                                                                                                                                                                                                        181 DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA
                                                                                                                                                                                                                                                                       1 PKHLLVPINPFGGKGOGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANOAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Platelet derived polypeptides with sphingosine kinase activity for
ovarian, breast, lung, colon, testicular, stomach and skin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, enzyme, haemostatic, sphingosine kinase 4; SPHK4; platelet transfusion; platelet stabiliser.
                                                                                                                                                                                                    Query Match 100.0%; Score 1717; DB 4; Best Local Similarity 100.0%; Pred. No. 2.3e-172; Matches 326; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOKK-) HOKKAIDO TECHNOLOGY LICENSING OFFICE (CHBI-) CHEM BIOLOGY INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLILIRKCSRFNFLRFLIRHTNQQDQ 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLILIRKCSRFNFLRFLIRHTNOODO 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR56301 standard; protein; 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-2001; 2001WO-JP008537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2001; 2001WO-JP008537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Igarashi Y, Kihara A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-354917/33.
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                                                                                                                                                                    Sequence 471 AA;
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                                                                                                                                   (SphK) protein
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                                                                                                                                                                                        GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180
                                                                                                                                                                                                                                                         DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; sphingosine kinase; SphK; restenosis; ischaemia; gene therapy; antisense therapy; cancer; sphingolipid; signalling molecule; asopticsis; cytostatic; tumour necrosis factor-alpha; TNF; atherosclerosis; lymphoma; leukaemia; vasotropic; cell proliferative disorder; vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An isolated Sphingosine kinase polypeptide useful for treating a SphK-associated disorder especially cancer, restenosis or ischemia in a human.
                                                                                                                                 9
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                                                                                                                   QQLEEEQKKALYGLEAAEDVBEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS
                                                                                                   PKHLLVFINPFGGKGOGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANOAKE
                                                                    Gaps
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                                   Length 326;
                                                                  Indels
                                 Score 1717; DB 5;
Pred. No. 1.4e-172;
                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human sphingosine kinase (SphK) protein #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLILIRKCSRFNFLRFLIRHTNOODO 326
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                                 100.0%;
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                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-514770/56.
                                                 Similarity
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N-PSDB; AAD14426.
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 Sequence 326
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                                 Query Match
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AAE07884

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The present sequence is that of human sphingosine kinase C (SKC), an enzyme that phosphorylates sphingosine to form sphingosine 1-phosphate. The sequence was deduced from that of a polynucleotide (see AAA50510) isolated from an HeLa CDNA library. The invention provides polynucleotides (see AAA50508-10) and polypeptides (see AAY96057-59) for the human sphingosine kinase (SK) homologues SKA, SKB and SKC. The colypeptides can be obtained using recombinant DNA methods, and host cells containing expression vectors including SK polynucleotides are used in a claimed method of screening for compounds that inhibit or activate human SK activity. Human SK specific antibodies, inhibitors, ligands or their analogues can be used as bloactive agents to treat inflammation or tisease including viral, bacterial or fungal infections, allergic responses, mechanical injury associated with trauma, hereditary diseases, lymphoma or carcinoma, and other conditions with activate the genes of kidney, lung, heart, lymphoid or tissues of the nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLYBINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180
    useful in e.g. chromosome and gene mapping, and detecting inflammation or
disease associated with abnormal levels of sphingosine kinase expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, enzyme; haemostatic, sphingosine kinase 4; SPHK4;
platelet transfusion; platelet stabiliser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1640.5; DB 3
Pred. No. 2.8e-164;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Sphingosine kinase 4-related protein
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96.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 96.3
Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003031627-A1
useful in e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
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                                                                                      for human sphingosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                       TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            58 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSEKKRWIGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCROSK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297
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                                                                                 The present sequence is the protein sequence for human sphingosine kins 4 (SHR4). The kinase can be used for the diagnosis and treatment of sphingosine related disorders. The kinase can also be potentially used for controlling toxicity of platelet transfusion and as a platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS
                                                                                                                                                                                                                                                                                                                                                          9 PKHLLVFINPFGGKGGKRIYERKVAPLFTLASITTDII------VTEHANQAKE
                                                                                                                                                                                                                                                                                                                                       1 PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sphingosine kinase C; SKC; human; drug screening; infection; antiinflammatory; antiallergic; anticancer; inflammation; allergy; cancer; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                     DB 6; Length 416;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                   95.5%; Score 1640.5; DB 6
llarity 96.3%; Pred. No. 2.4e-164;
Conservative 1; Mismatches 0;
  of sphingosine related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLILIRKCSRFNFLRFLIRHTNQQDQ 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 29-30; 39pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY96059 standard; protein; 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Falzone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2000; 2000WO-CA000223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human sphingosine kinase C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ALLX ) NPS ALLELIX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-572185/53
                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 314; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAAS0510
                                                                                                                                                                                                            Sequence 416 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200052173-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-1999;
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                                                                                                                                                                     stabiliser
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                                                                                                                                                                                                                                                     Query Match
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DB 3; Length 460;

281

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341

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New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous system disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 300
                                                                                                                                                                                                                                                                                                                The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g asthmá), autoimume diseases (e.g rheumatoid arthritis) and central and peripheral nervous system disorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.5%; Score 1640.5; DB 5; Length 537; Best Local Similarity 96.3%; Pred. No. 3.5e-164; Matches 314; Conservative 1; Mismatches 0; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLILIRKCSRFNFLRFLIRHTNQQDQ 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
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                                                                                                                                                                                                                                                                                 Claim 25; Fig 10; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             537
06-OCT-2000; 2000US-0238005P.
                 23-AUG-2001; 2001US-0314113P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
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                                                                                                                                  2002-340094/37.
                                                                                           Encinas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 537 AA;
                                                                                                                                                 N-PSDB; ABL40828
                                                        (FARB ) BAYER
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                                                                                             Kossida
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 셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                          The present invention relates to human sphingosine kinase 4 (SPHK4; ABE56301). The kinase can be used for the diagnosis and treatment of sphingosine related disorders. The kinase can also be potentially used for controlling toxicity platelet transfusion and as a platelet stabiliser. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKHLLVFINPFGGKGOGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human sphingosine kinase-like protein; intracellular signalling; cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma; autoimmune disease; rheumatoid arthritis; Parkinson's disease.
                                                                                                                                                                 Platelet derived polypeptides with sphingosine kinase activity for treatment of sphingosine related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                    8
                                                                                                                                                                                                                                                                                                                                                                                                             95.5%; Score 1640.5; DB 96.3%; Pred. No. 3e-164; ive 1; Mismatches C
                                  HOKKAIDO TECHNOLOGY LICENSING OFFICE CHEM BIOLOGY INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLILIRKCSRFNFLRFLIRHTNQQDQ 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human sphingosine kinase-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLILIRKCSRFNFLRFLIRHTNQQDQ
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                                                                                                                                                                                                                         Example 4; Fig 4; 39pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0S-OCT-2001; 2001WO-EP011516.
28-SEP-2001; 2001WO-JP008537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB07856 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 314; Conservative
                                                                                           Kihara A;
                                                                                                                                WPI; 2003-354917/33
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                            Sequence 481 AA;
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                                                                                         Igarashi Y,
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                                  (HOKK-)
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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2001US - 0327449P 2001US - 0327917P 2001US - 0328029P 2001US - 0328048P 2001US - 0328048P 2001US - 0328449P 2001US - 0330142P 2001US - 0330309P 2001US - 0341058P 2001US - 0343659P 2001US - 0343659P 2001US - 0349575P 2001US - 0349575P 2001US - 0349575P 2002US-0381042P. 2002US-0381642P. 2002US-0383656P. 2002US-0383831P. 2002US-0373815P. 2002US-0373817P. 2002US-0373826P. 2002US-0373884P. WO2003029424-A2 09-0CT-2001; 09-0CT-2001; 15-0CT-2001; 17-0CT-2001; 18-0CT-2001; 22-0CT-2001; 24-0CT-2001; 24-0CT-2001; 29-0CT-2001; 29-0CT-2001; 20-0CT-2001; 20-0CT-2001; 20-0CT-2001; 20-0CT-2001; 19-APR-2002; 19-APR-2002; Homo sapiens 02-OCT-2002; 17-APR-2002; 22-APR-2002; 09-OCT-2001; 19-APR-2002; 19-APR-2002; 05-OCT-2001; 10-APR-2003 

(CURA-) CURAGEN CORP.

2002US-00262511.

2002US-0391335P

2002US-0374977P. 2002US-0381037P.

2002US-0381038P

Smithson G, Millet I, reyman, ..., Bllerman A, ...., Catterton E; Patturajan M, Spytek KA, Edinger SR, Ellerman A, ..., Catterton E; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Raetelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Shimkets RA, Rothenberg ME, Spaderna SK;

N-PSDB; ADA05679

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1; Page 135; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the bove vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above (2) propeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for

use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating cor preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a companient of immunomodulator, cytostatic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian and antilipaemic activities, and can be used in gene therapy. The collypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic cid isorders such as diabetes or obesity, infections, cachexia, cancer, characters und and disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various cytobes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the Gaps 11; DB 6; Length 537; 0; Indels Score 1640.5; DB 6 Pred. No. 3.5e-164; 1; Mismatches 0; 95.5%; Best Local Similarity 96.3 Matches 314; Conservative present invention. Sequence 537 AA; Query Match 

240 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120 238 GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180 300 QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 418 09 GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 1 PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK QQLEEEQXKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 61 179 121 239 299 181 241 ઠે 셤 ઠે ď ò g ઠે ద ઠે

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셤 8 엄 RESULT

ADJ96664 standard; protein; 537 AA ADJ96664 

ADJ96664;

(first entry) 06-MAY-2004 Human lipid kinse KIAA1646 protein SeqID 121.

kinase; human; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease; eardiovascular disease, brain; neuronal associated disease; metabolic; inflammatory disorder; cytostatic; neuroprotective; immunomodulator; antiinflammatory; enzyme; lipid kinse; KIAA1646.

Homo sapiens

WO2004006838-A2.

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anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
              NOVX; metabolic disorder; diabetes; obesity; infectious disease;
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2001US-0341058P
2001US-0343626F
2001US-0349573P
2001US-0349573P
2002US-0373260P
2002US-0373817P
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2002US-0381037P
2002US-0381042P
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2001US-0327435P.
2001US-0327449P.
2001US-03299.
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MALYANKAR U M.
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EDINGER S R.
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PEYMAN J A.
KEKUDA R.
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CATTERTON E.
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                                                                     wasting disorder.
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09-0CT-2001;
12-0CT-2001;
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17-0CT-2001; 2
18-0CT-2001; 2
22-0CT-2001; 2
24-0CT-2001; 2
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16-MAY-2002;
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01-NOV-2001;
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29-MAY-2002;
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(PENA/)
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                 human;
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(PEYM/)
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(JUJJ/
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(SPYT/
(EDIN/
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 This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to buman tyrosine and serine/threonine protein kinases (FTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions in be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polypeptide sequence is a human kinase protein sequence
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                                                                                                                                                                            New nucleic acid molecule encoding a kinase polypeptide, useful for preparing a composition for treating diseases or disorders, e.g., cancer, or neurological, immunological or inflammatory disorders.
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Pred. No. 3.5e-164;
1; Mismatches 0; Indels 11;
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                         15-JUL-2003; 2003WO-US021730.
                                                     15-JUL-2002; 2002US-0395632P
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Matches 314; Conservative
                                                                                                          Whyte D, Manning G,
                                                                                                                                     WPI; 2004-122753/12
                                                                                (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 537 AA;
22-JAN-2004.
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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX by supplementing the patient our polymucleotides may be used to treat disorders associated with decreased complements of the patient our control or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypeptides and complementary sequences may also be used as DNA probles in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of crestorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. Complements and antagonists and antagonists and antagonists and antagonists and antagonists and complements. The anti-NOVX polypeptide antibodies, agonists and antagonists and antagonists and classified and polymucleotide expression and activity of NOVX polypeptides and polymucleotide expression of NOVX in samples.

Colypeptides and bolymucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, and the various dyslipidaemias, metabolic disorders associated with chronic diseases and various cancers. They may also be used as an
                                                                                                                                                            Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
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                                                                                                                                                                                                                                                                                                                                                                                                      Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
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Pred. No. 3.5e-164;
1; Mismatches 0;
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                                            EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
BERGHS C.
DIPIPPO V A.
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Best Local Similarity
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BERG/)
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New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous system
The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g. sthma), autoimmune diseases (e.g. theumatoid arthritis) and central and peripheral nervous system disorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSTDCVCXSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKHLIVFINPFGGKGÇGKRIYERKVAPLFTLASITTDII------VTEHANQAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                         Human sphingosine kinase-like protein; intracellular signalling; cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma; autoimmune disease; rheumatoid arthritis; Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1640.5; DB 5
Pred. No. 3.7e-164;
1; Mismatches 0;
                                                          326
                                                                                     444
                                                                                                                                                                                                                                              Human sphingosine kinase-like protein.
                                                                         DILIRKCSRFNFLRFLIRHTNQQDQ
                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; Fig 11; 120pp; English.
                                                                                                                                                          ABB07857 standard; protein; 562
                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-2001; 2001WO-EP011516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-OCT-2000; 2000US-0238005P.
23-AUG-2001; 2001US-0314113P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.5%;
96.3%;
                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
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N-PSDB; ABL40828.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 562 AA;
                                                                                                                                                                                                                                                                                                                                                                WO200228906-A2
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                   03-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kossida S,
                                                                                                                                                                                      ABB07857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allergy,
disorder.
                                                                                     419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
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                                                           301
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                                                                                                                                RESULT 10
                                                                                                                                               ABB07857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a human ceramide kinase designated hCERKI. The invention relates to hCERKI, nucleic acids encoding it, expression vectors and host cells containing hCERKI nucleic acids, the recombinant production of hCERKI and antibodies specific for hCERKI. The invention also encompasses methods of isolating hCERKI from samples, the use of hCERKI in drug screening, and the use of hCERKI incleic acid sequences in gene therapy. hCERKI mediates the APP-dependent 1-phosphorylation of cramides and can be used to screen for therapeutic and preventive agents for a wide range of disorders. Such disorders include neurological disease, inflammation, human immunodeficiency virus (HIV) infection, type 2 diabetes, obesity, sepsis, arteriosclerosis and cancer
                                                                                                                                                                         GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, ceramide kinase; hCERK1; drug screening; gene therapy; neurological disease; inflammation; human immunodeficiency virus; hIV infection; type 2 diabetes; obseity; sepsis; arteriosclerosis; cancer; neuroprotective; antiinflammatory; anti-HIV; antidiabetic; anorectic; antibacterial; antiseptic; antiarteriosclerotic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ceramide kinase gene and the enzyme encoded by it for screening substances as drugs for neurological, inflammatory and other disorders.
                                              QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1632.5; DB 5
Pred. No. 2.5e-163;
2; Mismatches 1;
                                                                                                                                                                                                                                                                          Claim 1; Page 54-57; 61pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                       AAM49115 standard; protein; 537 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-2000; 2000JP-00178039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ceramide kinase hCERK1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-JP004889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.7%;
Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kono K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-179513/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABA96945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 537 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200196575-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugiura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2001
                                                                                                                                                                                                384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM49115;
                                                                                                 324
  264
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238
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                                                                                                                                                                                                                                       359 QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 418
                                                                     GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180
                                                                                                                                                                               358
                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiatehmatic; antidiabetic; antiinflammatory; antipsoriatic; antirhyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an isolated PRO nucleic acid (I). Also described: (1) a vector comprising (I); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) tused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a
                    TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA
                                                                                        GPTDCVCYSTVGTSDAETSALHI VVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDI IK
                                                                                                                                               DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK
                                                                                                                                                                 DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK
                                                                                                                                                                                                                  QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS
TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schoenfeld J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO protein sequence SEQ ID NO:1224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1224; 3009pp; English.
                                                                                                                                                                                                                                                                                          DLILIRKCSRFNFLRFLIRHTNOODO 326
                                                                                                                                                                                                                                                                                                               DLILIRKCSKFNFLRFLIRHTNQQDQ 444
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                                                                                                                                                                                                                                                                                                                                                                                                                      ADP55248 standard; protein; 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-2003; 2003WO-US034381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-2002; 2002US-0422472P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virucide; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark H,
TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI: 2004-376182/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADP55247.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP55248;
                                   179
                                                                     121
                                                                                                         239
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                                                                                                                                                                                                                                                                                                                              419
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 61
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composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the antagonist of the polypeptide or an antibody that binds to the polypeptide in combination with a carrier; (8) an article of manufacture comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a mammal; (10) a method of baving the polypeptide; (11) a method of diagnosing an immune related disease or an inflammatory immune response in a mammal; (12) a method of identifying a compound that inhibits or minics the activity of or expression of a gene encoding a PRO polypeptide; and (13) a method of stimulating the immune response in a mammal. The PRO sequences have antialracysic, antianeamic, antiatheritic, antialabenic, antialmaency, antipsoriatic, antiantheumatic, antidiaberic, antialmaency, antipsoriatic, antiatheritic antidiaberic immunostimulant, immunosupressive, muscular, nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid (1) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune response. The present sequence represents a human containing an immune response. The present sequence represents a human containing an immune response. The present sequence represents a human containing an immune response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
             $$$$$$$$$$$$$$$$$$$$$$$$$$$
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1; 178 120 238 240 300 418 GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180 9 TLYEINTDSYDGIVCVGGDGMFSEVLHGVIGRTQQSAGIDPNHPRAVLVPSTLRIGIIPA QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS QOLEEBEKKALYGLENAEEVEEWOYTCGKFLAINATNMSCACPRSPGGLSPPAHLGDGSS PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRIQRSAGVDQNHPRAVLVPSSLRIGIIPA DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK Indels 87.6%; Score 1503.5; DB 8; 86.8%; Pred. No. 1.1e-149; ive 19; Mismatches 13; 326 DLILIRKCSRFNFLRFLIRHTNOODO Best Local Similarity 86.8 Matches 283; Conservative ٦ 61 179 121 239 181 299 241 359 301 419 ò a ઠે g ઠે g ઠ ద δ 셤 셤 ઠે

antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy. Human therapeutic protein - SEQ ID 1291 Ş ADS11054 standard; protein; 536 (first entry) Homo sapiens 16-DEC-2004 ADS11054; RESULT 13 

WO2004080148-A2

23-SEP-2004

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The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoletic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic protein of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 EVITEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
                                                                                                       Z, Ma Y;
Weng G, Zhou P;
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLITEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 EDRRIGEHVGPGENAGGLDGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 VPSSLRIGIIPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNST
                                                                                                                                                                                                       New polynucleotide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1414.5; DB 8; Length 536;
Pred. No. 2.9e-140;
2; Mismatches 0; Indels 67;
                                                                                                       , Wehrman T, Wang
Ghosh M, Xue AJ,
                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 1291; 718pp; English.
                                                                                                       ۵,
                                                                                                       Zhang J,
Wang J,
30-SEP-2003; 2003WO-US030720.
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                                  02-OCT-2002; 2002US-0416186P
                                                                                                   Asundi V, Ren F,
Chen R, Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 80.0
Matches 276; Conservative
                                                                                                                                                      WPI; 2004-668857/65.
                                                                    (NUVE-) NUVELO INC
                                                                                                                     Chen R,
                                                                                                                                                                            N-PSDB, ADS10370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 536 AA;
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                                                                                                                       Wang D,
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Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder. 326 CRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHTWQQDQ 443 CRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHTNQQDQ Novel human diagnostic protein #13532. ABG13541 standard; protein; 746 18-FEB-2002 ABG13541; 399 282 RESULT 14 ABG13541 g 8

281

279 LLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYBGTVSFLPAQHTVG 338

LLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVG

162

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SPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCA

222 339

SPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCA 398

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WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels 61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1400.5; DB 4; Length 746; Pred. No. 1.4e-138; 4; Mismatches 0; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 43900; 103pp; English.
                                                                                                                                                                                                                                                                                                Tang YT;
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80.8%;
                                                                                                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                    30-MAR-2001; 2001WO-US008631
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                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
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                                            WO200175067-A2
  Homo sapiens.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal catvity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and according to the trial to the casess biodiversity and according to the trial to the control of th
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288 GLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHTNQQDQ 326
                                                                                                                        636
                                                                     GLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHTNQQDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #13534.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG13543 standard; protein; 727
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23-AUG-2000; 2000US-00649167.
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61 GPKQMPAKGQVCRLPLLKLEASGLLRSEGRTCRSPDRLCSSCSIVCVGGDGMFSEVLHGL 120
                                                                 121 -----GSTDCVCYSTVGTSDAETSALH 142
                                                                                                                           181 FTLVTALGCEHRSHPHFMDEDRRTGEHVGPGENAGGLDGSTDCVCYSTVGTSDAETSALH 240
                                                                                                                                                       143 IVV------GDSLAMDVS 154
                                                                                                                                                                   155 SVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFL 214
                                                                                                                                                                                                               301 SVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRNLGLARYDFSGLKTFLSHHCYEGTVSFL 360
                                                                                                                                                                                                                                                         215 PAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEMQVVCGKFLAIN 274
TEHANQAKETLYEINIDKYDGCYTAHSRMPCPRNHSPAGKAAPVQGVGYGEGQRAFPWEP 60
                                                                                                                                                                                                                                                                                       ATNWSCACRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHTNQDQ 326
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Search completed: September 3, 2005, 04:37:38 Job time : 74.5726 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 3, 2005, 04:25:44; Search time 104.512 Seconds (without alignments) 2753.633 Million cell updates/sec Run on:

Title: Perfect score:

US-10-631-958-11 3025 1 HEAANGPAPLGVRAPPAWRT......QLVRLFARGIEENPKPDSHS 562 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           | 44     | nescribinou |            | Q8k4g7 mus musculu | Q6zpk5 mus musculu | Q6nx59 homo sapien |        |        |        |        | -      | Q6usk2 arabidopsis | Q6h6hl oryza sativ |        |        | O9tzil caenorhabdi |        |        | O65419 arabidopsis |        |        |        |        |        |        |        | Q7qip4 anopheles g |        | Q9vyy8 drosophila | Q9vzw0 drosophila | 014159 schizosacch | Q9nra0 homo sapien | Q6ayb2 rattus norv |
|-----------|--------|-------------|------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------|--------------------|--------------------|--------|--------|--------------------|--------|--------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------|-------------------|-------------------|--------------------|--------------------|--------------------|
| SUMMERIES | Ę      | T           | CEK1_HUMAN | CEX1_MOUSE         | Q6ZPK5             | Q6NX59             | Q6GLV1 | Q6GMF3 | Q9VNA6 | 095815 | Q7PRA8 | Q6USK2             | <b>Фенен1</b>      | Q6UZF6 | Q9LU45 | Q9TZI1             | Q949C3 | Q8L7L1 | 065419             | Q8H350 | Q9LRB0 | Q9FHL3 | Q6ZP59 | Q84S01 | Q94HY9 | Q7XCS9 | Q7QIP4             | Q7XN57 | Q9VYY8            | O9VZW0            | 014159             | SPH2_HUMAN         | Q6AYB2             |
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|           | Query  | nengtii     | 537        | 531                | 409                | 339                | 572    | 485    | 687    | 487    | 410    | 608                | 700                | 532    | 533    | 549                | 586    | 485    | 1240               | 480    | 763    | 732    | 280    | 446    | 757    | 757    | 685                | 748    | 641               | 661               | 458                | 654                | 616                |
| *         | Query  | marcii      | 95.5       | 80.3               | 65.9               | 59.9               | 56.6   | 49.4   | 26.5   | 25.2   | 22.0   | 21.4               | 20.5               | 19.6   | 19.3   | 18.8               | 15.9   | 14.1   | 13.8               | 12.3   | 12.2   | 11.6   | 11.3   | 11.0   | 10.9   | 10.9   | 10.7               | 10.4   | 10.3              | 6.6               | 9.6                | 9.5                | 8.8                |
|           | 94020  | arone       | 2888       | 2428               | 1904               | 1811               | 1713   | 1495.5 | 801.5  | 763    | 6.999  | 648                | 620.5              | 594    | 583.5  | 567.5              | 480    | 428    | 417.5              | 373.5  | 370.5  | 350    | 343    | 331.5  | 330.5  | 330.5  | 323                | 314.5  | 310.5             | 298.5             | 291.5              | 277                | 267.5              |
|           | Result |             |            | 7                  | m                  | 4                  | Ŋ      | 9      | 7      | 80     | 6      | 10                 | 11                 | 12     | 13     | 14                 | 15     | 16     | 17                 | 18     | 19     | 20     | 21     | 22     | 23     | 24     | 25                 | 56     | 27                | 28                | 29                 | 30                 | 31                 |

| =          | _          | Q96hv8 homo sapien | Q96gkl homo sapien | Q8n632 homo sapien | mus r  | Q86kf9 dictyosteli |        | Q8cil5 mus musculu | O88885 mus musculu | Q74ze3 ashbya goss |        | Q642f6 rattus norv | Q7jm91 caenorhabdi |
|------------|------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|
| ω          | 7          |                    |                    |                    |        |                    |        |                    |                    |                    |        |                    |                    |
| SPH2_MOUSE | SPH1 HUMAN | 096H <u>V</u> 8    | Q96GK1             | Q8N632             | 088886 | Q86KF9             | Q912N3 | Q8C115             | 088885             | Q74ZE3             | 006147 | Q642F6             | Q7JM91             |
| ч          | ч          | ~                  | 7                  | N                  | ~      | 7                  | 7      | ~                  | ~                  | N                  | ~      | ~                  | 0                  |
| 617        | 384        | 384                | 398                | 470                | 388    | 624                | 381    | 382                | 504                | 579                | 687    | 383                | 423                |
| 8.8        | 8.7        | 8.7                | 8.7                | 8.7                | 9.8    | 8.5                | 8.4    | 8.4                | 8.4                | 8.4                | 8.2    | 8.1                | 8.1                |
| 267.5      | 264.5      | 264.5              | 264.5              | 264.5              | 260    | 257.5              | 254    | 254                | 254                | 253.5              | 248.5  | 245.5              | 245.5              |
| 32         | 33         | 34                 | 35                 | 36                 | 37     | 38                 | 39     | 40                 | 41                 | 42                 | 43     | 44                 | 45                 |

## ALIGNMENTS

| G                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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| T.1  HUMAN STANDARD; PRT; 537 AA.  GGKZH HUMAN GGRZH GOUGES; 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 44, Last sequence update) 10-OCT-2003 (Rel. 44, Last sequence update) 10-OCT-2003 (Rel. 44, Last sequence update) 11-OCT-2003 (Rel. 46, Last sequence update) 11-OCT-2003 (Rel. 46, Last sequence update) 12-OCT-2003 (Rel. 46, Last sequence update) 13-OCT-2003 (Rel. 46, Last sequence update) 13-OCT-2004 (Rel. 46, Last sequence update) 13-OC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Ross<br>Ross<br>R.M<br>ing                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |         |
| (hCERK)  1eostom  o.  35200;  Spieg  g and  g A.K.,  e A.K.,  o.P.,  J.,  J.,  J.,  J.,  d.D.M.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | e in                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :       |
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| kinase) (b dae; Homo. dae; Homo. bc.M201535 ekura H., r cloning r, Babages. Bugases. Gonor F Connor F                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | [1] i                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Se de   |
| kin be ar ak                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Phi<br>Smi<br>Gwil                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :       |
| debr<br>A4/<br>A4/<br>Abin 138/<br>Cull Cull Cull Cull Cull Cull Cull Cull                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | D. Y. S. Y. | ig<br>S |
| T.1  HUMAN STANDARD; PRT; 537 AA.  GEKLHWAN STANDARD; PRT; 537 AA.  10-OCT-2003 (Rel. 42, Created)  10-OCT-2003 (Rel. 42, Last sequence update)  OS-JUL-2004 (Rel. 44, Last annotation update)  Ceramide kinase (EC 2.7.1.138) (Acylsphingosine kinase) (hCERK  Kinase 4) (LK4).  Name-CERK; Synonyms=KIAA1646;  Homo sapiens (Human).  Homo sapiens (Human).  COT-2003 (Rel. 44, Last annotation update)  NORDI TaxID=9606;  IL)  SEQUENCE FROM N.A., AND CHARACTERIZATION.  SEQUENCE FROM N.A., AND CHARACTERIZATION.  SEQUENCE FROM N.A., AND CHARACTERIZATION.  SEQUENCE FROM N.A., Shimizugawa T., Minekura H., Spi  (Caramide kinase, a novel lipid kinase. Molecular cloning and functional characterization.";  IL)  SEQUENCE FROM N.A.  A search for lipid kinases.";  SEQUENCE FROM N.A.  A search for lipid kinases.";  SEQUENCE FROM N.A.  A search for lipid kinases.";  SEQUENCE FROM N.A.  MEDLING=2005146;  Bagguley C., Bailey J., Barlow K.F., Bates K.N., Bababage A.K.  Bargully C., Bailey J., Barlow K.F., Bates K.N., Bargely O.P.  Bird C.P., Blakey S.B., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burlow N.S., Kimberley A.M., King A.,  Closgy S.M., Coobley V.B., Corelier R.B., Connor R., Consy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Daws Concry D., Corby N.R., Coville G.J., Cox A.V., Davis J., Daws Concry D., Corby W.B., Kershaw J., Kimberley A.M., King A.,  Burnill W.D., Burren M.B., Kershaw J., Kinberley A.M., King A.,  Hunt S.B., Hall-Taming W., Matthews L.H., Worthews L.H., Worthews L.H., Worthews L.H., Mashreghi-Mohammadi M., Matthews L.H., Morthews L.H., Mashreghi-Mohammadi M., Matthews L.H., Morthews L.H., Mashreghi-Mohammadi M., Morthews L.H., Matthews L.H., Mat                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | sey<br>wils                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Kak     |
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| en B. 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F. C. A. Sr. P. Dit.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |         |
| T.1  HUWAN CEKI, HUWAN CEKI, HUWAN CEKI, HUWAN CEKI, HUWAN CEKI, HUWAN  OBDED:  10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 44, Last sequence update) 11-OCT-2005 (Rel. 44, Last sequence update) 11-OCT-2005 (Rel. 44, Last sequence update) 12-OCT-2005 (Rel. 44, Last sequence update) 13-OCT-2005 (Rel. 44, Last sequence update) 14-OCT-2005 (Rel. 46, Last sequence update) 15-OCT-2005 (Rel. 46, Last seq                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | r.V.<br>Bay<br>Ird<br>Y.D.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ğ       |
| SACTOR SA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Se A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 988     |
| Created) Last seq Last seq Last ann 7.1.138) AA1646; AA1646; AA1646; AA1640  O CHARAC  D CHARAC  In H., S AVEL 11pj AA100."; 94-23300  Collins ANDECOUGH  ANDECOUGH  CONTILE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Skuc<br>Skuc<br>Skuc<br>Skuc<br>Ber<br>Ber                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :       |
| STANDARD; (Rel. 42, Created) (Rel. 42, Last sec (Rel. 44, Last and sec (Human). (Human                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | A. W.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ન<br>국  |
| STANDARD;  Q9UGES;  1. 42, La  203;  A.A. AND                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | H.K<br>H.K<br>Gon<br>gon<br>rrd                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sak     |
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                                              | e wa    |
| LT 1  HUMAN  CBEXL HUMAN  CBEXL HUMAN  CBEXL HUMAN  COST_2003 (Rel. 42, Created)  10-OCT_2003 (Rel. 44, Last sequ  OS-JUL_2004 (Rel. 44, Last ann  Ceramide kinase (EC 2.7.1.138)  Kinase 4) (LK4).  Name=CERK; Synonyms=KIAA1646;  HOMO sapiens (Human).  Eukaryota; Metazoa; Chordata; (Muman).  Eukaryota; Muman, Kono K., Liu H., Si  Sugiura M., Kono K., Liu H., Si  Sugiura M., Kono K., Liu H., Si  Sugiura M., Kono K., Liu H., Si  Submitted (APR-2002) to the EMI  Submitted (APR-2002) to the E                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Ser<br>Ser<br>Wall                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :       |
| T 1  HUMAN  CEKIL HUMAN  OBTITO; 09B  10-OCT-2003  10-OCT-2003  10-OCT-2003  CERMINAM  CETAMINAM  HOMO SADION  HOMO SADION  HOMO SADION  HOMO SADION  EUKATYOCA; 1  BUTILINESOU  CODITOY D., 1  EUKATYOCA; 1  BUTILINESOU  CODITOY D., 1  EUKATYOCA; 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | L L C C C C C C C C C C C C C C C C C C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ω<br>N  |
| T 1 HUWAN QGRCTTO; Q9 HU-OCT -200 GOS-ULL-200 HOMO SADIO [1] [1] HOMO SADIO [2] HOMO SADIO [3] HOMO SADIO [4] HOMO SADIO [5] HOMO SADIO [6] HOMO I TAXID [7] HOMO SADIO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Lips<br>C. C. C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | שלט     |
| HUMAN CEKI H 10-CCT- 10-CCT- 110-CCT- 110-CCT- 110-CCT- 110-CCT- 110-CCT- 110-CCT- 1110-CCT- 111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | der in                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | BOU     |
| RESULT 1  CEKI HUMAN  ID CCEKI  DAT 08-07  DD 08-07  DD 08-07  OS-07  Names  OS Kinas  Names  OS Kinas  NOBI  RR SEQUE  RR SEQ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | S S S S S S S S S S S S S S S S S S S                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Ξ       |
| THE STATE OF THE S                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ***                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | \$      |

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Shifteni A., Shibuya K., Yoshitaki Y., Aoki N., Mitauyama S., Dor., Dr. A., Dr. A., Dr. A., Dr. B. B., Chen F., Chu. Cachered. J., December S., Do., Dr. A., D
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                                                                                                                                                                                               241 TDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGATGAAEPLQSVLWVKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV
                                                                                                                                                                                86 EETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLR
                                                                                                                                                                                                                                                                 121 EMLEKUTSRPKHLLVFINPFGGKGGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
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                                                                                                              26 MGATGAAEPLOSVLWVKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV
                                                                                                                                                                                                                                                EMLEKLTSRPKHLLVFINPFGGKGOGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
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                                                                                                                                                                                                                                                                                                                                                                                                                                           326 EKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQ
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                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ceramide Kinase (EC 2.7.1.138) (Acylephingosine Kinase) (mCERK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22075121; PubMed=11956206; DOI=10.1074/jbc.M201535200;
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"Ceramide kinase, a novel lipid kinase. Molecular cloning and
                                                 DB 1; Length 537;
                                                                               0; Indels
               59977 MW; 3DBFC0ED8D679F7F CRC64;
                                             95.5%; Score 2888; DB 1; L 100.0%; Pred. No. 1.6e-227; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          531 AA
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 DAGKC
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                                                                                 Conservative
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132 2
537 AA;
                                                                  Similarity
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TISSUE=Brain;
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                                                                                 Matches 537;
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                  SEQUENCE
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Baldarelli R., Hill D.P., Bult C., Huma D.M., Quackenbush J.,
Baldarelli R., Hill D.P., Bult C., Huma D.M., Quackenbush J.,
Balda L., Mrandangi A., Shrughai H., Bardar C. Counins S.,
Balda L., Mrandangi T., Britcher C. P., Britcher C. Counins S.,
Balda L., Mrandangi T., Mrandawa W., Jacken I.J., Jarvis E.D.,
Randa A., Kawaji H., Kawasaw Y., Wadizeris R.M., King B.L.,
Randali A., Kawaji H., Kawasaw Y., Wadizeris R.M., King B.L.,
Randalin A., Kawaji H., Mrandawa W., Jacken I.J., Jarvis E.D.,
Randalin A., Kawaji H., Marandaw W., Jacken I.J., Jarvis E.D.,
Randalin A., Kawaji H., Marandaw W., Jacken I.J., Jarvis B.L.,
Randalin A., Kawaji H., Marandaw W., Jacken I.J., Jarvis B.L.,
Randalin A., Kawaji H., Marandawa W., Jacken I.J., Jarvis B.L.,
Randalin A., Kawaji H., Marandawa W., Jacken I.J., Jarvis B.L.,
Randalin A., Kawaji H., Marandawa W., Jacken I.J., Jarvis B.L.,
Randalin A., Kawaji H., Marandawa W., Jacken I.J., Jarvis B.L.,
Randalin A., Kaman W., Takenbar W., Jacken I.J., Shinadawa W.,
Randalin A., Kawaji H., Kawai U., Marandawa W., Jakan J.,
Randalin A., Kawai W., Takenbar W., Shinadawa W.,
Randalin A., Kawai W., Jacken W., Sandalin W.,
Randalin M., Sandalin W., Jacken W., Sandalin R.,
Randalin M., Sandalin W., Jacken W., Sandalin R.,
Randalin M., Sandalin W., Marandawa W., Sakana I.,
Randalin M., Sandalin W., Sandalin W., Marandawa W., Sakana I.,
Randalin M., Sandalin W., Sandalin W., Marandawa W., Sakana I.,
Randalin M., Sandalin W., Marandawa W., Sakana I
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                                                                         61 EEKDDCEKHASSGRWHKMENPFAFTVHRVKRVRHHRWKWARVTFWSADEQLCHLWLQTLR 120
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                  1 MGAMGAAEPLHSVLWVKRRRCAVSLEPARALLRWWRSPEPGPSAPGADARSVLVSEIIAV
                                                                                                                                                                                            EKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQ
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                                                           EETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLR
                                                                                                                  146 EMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
                                                                                                                                                                           206 YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS
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Saga Y., Nagase T., Ohara O., Koga H.;
"Prediction of the coding sequences of mouse homologues of KIAA gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              III. the complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones trandomly sampled from size-fractionated libraries.";
DNA Res. 10:167-180(2003).
EMBL. AK129416; BAC26225.1; .
GO, GO:0004143; F:diacylglycerol kinase activity; IEA.
GO, GO:0007205; P:protein kinase C activation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Wouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NORI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEE 554
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
MXIAA1646 protein (Fragment).
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Pred. No. 3.8e-147;
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Pfam; PF00781; DAGK cat; 1.
ProDom; PD005043; DAGKC; 1.
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TISSUE=Embryonic tail;
PubMed=14621295;
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80.3%; Score 2428; DB 1; Length 531; 85.1%; Pred. No. 7e-190; ive 33; Mismatches 46; Indels

Best Local Similarity 85.14 Matches 450; Conservative

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05-JUL-2004
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TISSUB-Peripheral Nervous System;

TISSUB-Peripheral Nervous System;

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jozdan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muray D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muray D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                   SRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDK 212
                                                                                                      272
                                                                                                                        66 YDGIVCVGGDGMFSEVLHGVIGRTQQSAGIDPNHPRAVLVPSTLRIGIIFAGSTDCVCYS 125
                                                                                                                                                                        TVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLG 332
                                                                                                                                                                                            186 LVRYDFSGLKTFLSHQYYEGTLSFLPAQHTVGSPRDNKPCRAGCFVCRQSKQQLEEEEEKK 245
                                                                                                                                                                                                                                                                                                               ALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCS 452
                                                                                                                                                                                                                                                                                                                                ALYGLENAEEVEEWQVTCGKFLAINATNMSCACPRSPGGLSPPAHLGDGSSDLILIRKCS 305
                                                                                                                                                                                                                                                                                                                                                                                 RFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSSH 512
                                                                                                                                                                                                                                                                                                                                                                                                   LARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQKK 392
                                                     SRPKHLLVPINPFGGKGOGKRIYEKTVAPLFTLASITTEIIITEHANOAKETLYEINTDS
                                                                                                      YDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYS
 Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEE 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSCTCSASRSSWNCDGEVMHSPAIEVRVHCQLVRLFARGIEE 407
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Last annotation update)
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 26; Mismatches
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TISSUE=Peripheral Nervous System;
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Matches 352; Conservative
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Strausberg R.L., Feingold E.A., Grouse I.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse I.H., Derge J.G.,

Rausner R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Rausner R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Batchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Raplatchenko L., Judin T.B., Toshiyuki S., Carninci P., Prange C.,

Rapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Ruhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

and mouse CDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                     LHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKT
                                                                                                                                                                                                                                                                                                                                                                         LHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 EEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRH
                                                                                                                                                                                                                                                                                                    1 MFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 FLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDV
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                      Query Match 59.9%; Score 1811; DB 2; Length 339; Best Local Similarity 100.0%; Pred. No. 1.2e-139; Matches 339; Conservative 0; Mismatches 0; Indels C
EMBL; BC067255; AAH67255.1; -.
GO; GO:0004143; F:diacylglycerol kinase activity; IEA.
GO; GO:0007205; P:protein kinase C activation; IEA.
InterPro; IPR001206; DAGKC.
                                                                                                                           37780 MW; A4C2ACDFF2E6F3D0 CRC64;
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Last annotation update)
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(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
                                                                          InterPro; IPR001206; DAGK
ProDom; PD005043; DAGKc;
SEQUENCE 339 AA; 37780
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NCBI_TaxID=8355;
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SEQUENCE FROM N.A.
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Name=MGC84197;
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Name=MGC81777
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                                                                                                                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                                        12 LCSVLSVKROSCEVTLDPGRSILS-WRELRPRHGRERSRPGICLTRVLHOTRGLVNRFTR
                                                                                                                                                                                                                                                                                                                                                                                                                                         AVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVSLLGYGFYGDVLKGSEKNRWLGPARYDVSGFKTFLTHHCYEGSVSFQPAKWVLGSPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNGLSPAAHLADGSADLILVRKCSRLDFLRHLIRHTSNKDOFDFPFVEVYRVKNFQFTPK
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                                                                                                                                                                                                                                                                                                                                                           FWCPBEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 RKPCRAGCFVCRQSKQQLEEEQKKALYGLBAAEDVEEWQVVCGKFLAINATNMSCACRRS
                                                                                                                                                                                                                                                          Gaps
                                     MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                              35 LQSVLWVKQQRCAVSLEPARALLRWWRSPGPGAG----APG----APG----
                                                                                                                                                                                                                                    Query Match 56.6%; Score 1713; DB 2; Length 572; Best Local Similarity 58.4%; Pred. No. 2.6e-131; Matches 320; Conservative 81; Mismatches 117; Indels 3
                                                                                                                TISSUE-Brain;

Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC074350; AAH74350.1; -.
GO; GO:0004143; F:diacylglycerol kinase activity; IEA.
GO; GO:0007205; P:protein kinase C activation; IEA.
InterPro; IPR01206; DAGKc.
Pfam; PP00781; DAGK cat; 1.
                                                                                                                                                                                                         SM00046; DAGKC; 1.
CE 572 AA; 64899 MW; E3D22DB2C93B5B77 CRC64;
Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                     Dev. Dyn. 225:384-391(2002).
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KLFARGIE 558
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                   SEQUENCE FROM N.A.
                                                                                                        SEQUENCE FROM N.A.
                                                                             initiative.
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MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altaener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Schmutz J., Marra M.A.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Richardson P., "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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55.3%; Pred. No. 1.3e-113;
ive 82; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO74110; AAH74110.1;
GO; GO:0004143; F:diacylgiycerol kinase activity; IEA.
GO; GO:0007205; P:protein kinase C activation; IEA.
InterPro; IPR001206; DAGKc.
Pfam; PF00781 DAGK cat; 1.
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SEQUENCE 485 AA; 54874 MW; E7C30C87AE52214F CRC64;
   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                Xenopus laevis (African clawed frog)
   27,
27,
27,
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05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                         MGC81777 protein.
                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
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485 AA.

PRT;

PRELIMINARY;

QGGMF3 QGGMF3;

RESULT 6 Q6GMF3

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Query Match
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RECUBERCE FROW N.B.

RECUBERCE R.A. Gorayne J.D.;

RECUBERCE R.A. Gorayne J.R.;

RECUBERCE R.A. Gorayne J.R.;

RECUBERCE R.A. Gorayne J.R.;

RECUBERCE R.A. Gorayne R. Gorayne J.D.;

RECUBERCE R.A. Gorayne R. Gorayne J.D.;

RECUBERCE R.A. Gorayne R. Gorayne J.D.;

RECUBERCE R.A. Gorayne R. Gorayne R.C.;

RECUBERCE R.A. Gorayne R. Gorayne R.C.;

RECUBERCE R.A. Gorayne R. Gorayne R.C.;

RECUBERCE R.A.;

RECUBERCE R.A.
KHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKYDG 215
                           217
                                                         IVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVG 275
                                                                                                                   276 TSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLAR 335
                                                                                                                                                                            YDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQLEEEQKKALY 395
                                                                                                                                                                                                                                                     GLE-AAEDVEEWOVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRF 454
                 Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAX-2000 (TrEMBLrel. 13, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
CG16708-PA (CG16708-pb)
0RFNames=CG16708;
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                           158
                                                         216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 VTFWCPEEQLCHLWLQTLREMLEKLT---SRPKHLLVFINPFGGKGQGKRIYERKVAPLF 183
Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDIJNE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Taminker J.S., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter C.,
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                                                                                                                                                                                                                                                                                                                              MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgon A., George K.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C. Weinstock G., Scherer S.E., Wars E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Harris N.L., Richter J.S., Ge Grey A.D., Drysdale R.A., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.5%; Score 801.5; DB 2; Length 687; 31.3%; Pred. No. 1.3e-56; ive 97; Mismatches 206; Indels 129;
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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Flymase; Frgmio03715; CG16708.
GO: 0048102; P: Partophagic cell death; IEP.
GO; GO:0035071; P:salivary gland cell death; IEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Pfam; PF00781; DAGK cat; 1.
SMART; SM00046; DAGKc; 1.
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SEQUENCE FROM N.A.
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ARYDFSGLKTFLSHHCYEGTVSFL------PAQHTVGSPRD-----RKPCRAGC 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQPITPPEEMTAHSS---STEFSSWNCDGEVVTDLDITMRSHCQLIEVFMRGPHSYSKP 464
                                                                                                                                                                                                   ||:| |:|:|:|:|| |:|:|| | |:|:|| | |:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:
                                                                                                                                                                                                                                                                                                                                                      241 QRCSFASSIQEQRSSLFIQEESKEA----ERNQQVETEDSHLAASEAALLRPRPRPGRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------EWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIR
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   DGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYST
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
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STRANT=BEST;
Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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(TrEMBLrel. 26, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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Live 59; Mismatches 140;
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Name=ENSANGG0000008356;
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Y. C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/Genbank/DDBJ databases.
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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Last annotation update)
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GO; GO:0048102; P:autophagic cell death; IEP.
GO; GO:0035071; P:salivary gland cell death; IEP.
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1-DEC-2001 (TrEMBLrel. 19,
1-MAR-2004 (TrEMBLrel. 26,
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SMART; SM00046; DAGKc; 1.
SEQUENCE 487 AA; 53711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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ORFNames=CG16708;
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                                                                                                                                                              399 AAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLR
                                                                                                                                                                                                                                        FLIRHTNQ-QDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 WLMKSSGEDRYLGQHGDIEEVSSSCW----SSIIMQPKLESKLKF-----SD
               --HHNSTL---LRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTV
                                                                                     SFLPAQ-----HT----VGSPRDRK-PCRAGCFVCRQSKQQLEEEOKKALYGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative ceramide kinase.

Name-P0519E06.23; Synonyms=OJ1003 B06.39;
Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 700;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005006; BAD25578.1; -.
EMBL; AP004676; BAD2537.1; -.
GO; GO:0004143; F:diacy1glycerol kinase activity; IEA.
GO; GO:0007205; P:protein kinase C activation; IEA.
InterPro; IPR001206; DAGKc.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Matches 193; Conservative
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                                                                       VSSVHH-------NSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARY 336
                                                                                                                                                 DFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQKKALYG 396
                                                                                                                                                                      TQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMD 295
                                                                                                                                                                                                                                            131 LAAFTEGHMDLQTCQSWMDQLNYSLIKEVERPRNLLVFVHPKSGKGNGSKVWE-TVSKIF
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                   TWMDCGIDIKYP-AYLPKPNIPIGVIPAGSTDTVACCLNGTTDIKTCIIHIILGQHSGLD
                                                                                           397 LEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 VPVSEIIAVEETDV------HGKHQGSGKWQKMEKPYAFTVHCVKRARRH--RWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 WAQVTFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGGGKRIYERKVAPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 TLASITTDIIVTEHANQAKETLYEI---NIDKYDGIVCVGGDGMFSEVLHG-LIGRTQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-2295668; PubMed=14563678; DOI=10.1101/gad.1140503; Liang H., Yao N., Song J.T., Luo S., Lu H., Greenberg J.T.; Caramides medulate programmed cell death in plants."; Genes Dev. 17:2636-2641(2003).

EMBL; AY362552; AA062904.1; -. GO; GO:0007143; F: Giacylglycerol kinase activity; IEA. GO; GO:0007205; P: Prototein kinase C activation; IEA. InterPro: JRN001206; DAGKC.

Pfam. PRO071206; DAGKC.
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31.6%; Pred. No. 4.2e-44;
ive 68; Mismatches 188; Indels
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Last annotation update)
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Matches 182; Conservative
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Name=CERK;
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77 RPAGDSKYDLLCKERFIELKDIFSVKLKRRCSVKQQRSGTLLGITLFICLKKEQNKLKNS 136
                                                                                                    QVTFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGGGKRIYERKVAPLFTL 185
                                                                                                                                         137 TLDLINLSEDHCDIWFRQFKKILAGFPNRPKSLKILLNPQSHKKEATQVYYEKVEPLLKL 196
                                                                                                                                                                                                                                 245
                                                                                                                                                                                                                                                                   246 HPRAVLVP--SSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNS 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHTNQQDQFDFTFVEVYRVKK 482
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similarity to unknown protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=20181125; PubMed=10718197;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. X. Seque truces of the regions of 3,076,755 bp covered by sixty Pl and Ti
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E 533 AA; 60153 MW; 1B851C7606B03E0E CRC64;
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DNA Res. 7:31-63(2000).

EMBL; AB023044; BAA97392.1; -.

GO; GO:0004143; F:dlacylglycerol kinase activity; IEA.

GO; GO:0007205; P:protein kinase C activation; IEA.

InterPro; IPR001206; DAGKC.
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Best Local S
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   KVKTKVIVTQRAGHAYDTLASLSDKDLKKFDGVIAVNTINACLSLFDIKHHNYKMSARPE 272
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                                                                                                                                                                                                                                                                                                                                                                 512 HQNRHRKTICRTNCLICKGTSTSEQNSEDENPDS---SRTACETPKWYWSKGRPLSVGAA
                                                                                                                               273 NTLSYDPQSAASGHKSMLIFYCFIINNMKCQEHRNNDLSNSELTGDDANAISGSSNTPDD
                                                                                                                                                                                                                                    CYSTVGTSDAETSALHIVVGDSLAMDVSSV-----HHNSTLLRYSVSLLGYGFYGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 GSPRDRKP-CRAGCFVCR---QSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINAT
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                      68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                causes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuson M., Marfany G., Gonzalez-Duarte R.;
"Mutation of CERKL, a novel human ceramide kinase gene, autosomal recessive retinitis pigmentosa (RP26).";
Am. J. Hum. Genet. 74:128-138(2004).
EMBL, AY357073; AAR13670.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 AA; 59602 MW; C73E590F7C25EED1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0004143; Fidiacylglycerol kinase activity; I GO; GO:0007205; P:protein kinase C activation; IEA. InterPro; IPR001206; DAGKC.
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Name=CERKL;
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                                                                                                                                                                                               HGLIGRTQRSAGVD
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Best Local Similarity
Matches 159; Conserv
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PubMed=14681825;
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WormBase; WBGene00020398; T10B11.2.
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                         131 LAAFTEGHMDLQTCQSWMDQLNYSLIKEVERPRNLLVFVHPKSGKGNGSKVWE-TVSKIF 189
                                                                                       TLASITTDIIVTEHANQAKETLYEI---NIDKYDGIVCVGGDGMFSEVLHG-LIGRTQ-- 237
                                                                                                               250 LPPSPSDSFNSVQSRGSSSVPEPGDEVHETDQKEHYP---LLPDSVQEVMNFRIEDPDHP 306
                                                                                                                                                                                                                                                                     -----RIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSV-----HHNSTL 305
                                                                                                                                                                                                                                                                                              307 FSSERPRFGLIPAGSTDAIVMCTTGARDPVTSALHIILGRKLFLDAMQVVRWKTASTSTI 366
                                                                                                                                                                                                                                                                                                                                                           ---LRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQ-- 360
                                                                                                                                                                                                                                                                                                                                                                                  -----HT------VGSPRDRK-PCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEW 406
  WAQVTFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427 NSKASLHTRSKTWPFRNTTRSEKILCRANCKICNS----KVGWNSASTTLNPCPEKTRW 481
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Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFL 457
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STRAIN=Bristol N2;
Minx P., Kemp K.,
"The sequence of C. elegans cosmid T10B11.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF0989993; AAC67466.1; -.
PIR; T33517; T33517.
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein T10811.2.
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MEDLINE=99069613; PubMed=9851916;
WormBase Consortium;
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Submitted (JUN-2003)
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 VIHGLIGRIORSAGVDONHPRAVIVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIV 287
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                                                                                                                                                                                                                                                                                                                                                                                                               172 KRIYERKVAPLFTLA-SITTDIIVTEHANQAKETLYEINIDKY---DGIVCVGGDGMFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                          407 QVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHT--
                                                                                                                                                                                                                                    Gaps
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MEDLINE=21329048; PubMed=11435398; DOI=10.1101/gr.GR-1617R;
MAyer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T.,
Buesterhoeft A., Stiekema W., Entian K.D., Terryn N., Lemcke K.,
Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W.,
Bevan M., Bancroft I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Conservation of microstructure bewtween a sequenced region of the genome of rice and multiple segments of the genome of Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                    61;
                                                                                                                                                                              Length 549;
                                                                                                                                                                                                                                    Indels
WormPep; T10B11.2; CE18241.
InterPro; IPR001206; DAGKC.
Pfam: PF00781; DAGK cat; 1.
Hypothetical protein.
SEQUENCE 549 AA; 62425 WW; DE95737555534EEB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C875ERIPDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464 GGKOLYELD-PSLNCYRVTKWSY-----OPDADOEDPG---
                                                                                                                                                                        18.8%; Score 567.5; DB 2; 30.8%; Pred. No. 1.4e-37; ive 91; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            523 SWNCDGEVLHSP---AIEVRVHCQLVRLFAR 550
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EMBL; AJ307662; CAC39069.1; -.
                                                                                                                                                                        Query Match
Best Local Similarity 30.8%
Matches 139; Conservative
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21;
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                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                               Query Match 15.9%; Score 480; DB 2; Length 586; Best Local Similarity 26.8%; Pred. No. 2.2e-30; Matches 152; Conservative 81; Mismatches 173; Indels 162;
InterPro; IPR001206; DAGKc.
ProDom; PD005043; DAGKc; 1.
Hypochetical protein.
SEQUENCE 586 AA; 64892 MW; 1C45DFBB670E1E22 CRC64;
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Search completed: September 3, 2005, 04:43:18 Job time : 106.512 secs

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Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630056D11 product:DA59H18.2 (NOVEL PROTEIN SIMILAR TO HUMAN, MOUSE, YEAST, WORM AND PLANT (PREDICTED) PROTEINS) (FRAGMENT) homolog (Homo sapiens), full insert sequence.
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AGENCOURT
UI-HF-BNO
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                               BX552302
CNC265312
BCN245312
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BP274786
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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BX952312
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CCK603033
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CCK603033
BP3749990
CCK364327
CCK36437
CCK3643
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Mus musculus (house mouse)
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Mus musculus
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CK000755 AGENCOURT
BQ057191 AGENCOURT
CK000525 AGENCOURT
CK000525 AGENCOURT
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
Lof 60,770 full-length CDNAs
Lotture 420, 563-573 (2002)
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Yoneda,Y., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer 20530913
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/db_xref="raxon:10090"
/clone="A630056D10"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Fissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Adenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please vist our web site for further details.

URL:http://genom.gsc.riken.jp/
URL:http://fancom.gsc.riken.jp/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                      The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
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/protein_id="BAC31157.1"
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/strain="C57BL/6J"
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PNHPRAVLVPSTLRGIIPAGSTDCYCYSTVGTNDAFTSALHIIGDSLAJIDVSSVHY
HNTLLRXSVSLLGYTGGIIPAGSTCOCYCYSTVGTNDAFTSALHIIGIGDSLAJIDVSSVHY
HNTLLRXSVSLLGYFTGDLIKDSEKKRWMGLIVRYDFSGLKYFFLSHQYYEGTLSFLPA
QHTVGSPRDNKPCRAGCFVCRQSKQQLEBEBKKALYGLENNEEMEBWQYTCGKFLAIN
EVYRNKKFHFTSKHVBDBNDSKEGEBKKALYGLENNEEMEBWQDPFTFV
BVYRVKKFHFTSKHVBDBNDSKEGERQKFGKICKDRPSCTCSASRSSWNCGGEVMHS
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Conservative:
Mismatches:
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                                     1.09e-219
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                                                Pred. No.:
Alignment
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792

733

CDS

FEATURES

| KEYWORDS<br>SOURCE<br>ORGANISM                                           | REFERENCE<br>AUTHORS                                                     | TITLE<br>JOURNAL<br>MEDLINE<br>PUBMED                                          | REFERENCE<br>AUTHORS<br>TITLE                                            | JOURNAL<br>MEDLINE<br>PUBMED | REFERENCE<br>AUTHORS                                                     | !                                                                           | TITLE<br>JOURNAL<br>MEDLINE                                                   | PUBMED<br>REFERENCE<br>AUTHORS                                           | TITLE<br>JOURNAL<br>REFERENCE<br>AUTHORS                     | TITLE<br>JOURNAL                                                         | REFERENCE<br>AUTHORS                                         |                                                                      |                                                                      | TITLE<br>JOURNAL                                      |                                                                | COMMENT                                                           |
|--------------------------------------------------------------------------|--------------------------------------------------------------------------|--------------------------------------------------------------------------------|--------------------------------------------------------------------------|------------------------------|--------------------------------------------------------------------------|-----------------------------------------------------------------------------|-------------------------------------------------------------------------------|--------------------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------------------|--------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------|----------------------------------------------------------------|-------------------------------------------------------------------|
| 262 ProAlaGlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGluThr 281<br> | 282 SeralaLeuhisIlevalValGlyAspSerLeuAlaMetAspValSerSerValhisHis 301<br> | 302 AsnSerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspIle 321<br>:::::: | 322 IleLysAspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeu 341<br> |                              | 362 ThrValGlySerProArgAspArgLysProCysArgAlaGlyCysPheValCysArgGln 381<br> | 382 SerLysGlnGlnLeuGluGluGluGluGlnLysLysAlaLeuTyrGlyLeuGlualaalaGlu 401<br> | 402 AspvalGluGluTrpGlnValvalCysGlyLysPheLeuAlaIleAsnAlaThrAsnMet 421<br>::::: | 422 SerCysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGly 441<br> | SerSerAspLeulleLeulleArgLysCysSerArgPheAsnPheLeuArgPheLeulle | 462 ArgHisThrAsnGlnGlnAspGlnPheAspPheThrPheValGluValTyrArgValLys 481<br> | LysPheGlnPheThrSerLysHisMetGluAspGluAspSerAspLeuLysGluGlyGly | 502 LysLysArgPheGlyHislleCysSerSerHisProSerCysCysCysThrValSerAsn 521 | 522 SerSerTrpAsnCysAspGlyGluValLeuHisSerProAlaIleGluValArgValHis 541 | 542 CysGlnLeuValArgLeuPheAlaArgGly1leGluGluAsnPro 556 | 557 LysProAspSer 560<br>            <br>1693 AAGCCCAGGAGC 1704 | RESULT 2<br>AKO52269 AKO52369 4248 hn mRNA linear HTC 01-ADR-2004 |
| දු දු                                                                    | දු දු                                                                    | දු දු                                                                          | දු දු                                                                    | දු දු                        | දි දි                                                                    | දි සි                                                                       | & g                                                                           | දු පු                                                                    | දු අ                                                         | & a                                                                      | 중<br>음                                                       | දු පු                                                                | & g                                                                  | දු දු                                                 | è 4                                                            | AK05                                                              |

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Es dachi,J., Alzawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Intoh,M., Kagawa,T., Kagawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Komno,H., Kouda,M., Nakamira,M., Nishi,K., Nomura,K., Numazaki,A., Murata,M., Ohsato,N., Okazaki,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Takeda,Y., Tanaka,T., Tomaru,A., Takahashi,F., Takaku-Akahira,S., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Li Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 210-0045, Japan (E-mail:genome-resegneriken.jp, Well-inttp://genome-gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komo, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togwa, Y., Izawa, M., Ohara, E., Watshikayi, K., Yongawa, Y., Itanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs
Nature 470, 1410, 163-573 (2002)
6 (bases 1 to 4248)
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                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                           Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
HTC; CAP trapper.
Mus musculus (house mouse)
                                                                                     Mus musculus
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FEATURES

HTC 03-APR-2004

linear

4248 bp

AK052269

LOCUS

ACCESSION VERSION

Mus musculus 13 days embryo hart cDNA, RIKEN full-length enriched library, clone:D330016D08 product:DA59H18.2 (NOVEL PROTEIN SIMILAR TO HUMAN, MOUSE, YEAST, WORM AND PLANT (PREDICTED) PROTEINS) (FRAGMENT) homolog [Homo sapiens], full insert sequence. AK052269.1 GI:26342491

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1687
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         LeuPheThrLeuAlaSerIleThrThrAspIleIleValThrGluHisAlaAsnGlnAla
                                                 LysGluThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIleValCysValGlyGly
                                                                                                                      AspGlyMetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGly
                                                                                                                                   GACGGCATGTTCAGCGAGGTGCTGCATGGGGTGATTGGGAGGACGCGCAGAGCAGAGCGCTGGT
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260. 1855
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Matches:
Conservative:
Mismatches:
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                                       xref="FANTOM_DB:D330016D08"
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        organism="Mus musculus"
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                   'mol_type="mRNA"
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BQ054406 1059 bp mRNA linear EST 29-MAR-2002
AGENCOURT 6771237 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5803668
5', mRNA Sequence.
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    GGCGGAGATGGTATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGG
                                                                                                                                                                        301 GARACCICGGCGCIGCAIAICGIIGITGGGGACICGCIGGCCAIGGAIGIGICCICAGIC 360
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NIH-WGC http://mgc.noi.nih.gov/.
                                                                                     260 IlelleProAlaGlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAla
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                                               GCCGGGGTCGACAGAACCACCCCCGGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGA
                                                                                                             241 ATCATTCCCGCAGGGTCAACGGACTGCGTGGTTACTCCACCGTGGGCACCAGCGACGCA
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                               AlaGlyvalAspGlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGly
                                                                                                                                              GluThrSerAlaLeuHisIleValValGlyAspSerLeuAlaMetAspValSerSerVal
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Homo sapiens cDNA clone IMAGE:5502281
                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: AFCC
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12140 row: c column: 18
High quality sequence stop: 665.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1063)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mismatches:
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AGENCOURT_6418742 NIH_MGC_67 Ho
5', mkNA sequence.
BM479389 GI:18528431
EST.
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JOURNAL
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/tissuc_type="lymphona, cell line"
/clone lib="NIH MGCpape-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lymph; Vector: poTB7; Site_1: XhoI; Site_2: SecRI; CpNR made by Oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BUU63738 1078 bp mRNA linear EST 02-APR-2002 AGENCOURT_6873251 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5925382 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1078)

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2096 row: p column: 23
High quality sequence stop: 640.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/organism="Homo sapiens"
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/lab_host="hylloB (phage-resistant)"
/clone_lib="NIH MGC_90"
/clone_
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                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nh.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llni.gov
Plate: LLCM2040 row: a column: 13
High quality sequence stop: 601.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5803668"
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1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg, 31 RanloAO7 Bethesda MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: James Martin, University of Iowa

CDNA Library Preparation: Wh Bento Soares, University of Iowa

CDNA Library Preparation: Wh Bento Soares, University of Iowa

CDNA Library Preparation: Wh Colone Library Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be

found through the I.M.A.G.E. Consortium/Libra at:

Clone distribution: MGC column: 20

High quality sequence stop: 656.

S. 1. 797

Location/Qualifiers

J. 1. 797

Adb xref=raxon:960s"

Adb xref=raxon:9
                                                                                                                      797 bp mRNA linear EST 26-NOV-2003
AGENCOURT 16363467 NIH MGC 221 Homo sapiens cDNA clone
CK000755 5', mRNA sequence.
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11H-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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/tissue_type="lymphoma, cell line"
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/clone_lib="NIH MGC_99"
/clone_lib="NIH MGC_99"
/note="Organ: lymph, Vector: pOTB7; Site_l: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/KhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
li RT [Life Technologies). Note: this is a NIH_MGC
Library."
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                 /organism="Homo sapiens"
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Plate: LLCM2062 row: 1 column:
High quality sequence stop: 535.
Location/Qualifiers
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I (Dases 1 to 1047)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
Cloud through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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// mol type="mRNA"
// db_xref="texon:960"
// db_xref="texon:960"
// clone="InMAGE:3070859""
// lab host="DH10B TonA"
// clone="Lib-WIH MGC_221"
// note="Organ: mixed; Vector: pYX-A8c; Site 1: EcoRI;
// note="Ordan: mixed; Vector: primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according tomRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-A8c vector. Average insert size 4-5Kb. Adaptors 5' (AATTCGGCACGAGG(3) and 5' and 5' d
(CCTCGTGCCG(3) a. 3' Linker sequence - GCGCCCTCAGAGGC T18. Sequencing primers 3' end: T3 promoter primer 5' d
(ATTAACCCTCACTAAAGGAN) 3' . 5' End: T7 promoter primer 5' d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 713)

NH-MGC http://mgc.nci.nih.gov/.

I (bases I to 713)

L (brighlished (1999)

Office of Cancer Genemato, Ph.D.

Office of Cancer Genemato, Ph.D.

Office of Cancer Genemato, Ph.D.

Office of Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Martin, University of Iowa cDNA Library Preparation: M Bento Sorses, University of Iowa cDNA Library Preparation: The I.M.A.G.E. Consortium (Libri)

DNA Sequencing by: Agencourt Bioscience Corporation clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libri at: http://image.llnl.gov

Plate: NDAM1075 row: a column: 22 High quality sequence stop: 689.

High quality sequence etop: 689.
                                                                                                                                                                                                                                                                                                                                                                                            CK000525
AGENCOURT 16369000 NIH MGC 221 Homo sapiens cDNA clone
IMAGE:30708597 5', mRNĀ sequence.
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PheVal-CysArgGlnSerLysGlnGlnLeuGluGlu--GlnLysLysAlaLeuTyr
                                                               alleAsnAlaThrAsnMetSerCys-AlaCysArgArgSerProArgGlyLeuSer---P
                                                                                                                                                                                           GlyLeuGluAlaAlaGluAspValGluGluTrpGlnValValCys-GlyLySPheLeuAl
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AGENCOURT_14552675 NIA Human HI Embryonic Stem Cell cDNA Library (Long) Homo sapiens cDNA clone IMAGE:30426593 5', mRNA sequence. CD655311.1 GI:31895467
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(TAATACGACTCACTATAGGG)3'. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC Library"
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372 CysArgAlaGlyCysPheValCysArgGlnSerLysGlnGlnLeuGluGluGluGlnLys 391
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This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001). [PMID: 1154199]) from WAO1 cell line. Undifferentiated human ES cell line WAO1/HI was obtained from WiCell Research Institute, Inc., Wadison, Wi, cultured according to their instructions, on MEF feeders. They formed according to their instructions, on MEF feeders. They formed colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UFF, TERT, SOX2, CX43 and CX45, They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FIT3, SSEA-1, TUBB3, NES, GFRP, and EDWES. When confluent (18-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRIZOl Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:11544199]) Double-stranded cDNA8 were synthesized with an Oligo(dT) primer [Invitrogen:
                                                                                                   undividual Association (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Irrene Ginis and Mahendra Rao, NIA
CDNA Library Preparation: Yulan Pico and Minoru Ko
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC lone distribution information
can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: NDAMSIZ row: k column: 18
High quality sequence stop: 673.
I. .820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:30426593"
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(Long)"
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 820)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Conservative:
Mismatches:
Indels:
Gaps:
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CF135528 732 bp mRNA linear EST 09-SEP-2003 UI-HP-BNO-amf-g-10-0-UI.rl NIH MGC_50 Homo sapiens cDNA clone IMAGE33090211 5', mRNA sequence.
511
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                                                                                                                                   ---ACCCTCTGCTGCTGCACGC---TCTCACAGCTCTG---GACTGCGACGGAGTCTG--- 777
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
GATGAGGACAGCGACCTCAAGGAGGGGAAGAGCGCCTTGGGCACAT---TGCAGCAGC
                                                                                                                                                                                                               532 HisSerProAla -- - IleGluValArgValHisCysGlnLeuValArg 546
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US-10-631-958-11 (1-562) x CD655311 (1-820)

Query Match: DB:

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/mol trype="mcMon"
/db xref="taxon:9606"
/clone="lunAgs:3090211"
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(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Standt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                       University of Iowa 135 MEBRF, Iowa City, IA 52242, USA Tel: 319 315 8260
Fax: 319 315 8260
Fax: 319 315 8260
Fax: 319 315 8260
Fax: 319 316 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Louis Staudt
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfi.html
Seq primer: pXx-5.
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                                              Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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Genome Res. 6 (9), 791-806 (1996)
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/db xref="Taxxon:10090"
/db xref="Taxxon:10090"
/clone="IMAGE:6835595"
/tissue type="whole brain"
/dev stage="embryo 12.5dpc"
/lab_host="mbryo 12.5dpc"
/lab_host="bh108 (T1 phage resistant)"
/clone lib="NHH BMAP_F10"
/clone located between the Not I site and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCAGGAC. This library was created for the University lows Brain Anatowny Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 758)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Nutional Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CHA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be thttp://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
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PheThrPheValGluValTyrArgValLysLysPheGlnPheThrSerLysHisMetGlu
                                                                            429 TTCACTTTTGTTGAAGTTTTATCGCGTCAAGAAATTCCAGTTTACGTCGAAGCACATGGAG
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CB246749
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Location/Qualifiers
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Mus musculus
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EST.
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421
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 653)
Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
Fobo,G., Han,M. and Wiemann,S.
Unpublished (2003)
Contact: MIPS
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/clone_lib="781 (synonym: hlcc4)"
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cDNA-collection"
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                                                                                                          Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp781L11183) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysThrPheLeuSerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHis
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Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
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sapiens (human)
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Mismatches:
Indels:
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program coordinator."
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88.49%
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Best Local Similarity:
Query Match:
DB:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

B. 1 (Bases I to 1017)

B. 1 (Bases I to 1017)

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

High quality sequence stop: 570.

High quality sequence etop: 570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ879739 1017 bp mRNA linear EST 16-AUG-2002
AGENCOURT 7981067 Lupski_dorsal_root_ganglion Homo sapiens cDNA
clone_IMAGE:6185601 5', mRNA sequence.
                                                                                                                        ValGluGluTrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSer 422
                                                                                                                                                                                                   CysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySer 442
                                                                                                                                                                                                                                                              363 TGTGCTTGTCGCCGGAGCCCCAGGGGCCTCTCCCCGGCTGCCCACTTGGGAGACGGGTCT 422
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                                  ThrPheLeuSerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThr
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/organism="Homo sapiens"
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BQ879739.1 GI:22271747
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Homo sapiens
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AUTHORS
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                                                                                                                                                                                                                                                           EST 16-MAY-2004
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I (bases I to 661)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.

Control human Es cell growth and differentiation

Nat. Blotechnol. 22 (6), 707-716 (2004)
                                                                                                      Ly8PheGlnPheThrSerLy8HisMetGluAspGluAspSerAspLeuLy8GluGlyGly
                                                                       482 AAATTCCAGTTTACGTCGAAGCACATGAGGATGAGGACAGCGACCTCAAGGAGGGGGGG
                                                                                                                                                                linear EST 105', mRNA sequence
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                           mRNA
CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geron Corporation
230 Constitution Drive, Menlo Park, CA
Tel: 650 473 7656
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 661 Std Error: 0.00.
Location/Qualifiers
                                                                                                                                                                                                                                                      661 bp
17000532197874 GRN_EB Homo sapiens
CN296312
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/mol_type="mRNA"
/db_xref="taxon:9606"
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EST.
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/lissue_type="heart, pooled"
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/cloon=lib="hulf MGC_234"
/cloon=lib="hulf MGC_234"
/note="Organ: heart; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from pooled heart tissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (Tri-reagent method). CDNA was primed using oligo-dT primer:
5.-pGACTAGTTCTAGATCGCAGCGCCCC(T)25-3' and cloned into the EcoRV/Not1 sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.2 kb. This primary library is normalized (non-normalized primary library is NIH MGC_233) and was constructed by Express Genomics (FrederIck, MD). Note: this is a NIH_MGC library."
                                                                   AGENCOURT 17899852 NIH MGC 234 Rattus norvegicus cDNA clone
IMAGE:7193195 5', mRNA sequence.
                                                                                                                                                                                                                                      Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Daniela 13.9.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Profurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15055 row: b column: 09
High quality sequence stop: 657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 VallysGlnGlnArgCysAlaValSerLeuGluProAlaArgAlaLeuLeuArgTrpTrp
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646 CCCCCCGGGCTGTGCTGCTCCCCAATAGCCCTTCCGGATTGGGAATCATTCCC 699
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Mismatches:
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/mol_type="mRARA"
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/clone="IMAGE:7193195"
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                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
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                                                                                                    5'-GACTAGTTCTAGATCCCGAGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified, Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValThrPheTrpCysProGluGluGluGlnLeuCysHisLeuTrpLeuGlnThrLeuArgGlu 146
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Not1; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyAlaThrGlyAlaAlaGluProLeuGlnSerValLeuTrpValLysGlnGlnArgCys
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 3, 2005, 04:10:49; Search time 24.8463 Seconds (without alignments) 2176.332 Million cell updates/sec Run on:

US-10-631-958-11 3025 1 HEAANGPAPLGVRAPPAWRT.....QLVRLFARGIEENPKPDSHS 562 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | hypothetical prote | hypothetical prote |        | ч     |        | _      |       |     | conserved hypothet | conserved hypothet | hypothetical prote | involved in polyke | conserved hypothet | hypothetical prote | hypothetical prote | hyp    | multidrug resistan | cathepsin Q (EC 3. | fibroblast growth | hypothetical prote | protein B0272.5 [i | | | | | | | | |
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| SUMMARIES | ID            | T33517             | T05162             | T38776 |       | T19707 | 867059 |       | •   |                    |                    | T16422             | AH1528             |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    | A89978 |                    | JC7183             | JC1450            | T18688             |                    |
|           | Length DB     |                    |                    | 458 2  | 687 2 |        |        |       |     |                    |                    |                    |                    | 295 2              |                    |                    | •                  | 433 2              |                    |                    | 345 2              |                    |                    |                    |        |                    | 343 2              |                   | •                  | 973                |
| 940       | Query         | 8                  | 13.8               | ٠.     | 8.2   | 8.1    |        | 6.3   | ٠   | 4.9                | 4.5                | 4.5                | 4.3                | 4.3                | 4.2                | ٠                  | 4.1                | •                  | •                  | 3.8                | 3.7                | •                  | 3.5                | 3.4                | 3.4    | •                  | •                  | •                 | 3.3                | 3.3                |
|           | Score         |                    | 417.5              | 291.5  | 248.5 | 245.5  | 210.5  | 189.5 | 176 | 147                | 136.5              | 136                | 130.5              | 129                | 126.5              | 125.5              | 125.5              | 122.5              | 115.5              | 114                | 112                | 111.5              | 105                | 103.5              | 102.5  | 102                | 102                | 100               | 66                 | 66                 |
|           | Result<br>No. | -                  | 7                  | e      | 4     | S      | 9      | 7     | 80  | 0                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24     | 25                 | 56                 | 27                | 28                 | 29                 |

| hypothetical prote<br>protein C23F12.1 | hypothetical prote<br>probable membrane<br>conserved hypothet | hypothetical prote conserved hypothet hypothetical arguments | hypothetical proce<br>conserved hypothet<br>indoleacetamide hy                 | probable ClpA/B pr<br>hypothetical prote<br>ornithine decarbox | ubiquitin carboxyl<br>hypothetical prote |
|----------------------------------------|---------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------------------------|----------------------------------------------------------------|------------------------------------------|
| T18686<br>B89608                       | T15571<br>S60932<br>F72386                                    | H70861<br>A82377<br>G71901                                   | E64975<br>A86842<br>B25493                                                     | A83589<br>B83973<br>T37671                                     | T40647<br>B75125                         |
| 000                                    | 0 0 0                                                         | 000                                                          | 9 6 6                                                                          | 000                                                            | 7 7                                      |
| 1973                                   | 2305<br>1511<br>304                                           | 309<br>708<br>338                                            | 300<br>300<br>400<br>500<br>500<br>500<br>500<br>500<br>500<br>500<br>500<br>5 | 850<br>349<br>432                                              | 337                                      |
|                                        | <br>                                                          | 999                                                          |                                                                                |                                                                | 3.0                                      |
| 9 9 9                                  | 98.5<br>96.5                                                  | 96<br>96<br>5.55                                             | 0 0 0<br>0 0 0                                                                 | 9 9 9<br>9 9 9                                                 | 92.5                                     |
| 31                                     | 3 3 3<br>4 3 3                                                | 35<br>36                                                     | . w w 4                                                                        | 4 4 4<br>1 2 5                                                 | 4.4.<br>4.7                              |

## ALIGNMENTS

|   | RESULT 1<br>T33517                           |                                                                                                                                                   |
|---|----------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------|
|   | hypothetical pro<br>C;Species: Caeno         | hypothetical protein T10B11.2 - Caenorhabditis elegans<br>C:Species: Caenorhabditis elecans                                                       |
|   | C,Date: 29-Oct-1<br>C,Accession: T33         | Cibite: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004<br>C;Accession: T33517                                                |
|   | R;Minx, P.; Kemp                             | R;Minx, P.; Kemp, K.<br>submitted to the EMBT Data Library. October 1998                                                                          |
|   | A; Reference number: 221363                  | he sequence of C. elegans cosmid T10B11.<br>er: 221363                                                                                            |
|   | A, Accession: T33517                         | 517                                                                                                                                               |
|   | A;Status: preliminar<br>A;Molecule type: DNA | A;Status: preliminary; translated irom GB/EMBL/DDBJ<br>A;Molecule type: DNA                                                                       |
|   | A;Residues: 1-549 <min></min>                |                                                                                                                                                   |
|   | A; Experimental s                            | A;Cross-rererences: UNIPKOI:UPTZII; EMBL:AFU98993; FIDN:AAC6/466.1; GSFDB:GNU0019; CESP<br>A;Experimental source: strain Bristol N2; clone T10B11 |
|   | C; Genetics:<br>A; Gene: CESP: T10B11.2      | 111.2                                                                                                                                             |
|   | A; Introns: 26/1;                            | A;Map poelcion: 1<br>A;Introne: 26/1; 76/2; 109/3; 159/1; 187/3; 229/3; 353/1; 398/2; 434/1; 467/3                                                |
|   | Query Match<br>Best Local Sim                | Query Match 18.8%; Score 567.5; DB 2; Length 549;<br>Best Local Similarity 30.8%; Pred. No. 2.1e-38;                                              |
|   | Matches 139;                                 | Conservative 91; Mismatches 160; Indels 61; Gaps 13;                                                                                              |
|   | Oy 114 VK                                    | 114 VKRARRHRWKWAQVTFWCPERQLCHLWLQTLREMLEKLITSRPKHLLVFINPFGGKGQG 171                                                                               |
|   | Db 123 VY                                    | KKDKOKWRLKQIPVIFYTTSERDYWHSLIDTTLRYKNRPKNIIIFINPFGGNGKA 180                                                                                       |
|   | Qy 172 KR                                    | IYERKVAPLFTLA-SITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSE 227                                                                                       |
|   | ::<br>DD 181 QK                              |                                                                                                                                                   |
|   | Oy 228 VL                                    | 228 VLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIV 287                                                                              |
|   | Db 241 LL                                    | SGALLRTQTDAGRNIDNPSSHLVTPHIRFGIIGAGSANSIVSTVHETNDHATSAVHIA 300                                                                                    |
|   | Oy 288 VG                                    | 288 VGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRNLGLARYDFSGLKTFLSH 347                                                                              |
|   | DD 301 iG                                    | SECNVDVCTVHQHQKLIRISANAISYGWLGDVLRDSBEVRCLGPIRYQWSALRTTIRH 360                                                                                    |
|   | Qy 348 HC                                    | 348 HCYEGTVSFLPAQHTVGSPRDR-KPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEW 406                                                                              |
|   | Db 361 PI                                    | 361 PIYRGMVQFSLSHKENVNPKDQLPPCLEPCPVCMKPQGNDKYDYHWHAEFT 411                                                                                       |
|   | Oy 407 OV                                    | 407 QVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHT 464                                                                                |
|   | Db 412 HV                                    | CCVIPTVTPFTPYGLAPFTGIGDGTLDLALVPRISRFHNMQFMRKVAMY 463                                                                                             |
|   | Qy 465                                       | NQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNS 522                                                                                    |
| _ | Db 464 GG                                    | 464 GGKQLYELD-PSLNCYRVTKWSYQPDADQEDPG                                                                                                             |

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A;Molecule type: DNA
A;Residues: 1-458 <5KE>
A;Residues: 1-458 <5KE>
A;COSS-references: UNIPROT:O14159; EMBL:Z98762; PIDN:CAB11477.1; GSPDB:GN00066; SPDB:SPJ
A;Experimental source: strain 972h-; cosmid c4A8
C;Genetics:
A;Gene: SPDB:SPAC4A8.07c
A;Gene: SPDB:SPAC4A8.07c
A;Amp position: 1
A;Introns: 39/1; 101/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-references: UNIPROT: Q06147; EMBL: U17244; NID: 9577171; PIDN: AAB67377.1; PID: 95771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 ----VCMIPGGSGNAFSYNATGQLKPALTALEILKGRPTSFDLMTFEQKGK-KAYSFLTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- CRAGCFVCROSKOOLEE-- BOXKALYGLEAAED-------VEEWQVVC 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 WKCSIEMDVVSSDRTEIKHMYEKSKNLAPMSESSDSDKTVSTSPESHLLTFEINDLSIFC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 GKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHTNQQDQF 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 GYGFYGDIIKDSEKKRWLGLAR-YDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKP- 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein YLR260w - yeast (Saccharomyces cerevisiae)
hypothetical protein 18479.7
N.Alternate names: hypothetical protein 18479.7
S.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Species: 05-May-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C.Speciesion: S51398
S.Miller, N.
Submitted to the EMBL Data Library, November 1994
A.Specription: The sequence of S. cerevisiae cosmid 8479.
A.Reference number: S51395
A.Accession: S51398
                                                                                                                                                                                                                                                                                                                                                                                                                            35 CSIPVS----ARNVDLAIPFKNI-LWVDKTGPNSVTLSYVSRSSKVATKCW--VDFVENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 CSVPVSEIIAVEETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWK-WAQVTFWCPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 VTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 EQLCHLWLQTLREMLEKUTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 ADACSVPVSEIIAVEETDVHGKHQGSGKWQKM---EKPYAFTVHCV-KRARRHRWKWAQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 8.2%; Score 248.5; DB 2; Length 687; Best Local Similarity 21.7%; Pred. No. 4.1e-12; Matches 99; Conservative 75; Mismatches 175; Indels 107;
                                                                                                                                                                                                                                                                     9.6%; Score 291.5; DB 2; 23.9%; Pred. No. 7e-16; ive 72; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 NYGIIADCDIGTENWRFMGENRAYLGFFLRLF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : : |:||
395 GFYYSKHLNYYKVRSFRFT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 DFTF---VEVYRVKKFQFT
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A;Cross-references: SGD:S0004250
A;Map position: 12R
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 105; Conserv
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A; Residues: 1-687 < MIL>
                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                  Mey
                                                                                                                                                                                                                             hypothetical protein F18E5.160 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (5pecies: Arabidopsis thaliana (mouse-ear cress) (5pecies: Arabidopsis thaliana (mouse-ear cress) (5pace: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 09-Jul-2004 (5,Accession: T05162 (5)A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Me submitted to the Protein Sequence Database, August 1998 (7)Accession: T05162 (7)Acce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      527
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03.Dec-1999 #sequence_revision 03.Dec-1999 #text_change 09-Jul-2004
C;Accession: T38776
R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
A;Reference number: Z21751
A;Reference number: Z21751
A;Accession: T38776
A;Accession: T38776
A;Accession: T38776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 WCYKLRQYLDSL-GRPKRLLVFVNPFGGKKSAREIFVKEVKPLFEDADVQLEIQETKYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |::|||: : | : | : | : | : | : | CRVPAGTGNGMIKSLDTVGLRCCANSATISIIRGHKRSVDVATIAQGNTKF-FSVLMLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 WLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQ-RSAGVDQNHPRAVLVPSSLRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 417.5; DB 2; Length 1
28.9%; Pred. No. 1.3e-25;
tive 75; Mismatches 162; Indels
                                    550
                                                                      || |||:| | : ::| ||: | | 496 VWNLDGEILEQPKDEPLHFKLHPQLISFFGR
                                    SWNCDGEVLHSP---AIEVRVHCQLVRLFAR
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Matches 129; Conservative
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Best Local Similarity
                                    523
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87;

Length 458; Indels 286

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127 233

| QY 128 TFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVA:                                                                                                                   | 180                             | Qy 397 -LEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKC-S 452<br>                                                                                                                                                                                                                                                                                                                                                                        |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| OY 181 PLFTLASITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSA :                                                                                                           | 240                             | QY 453 RENFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHIC 509                                                                                                                                                                                                                                                                                                                                                                             |
| OY 241 GVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVH :                                                                                                           | 300                             | QY         510 SSHPSCCCTVSNSSWNCDGEVLHSPAIEV 538           Db         447LDGEVVDTKTIEV 459                                                                                                                                                                                                                                                                                                                                                       |
| Qy 301 HNSTLLRY-SVSLIGYGFYGDIIKDSEKKRWLGLARYDF                                                                                                                                  | 338                             | RESULT 6<br>S67059                                                                                                                                                                                                                                                                                                                                                                                                                               |
| QY 339SGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCF                                                                                                                                   | 377                             | <pre>!ypothetical protein YOR171c - yeast (Saccharomyces cerevisiae) !Alternate names: hypothetical protein 03615 ;} Saccharomyces cerevisiae ;} Baccharomyces cerevisiae ;} Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 09-Jul-2004</pre>                                                                                                                                                                                     |
| QY 378VCRQSKQQLEEEQKKALYGLEAAEDV-EEWQVVCG (<br>                                                                                                                                 | 411<br>576                      | .; Accession: 867059<br>; Bordonne, R.; Camasses, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarassov, I.A.; Winso<br>winditted to the Protein Sequence Database, July 1996<br>; Reference number: 867032                                                                                                                                                                                                                                          |
| QY         412 KFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLIL 447           D         577 KMPYVAADTKFPPAALPSDGTMDMVI 602                                                                  |                                 | .;Accession: S67059<br>;;Molecule type: DNA<br>;Kasidues: 1-624 <bor><br/>;;Cross-references: UNIPROT:012246; EMBL:275078; NID:91420415; PID:91420417; GSPDB:GN000</bor>                                                                                                                                                                                                                                                                         |
| RESULT 5<br>T19707<br>hypothetical protein C34C6.5 - Caenorhabditis elecans                                                                                                     |                                 | A;Experimental source: strain S288C<br>C;Genetics:<br>A;Gene: SGD:LCB4; MIPS:YOR171c<br>A;Cross-references: SGD:S0005697                                                                                                                                                                                                                                                                                                                         |
| C,Species: Caenorhabditis elegans<br>C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004<br>C;Accession: T19707<br>R:Percy, C.                          |                                 | Query Match  Query Match  7.0%; Score 210.5; DB 2; Length 624;  Best Local Similarity 26.3%; Pred. No. 4.7e-09;  Matches 66; Conservative 46; Mismarches 102;                                                                                                                                                                                                                                                                                    |
| <pre>submitted to the EMBL Data Library, October 1995 A.Reference number: Z19167 A.A.Cession: T19707 A.Status: preliminary; translated from GB/EMBL/DDBJ</pre>                  |                                 | 143 TLREMLEKI TSRPKHLIVFINPFGGKGGKRIVERKVAPLFTLASITTDIIVTEHAN 19                                                                                                                                                                                                                                                                                                                                                                                 |
| A;Molecule type: DNA<br>A;Residues: 1-473 <wll><br/>A;Cross-references: UNIPROT:Q18425; EMBL:Z66494; PIDN:CAA91259.1; GSPDB:GN0002<br/>A;Experimental source: clone C34C6</wll> | 0; CESP:C3                      | QAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIG                                                                                                                                                                                                                                                                                                                                                                                     |
| .;Gene.: CESP.C34C6.5<br>A;Gene: CESP.C34C6.5<br>A;Map position: 2<br>A;Introns: 82/1; 126/1; 158/3; 276/1; 311/3; 427/3                                                        |                                 | Qy 260 IIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYG 316         :     :                                                                                                                                                                                                                                                                                                                                                             |
| Query Match  8 1%; Score 245.5; DB 2; Length 473; Best Local Similarity 24.3%; Pred. No. 4.3e-12; Matches 109; Conservative 66; Mismatches 159; Indels 115; Gaps                | 18;                             | Qy 317 FYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGC 376<br>  : :           : :                                                                                                                                                                                                                                                                                                                                                   |
| QY 149 EKLTSRPKHLLVFINPFGGKGGGKRIYERKVAPLFTLASITTDIIVTE 1                                                                                                                       | 196<br>126                      | Qy 377 FVCRQSKQQLE 387<br>   :: :<br> Db 420 KYAAKSKKELK 430                                                                                                                                                                                                                                                                                                                                                                                     |
| 197 HANQAKETLY-EINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSS                                                                                                                | 255<br>175<br>312<br>231<br>361 | RESULT 7 AG1665 hypothetical protein homolog lin1865 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AG1665 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst. U. |
| Db 232 DNQSYASFLSIGWGLMADIDIDSEKWRKSLGHHRFTVWGFIRSCNLRSYKGRLTYRFYK- 2  Qy 362 TVGSPRDRKPCRAGCFVCRQSKQQLEEEQKKALYG                                                               | 290<br>396<br>346               | cience 294, 849-852, 2001<br>;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma<br>k, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,<br>!Title: Comparative genomics of Listeria species.<br>;Reference number: AB1077; MUID:21537279; PMID:11679669                                                                                                                  |

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390 QKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIR 449
212 KYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCY
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                                                                                                                                                                                157 MLGQLAYYLKG-
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A;Gene: yerQ
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C; Species: Listeria monocytogenes
C; Species: Listeria monocytogenes
C; Species: Listeria monocytogenes
C; Species: Listeria monocytogenes
C; Accession: Al1293
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R; Glaser, P.; Frangeul, L.; Duchaud, E.; Durand, L.; Dassurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852. 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Accession: Al1293
A; Stetus: preliminary
A; Wolecule type: DNA
A; Residues: 1-310 < GLA>
A; Cross-references: UNIPROT:Q8YED4; GB:NC_003210; PIDN:CAC99831.1; PID:g16411207; GSPDB:
A; Genetics:
C; Genetics: Lmo1753
                  A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Cross-references: UNIPROT: Q92AQ5; GB:AL592022; PIDN:CAC97095.1; PID:g16414366; GSPDB:G
A, Experimental source: strain Clip11262
G, Genetics:
A, Gene: lin1865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 KHLLVFINPFGGKGGKRIYERKVAPLFTLAS----ITTDIIVTEHANQAKETLYEINID 211
                                                                                                                                                                                                                                                                                                                                                                                  STVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD--SEKKR 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450 KCSRFNFLRFL-----IRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGG 501
                                                                                                                                                                                                                                                                                                                                              3 KHARVIYNP----TSGREIIKKNLADVLSILEQAGYVTSAHATTAEPGDAKHAAEEAVRD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 KKRFGHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPD 559
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                                                                                                                                                                                                     Indels 131;
                                                                                                                                                                 Length 310;
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                                                                                                                                                               6.3%; Score 189.5; DB 2;
21.8%; Pred. No. 9.5e-08;
trive 57; Mismatches 139;
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conserved hypothetical protein yerQ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69795
R;KunGt, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V.; Berterr
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho.
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A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Accesiance number: A69580; MUID:98044033; PMID:9384377
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329
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                                                                                                        STVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD--SEKKR
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A;Status: preliminary; nucleic acid sequence not shown; translation not
A;Molecule type: DNA
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A,Residues: 1-732 <FAV>
A;Cross-references: EMBL:U39850; NID:g1055052; PID:g1055058; PIDN:AAA81060.1; CESP:F52C9
C;Genetics:
A;Gene: GESP:F52C9.3
A;Introns: 63/1; 106/3; 148/2; 303/1; 347/1; 408/2; 650/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Listeria innocus
C;Species: Listeria innocus
C;Species: Listeria innocus
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21837279; PMID:11679669
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A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein lin0768 [imported] - Listeria innocua (strain Clip11262)
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                                                                                                                                                                                                                                                                                                                             153 SRPKHLLVFINPFGGKGGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDK 212
                                                                                                                                                                                                                                                                                                                                                                         313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 MLPSVFENSDDVRHACETAMAVIEDQKKSVY-----AFELTT--EGSTLAPBYGLGDV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYGFYGDIIKDSEKKRW-LGLAR----YDFSGLK----TFLSHHCYEGTVSFLPAQHTVG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 SPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 CRRSPRGLSPAAHLGDGSSDL--ILIRKCSRFNFL----RFLIRHTNQQDQFDFTFVEV 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 VGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSD 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 YDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAG-
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                                                                                                                                                                                              4.5%; Score 136; DB 2; L. 19.9%; Pred. No. 0.0075; ive 56; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 YSQIRFRMGDPYMPEEFFEWNE 359
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Matches 42; Conservative
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                            Best Local Similarity
Matches 76; Conserv
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                                                                                                                                                                                              Query Match
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D.; Jones, L.M.; Karst, U. Science 294, 484-852, 201.

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Reterence number: AB1077; MUID:21537279; PMID:11679669

A; Residues: preliminary
A; Residues: 1-306 cGLA>
A; Residues: 1-3
                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein lin2702 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;C;Date: 27-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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: | | | | | | : ::: 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 TLYBINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYS----VSLLGYGFYG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIIKOSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVC 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::||:|
-----KLGILPV 93
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T16422
R;Favello, T
Rubbit Co the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F52C9.
A;Reference number: Z18511
A;Accession: T16422
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                         226 KANLAEFIRVATMALRGEHINDQ---HIIYTKANRVK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.5%; Score 136.5; DB 2; Best Local Similarity 19.6%; Pred. No. 0.0021; Matches 62; Conservative 55; Mismatches 91;
                                                                                                450 KCSRFNFLRFLI-----RHTNQQDQFDFTFVEVYRVK
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58 AGYEV-----VIAAGGDGTVNEVVNGLMQVEKRP--
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                                 184 GK--LFOGEI---
                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: AH1769
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A;Molecule_type: DNA
A;Residues: 1-306 <GLA>
A;Cross-references: UNIPROT:Q8Y497; GB:NC_003210; PIDN:CAD00635.1; PID:g16412045; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2557
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Takkami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiram Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and careference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues 1.255 csTo-
A;Cross-references: UNIPROT:Q9KF21; GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB043°
A;Experimental source: strain C-125
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                                                                                                                                                                                                                                                                                                                           156 KHLLVFINPFGGKGQGKRI-----YERKVAPLFTLASITTDIIVTEHANQAKE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                           204 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYS----VSLLGYGFYG 319
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                                                                                                                                                                                                                                                                                                                                                               -----TVLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein BH0676 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 AGGDGTIYEVVNGLAGLEKRPT------LGLIPAGTTNDFARALNIPRD
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21.9%; Pred. No. 0.016;
tive 44; Mismatches 119;
                                                                                                                                                                                                        4.2%; Score 126.5; DB 2;
19.1%; Pred. No. 0.014;
tive 51; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---VKESMKSKW-GRLAYLFSGL----
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Best Local Similarity 21.9%
Matches 73; Conservative
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Best Local Similarity
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A; Accession: D83734
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                                                                                                                                                                                                                                                                                                               hypothetical protein BH1953 (imported) - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 0.1-6c-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A83894
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83850; MUID:20512582; PMID:11058132
A;Accession: A83894
A;Accesi
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A;Reference number: AB1077; MUD:21537279; PMID:11679669
      336
                                       160 VFINPFGGKGOGKRIYERKVAPLFTLASITTDIIV--TEHANDAKETLYEINIDKYDGIV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 CVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAE-----TSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK---DSE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQL 386
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      AETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK--DSEKKRWLGLARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.3%; Score 129; DB 2; Length 29: 22.8%; Pred. No. 0.0081; Live 45; Mismatches 104; Indels
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                                                                                                                                                                            FLEGLKAF 169
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Matches 71; Conserv
                                                                                                                      DFSGLKTF
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| 178   | 456                              | 231 |                                   |                                     |                                                                          |
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| :<br> | KFLAINATNMSCACRRSPRGLSPAAHLGDGSS |     | 457 LRFLIRHTNQQDQFDFTFVEVYRVK 481 | 232 LHLAGLALRGEHIKHPKVLYVQANRIK 258 | Search completed: September 3, 2005, 04:38:45<br>Job time : 25.8463 secs |
| 162   | 397                              | 179 | 457                               | 232                                 | plet<br>25.                                                              |
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Sequence 12897, A Sequence 15682, A Sequence 15682, A Sequence 6505, App Sequence 991, App Sequence 1961, App Sequence 1961, App Sequence 29, App Sequence 29, App Sequence 29, App Sequence 29, App Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli

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APPLICANT: dunot, ring
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
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US-09-248-796A-1756
US-09-949-016-3940
US-09-614-211A-799
US-09-620-312D-796
US-09-107-132A-350
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US-09-252-991A-5922
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Patent No. 6743619
GENERAL INFORMATION:
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Ren, Felyan
Zhang, Jie
Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
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ORGANISM: Homo sapiens

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-Q=/cgn2_1/USPTO spool/US10631958/runat_02092005_165811_4432/app_query.fasta_1.1941
-Q=/cgn2_1/USPTO spool/US10631958/runat_02092005_165811_4432/app_query.fasta_1.1941
-Da=Lesued Patents NA -QFWT=fastap -SUFFIX=ni -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Eits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                               OM protein - nucleic search, using frame plus p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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length: 2000000000
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                           LysaspSerGluLysLysargTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLys
                      ThrPheLeuSerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThr
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Matches:
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Patent No. 6703491;
GENERAL INFORMATION:
APPLICANT: Homburger et al.;
TITLE OF INVENTION: Nucleic acids and proteins of;
FILE REFERENCE: File Reference: 7326-094;
CURRENT APPLICATION NUMBER: US/09/270,767;
CURRENT PILING DATE: 1999-03-17;
NUMBER OF SEQ ID NOS: 62517;
SOFTWARE: PatentIn Ver. 2.0;
SEQ ID NO 14306
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; ORGANISM: Drosophila melanogaster
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                                                GlyProAlaProLeuGly-----ValArgAlaProProAlaTrpArgThrSerPro
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Length:
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1765 AGGAATTCCGGTTCAGAACTTTTTCTGCCAGCAGGAGACTACAGCTTGGCAGGGTCT 1824
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                                         GAGAACTACCGCTGGATGGGACCGCGCGCGGTACGAGTACAGTGGCGTCAAGGCCTTCCTG
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CTCAGATTCTGTGCCAGTGTCCTGAGCTACGGGTACCTGGGCGATGTGGCCAGGCCCAGAGC
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| IGCTGAACAACTTCCAGCTTAAGAAGAAGAAGCTACAGGGTCCTGCTTCACGGA-CAGCAG 180
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|CCATTAGCTCTACGAGTGCCTCCAAGTTCACGCCCTGCTCCGACCACCACAATGTCC 121
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            US-10-631-958-11 (1-562) x US-09-270-767-14306 (1-2064)
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US-09-270-767-15155/c
; Sequence 15155, Application US/09270767
; Patent No. 670491
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster 512 HisProSerCysCysCysThrValSerAsnSerSerTrpAsnCysAspGlyGluValLeu 532 HisSerProAlaIleGluValArgValHisCysGlnLeuValArgLeuPheAlaArgGly

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GluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspValGlu-
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Matches:
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Mismatches:
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CRGANISM: Drosophila melanogaster
US-09-270-767-30448
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41.24%
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Query Match:
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687 CACGGCACGGCGGATGTGAGGACAGCGGCTATCCATGTGATTCTGGGCCAGCATCGGGGA 628
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627 TTGGATGTGCAGTATGGCCAGTCCCTGCTGAATTCTGTGCCAGTGTCCTG 568
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Conservative:
Mismatches:
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Gaps:
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FILE REFERENCE: File Reference: 7326-094
CURRENT PEPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15155
LENGTH: 1084
                                                                                            TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-15155
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585.50
51.14%
35.51%
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Sequence 10.67034 Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.
FILE REFERENCE: File Reference: 7326-094
CURRENT ELING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
LENGTH: 901
                                                                                                                                                                                                                              TIGCCCACTGGCTCCATTTCATCAATGAGGAACCTCGGCAACGATCAGTGGAAGGTTGTG
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    GCTGGCAGTGTAAAAACCACGTGCTTCCCATGATCTCTGAAAGCTGGGCTGTCTTC
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                                                                                              GlyAlaAspAlaCysSerValProValSerGluIleIleAlaValGluGluThrAspVal
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TITLE OF INVENTION: Induction of blood vessel formation through administration of ITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REPERRNCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3
ATGAGGAACCTCGGCAACGATGAGGTTGTGCGGGGCAATTTCTTTATGATCTGC 409
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GTATATCGCAAGGGAATTCCGGTTCAGAACTTTTTCTGCCAGCGAGGAGGACTACAGC
                                      AlaThrAsnMetSerCysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHis
                                                                                                      -----SerSerHisProSerCysCysCysThrValSerAsnSerTrpAsnCysAsp
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                                                                                                                                               ArgPheLeuIleArgHisThrAsnGlnGln---AspGlnPheAspPheThrPheValGlu
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Patent No. 6610534
GENERAL INFORMATION:
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288.50
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26.58%
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ORGANISM: Homo sapiens
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Percent Similarity:
Best Local Similarity:
Query Match:
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OTHER INFORMATION
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NAME/KEY: CDS
LOCATION: (1).
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US-09-970-516-3
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Sequence 1155, Application US/09949016

Sequence 1155, Application US/09949016

Fatent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: BOLYMORHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1155

LEMPORAL. 10-03

SEQ ID NO 1155
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424 CTGCTACCTCGGCCGCCCCGGTTGCTTCTATTGGTCAATCCCTTTGGGGGGTCGGGGCCTG 483
                                       GlyLysArgileTyrGluArgLysValAlaProLeuPheThrLeuAlaSerIleThrThr 190
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                                                                                                                        191 AspilelleValThrGluHisAlaAsnGlnAlaLysGluThrLeuTyrGluIleAsnIle
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664 GGCTCCTAGATCGC-
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ORGANISM: Human
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                                                                          APPLICANT: Kohama, Takatumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE PETERRENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 13
LENGTH: 2380
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Matches:
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DATABASE ACCESSION NUMBER: AF245447
DATABASE ENTRY DATE: 2000-06-27
Sequence 13, Application US/09817676A
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PUBLICATION INFORMATION:
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ORGANISM: Homo sapiens
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Query Match:
DB:
                     Patent No. 6800470
GENERAL INFORMATION:
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PAGES: 19513-19520
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                                                                                       GluAlaAlaAsnGlyProAlaProLeu-----GlyValArgAlaProProAlaTrpArg
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    143
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148
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            Conservative:
Mismatches:
Indels:
Gaps:
                                                                  US-10-631-958-11 (1-562) x US-09-949-016-1155 (1-1783)
  280.50
37.82%
24.03%
9.27%
.ercent Similarity:
Best Local Similarity:
Query Match:
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; Sequence 11, Application US/09817676A; Sequence 11, Application US/09817676A; Patent No. 6800470
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; APPLICANT: Schema, Takafumi
; TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
; TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms,
; FILE REFERENCE: 01170/HG
; CURRENT APPLICATION NUMBER: US/09/817,676A
; CURRENT PILING DATE: 2001-03-26
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2698
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337 AspPheSerGlyLeuLysThrPheLeuSerHisHisCysTyrGluGlyThrValSerPhe
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                                                                                                                      -----TyrSerThrValGlyThrSerAspAlaGluThrSerAlaLeuHisIleValVal
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-----CCAGACTGGGAGGATGCCGTGCGGATGCCC--
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Matches:
Conservative:
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APPLICANT: Pu, XIA
APPLICANT: Pu, XIA
APPLICANT: Richard, D'ANDREA J
APPLICANT: Richard, D'ANDREA J
APPLICANT: Jennifer, BAMBLE R
APPLICANT: Mathew, VADAS A
ITILE OF INVENTION: SPHINGOSINE KINASE ENZYME
FILE OF INVENTION: SPHINGOSINE KINASE ENZYME
FILE OF INVENTION: SPHINGOSINE KINASE ENZYME
FILE PRICATION NUMBER: US/09/959,897
CURRENT FILING DATE: 2001-05-12
PRICA APPLICATION NUMBER: PCT/AU00/00457
PRICA APPLICATION NUMBER: AU PQ 0339
PRICA FILING DATE: 1999-05-13
PRICA FILING DATE: 1999-07-08
NUMBER: OF SEQ ID NOS: 56
SOFTWARE: PATENTIN VETSION 3.1
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Patent No. 6730480
GENERAL INFORMATION:
APPLICANT: PITSON, STUART M
APPLICANT: Brian, WATTENBERG W
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ORGANISM: Homo sapiens
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LOCATION: (33)..(1184)
OTHER INFORMATION:
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LENGTH: 1205
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606 GAGGACACTGCAGCCTACTTCTGCATCTACCCTACCCACGTGGCCGTCGAGGGGGCCGG 665
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                                                                              LOCATION: (387)..(2237)
PUBLICATION INFORMATION:
TITLE: Molecular cloning and functional characterization
TITLE: movel mammalian sphingosine kinase type 2 isoform
VOLUME: J. Biol. Chem.
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Conservative:
Mismatches:
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DATE: 2000-06-30
DATABASE ACCESSION NUMBER: AF245448
DATABASE ENTRY DATE: 2000-06-27
                                                                                                                                                                                                                                                                                                                                                                           4.04e-16
269.00
41.64%
25.99%
8.89%
                 ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Sequence 1, Application US/09970516

Sequence 1, Application US/09970516

Patent No. 6610534

GENERAL INFORMATION:
TITLE OF INVENTION: Induction of blood vessel formation through administration of TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT PILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 1155 1086 GGCCAGGTGCACCCCAAACTACTTCTGGATGGTCAGCGGTTGCGTGGAGCCCCCGGCCAGC 1145 276 213 309 ... CCCCTGTGTAGCCTCCCAGCAGCTCTGGCAACGCGCTGCCAGCTTCCTTG 360 154 ArgProlysHisLeuleuValPhelleAsnProPheGlyGlyLysGlyGlnGlyLysArg 173 174 IleTyrGluArgLysValAlaProLeuPheThrLeuAlaSerileThrThrAspIleIle 193 SerSerLeuArglleGlyIleIleProAlaGlySerThrAspCysValCys----- 270 96 ------GTGGATGGGAATTGATGCTTAGCGAGGCGTGCAG 194 ValThrGluHisAlaAsnGlnAlaLysGluThrLeuTyrGluIleAsnIleAspLysTyr 214 AgpGlyIlevalCysValGlyGlyAgpGlyMetPheSerGluValLeuHisGlyLeuIle 518 ThrValSerAsnSerSerTrpAsnCysAspGlyGluValLeuHisSerProAlaIleGlu 234 GlyArgThrGlnArgSerAlaGlyValAspGlnAsnHisProArgAlaValLeuValPro 538 ValArgValHisCysGlnLeuValArgLeuPheAlaArgGlyIleGluGluAsnPro---277 GAGCGCCTGACTGGGAGCCGCCATCCAGAAG------

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APPLICATION NUMBER: PCT/US98/11422
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APPLICATION NUMBER: 60/049,020
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,876
FILING DATE: 1997-06-06
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APPLICATION UNMBER: 60/048,875
APPLICATION DATE: 1997-06-06
APPLICATION NUMBER: 60/049,374
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APPLICATION NUMBER: 60/048,917
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/049,375
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APPLICATION NUMBER: 60/048,880
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
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APPLICATION WUMBER: 60/048,901
ELING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,892
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APPLICATION NUMBER: 60/048,915
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/049,373
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                                        APPLICATION NUMBER: 60/048,885
                                                                                                          FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,881
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APPLICATION NUMBER: 60/
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FILING DATE: 1997-06-06
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               361 AACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTA 420
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                                                             IleValValGlyAspSerLeuAla---MetAspValSerSerValHisHisAsnSerThr 304
                                                                                                                                                   LeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspIleIleLysAsp 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                           658 TCCAAGACACCTGCCTCCCCC-----GTTGTGGTCCAGGAGGGCCCGGTA 702
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CACCTGGGCAGTGAGTTTTGCTGCACCCATGGGCCGCTGTGCAGCT------
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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
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Patent No. 6525174
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Sequence 5, Application US/09970516
; Sequence 5, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
    APPLICANT: No. 6610534artis AG
    APPLICANT: No. 6610534artis AG
    TITLE OF INVENTION: Induction of blood vessel formation through administration of TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
    FILE REPRESENCE: 4.31617
    CURRENT APPLICATION NUMBER: US/09/970,516
    CURRENT APPLICATION NUMBER: US/09/970,516
    CURRENT FILING DATE: 2001-10-04
    NUMBER OF SEQ ID NOS: 6
    LEMENTRE: Patentin version 3.1
    SEQ ID NO 5
    LEMETH: 1149
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       304 rieuleuArgTyrSerValSerLeuleuGlyTyrGlyPheTyrGlyAspIleIleLysAs 324
                                                                               324 pSerGlulysLysArgTrpleuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThrPh 344
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                            404 -GluGluTrpGlnValValCysGlyLys------PheLeuAlaIleAsnAlaTh
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730 TTCCAAGACACCTGCCTCCCCC-----GTTGTGTCCAGCAGGCCCGGT
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Matches:
Conservative:
Mismatches:
Indels:
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER PILING DATE: 1999-12-18
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 90
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OTHER INFORMATION: n
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us-10-631-958-11.rni

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Sequence 1756, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POR DIAGNOSTICS AND THERABEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                      -----TGCACCCAAACTTTGGATGGTCTGTGGCAGCAGAGATGCCCCAT---CCG 1108
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CTGGTTCATGTGCCCGTGGTTGCTTTCCGCCTGGAGCCCAGGAGCCAGAGGGGCGTGTTT 1011
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                                                                                                                456 PheleuArg---PheleulleArgHisThrAsnGlnGlnAspGlnPheAspPheThrPhe 474
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                                                                                                                                      SerAspLeuLysGluGlyGlyLysLysArgPheGlyHisIleCysSerSerHisProSer
                                                  HisLeuGlyAspGlySerSerAspLeuIleLeuIleArgLys---CysSerArgPheAsn
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Conservative:
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                                                                                                                                                                                                                                                                                                                            .71 GlyLysArglleTyrGluArgLysValAlaProLeuPheThrLeuAlaSerileThrThr 190
                                                                                                                                                                                                                                                                                                                                                GCTCTGCAGACTCTTCCAGAGCCGTGTGCAGCCCTTCCTGGAGGAGGAGAGATAACCTTT 147
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                              247.50
41.65%
24.94%
8.18%
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                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(114
; OTHER INFORMATION:
US-09-970-516-5
                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                   62 GAGCTTGGGACGAGCTGCGTTCCGCCCAGGCCATGTAGGGAACGGCGGTGGCGTCC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProAlaArgAlaLeuLeuArgTrpTrpArgSerProGlyProGlyAlaGlyAlaProGly 71
                                                                                                                                                                                                                                                                                                 GluAlaAlaAsnGlyProAlaProLeu----GlyValArgAlaProProAlaTrpArg
                                                                                                                                                                                                                                                                                                                                                                           -ThrSerProAlaAlaGluMetGlyAlaThrGlyAlaAlaGlu
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Mismatches:
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217.50
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23.48$
7.19$
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Best Local Similarity:
Query Match:
DB:
SEQ ID NO 3940
LENGTH: 1764
TYPE: DNA
ORGANISM: Human
                                                                         US-09-949-016-3940
                                                                                                              Alignment Scores:
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Fatent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION WUMBER: 60/237,768
FRIOR FILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASELSEQ for Mindows Version 4.0
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                                    MetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp
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APPLICANT: Karunanandaa, Balasulojini
APPLICANT: Yu, Jaehyuk
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
                                                                                        SerAspAlaGluThrSerAlaLeuHisIleValValGlyAspSerLeuAla---MetAsp
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Patent No. 6723837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValPheileAsnProPheGlyGlyLysGlyGlnGlyLysArgileTyrGluArgLysVal 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GICATIATIAATCCCCACGGTGGTAAAGGTACTGCTAAAAATTTATTCCTGACAAAGCA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 AlaProLeuPheThrLeuAlaSerIleThrThrAspIleIleValThrGluHisAlaAsn 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         927
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66
46
102
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Matches:
Conservative:
Mismatches:
Indels:
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                                                            US/09/614,221A
FILE REFERENCE: 16516.075

CURRENT APPLICATION NUMBER: US/09/614,221A

CURRENT FILING DATE: 2000-07-12

PRIOR PPLICATION NUMBER: US 60/142,981

PRIOR FILING DATE: 1999-07-12

NUMBER OF SEQ ID NOS: 626

LENGTH: 1875
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.37e-10
210.50
44.62%
26.29%
6.96%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-614-221A-399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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Search completed: September 6, 2005, 02:35:04 Job time: 367.875 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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23:41:54 ; Search time 1583.07 Seconds (without alignments) 2324.913 Million cell updates/sec
OM protein - nucleic search, using frame_plus_p2n model
                                                5, 2005,
                                                September
                                                Run on:
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1 HEAANGPAPLGVRAPPAWRT.....QLVRLFARGIEENPKPDSHS Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-10-631-958-11 3025 **BLOSUM62** Perfect score: Scoring table: Sequence:

562

7338684 seqs, 3274456166 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

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-LOOPCL=0 - LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62
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-MAXIZEN=200000000 - USER=B13.63.1958 @ GCN 1 1 1588 @ runat 0.2092005 165813\_470
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-FGAPOP=6 - FGAPEXT=7 - YGAPOP=10 - YGAPEXT=7 - DELOP=6 - DELOEXT=7

Published Applications NA:\*

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is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | Description  | <br>-262-511-39 Sequenc | -969-896-16 Sequence 1 | -631-958-16 Sequence 1 | -618-941-55 Seguence 5 | -315-597A-1 Sequence 1 | -120-988-148 Sequence 1 | -969-896-9 Sequence 9 | 631-958-9 Sequence 9 | 84-810A-5 Sequence 5, | 876-281-5 Seguence 5 | 969-896-1 Sequence 1 | 631-958-1 Sequence 1 | 115-635-247 Sequence 2 | 9-896-8 Sequence 8 | 958-8 Sequence 8 | 9-896-4 Sequence 4 | 958-4 Seguence 4 | .810A-7 Seq | i-281-7 Sei | 5-115-176413 Se | 5-114-34530 Se | i-115-86211 Se | 9-896-5 Se | 958-5 Se | 7-963-92801 Se | 7-445-46 Se | 7-963-30650 Se | -115-64890 Se | 1-599-47396 Se | 5-114-34806 Se | .590-5271 Se | -115-29002 Sec | -599-594LV SE | 25 25 25 25 25 26 26 26 26 26 26 26 26 26 26 26 26 26 | -963-58/UI Se | 784-810A-9 Seq | -876-281-9<br>Sec | -425-114-34081 Se | -437-963-95148 Se | -437-963-77896 Se | -348-052-25 Set | -622-011-25 Se | -425-114-32139 Se | -425-115-97849 Sec | -425-115-79424 Sec |
|-----------|--------------|-------------------------|------------------------|------------------------|------------------------|------------------------|-------------------------|-----------------------|----------------------|-----------------------|----------------------|----------------------|----------------------|------------------------|--------------------|------------------|--------------------|------------------|-------------|-------------|-----------------|----------------|----------------|------------|----------|----------------|-------------|----------------|---------------|----------------|----------------|--------------|----------------|---------------|-------------------------------------------------------|---------------|----------------|-------------------|-------------------|-------------------|-------------------|-----------------|----------------|-------------------|--------------------|--------------------|
| SUV       | ID           | <br>8 US-1              | o as-o                 | 9 US-1                 | 9 US-1                 | 9                      | 7 US-1                  | o us                  | 9 US-1               | 0S-09                 | 2 US-1               | 0 ns-0               | 9 US-1               | 9 US-1                 | 0                  | σ                | 0                  | σ                |             | 2           | 0               | æ              | 0              | 0          | σ        | σ              | 2           | o.             | 0             | ω.             | œ              | 9 US-09-783- | <b>5</b> 0     | oσ            | 0                                                     | ת             | -60-SD 6       | Z US-1            | 8 US-1            | sn 6              | 9 US-1            | v us            | 6              | 8 US-1            | 0 118-1            | 0 US-1             |
|           | Length       | <br>_                   | 4                      | 4.                     | 4                      | 4                      | 4                       | -                     | ٦                    | -                     | _                    |                      |                      |                        |                    |                  |                    |                  |             |             | ~               | ~              | ~              |            |          | ~              |             | -              | ~             | ~              | _              |              | ~ (            | 7.            | ٠,                                                    | 1             |                |                   | _                 | -                 | n                 | ~               | N              | 185               | 224                | 2284               |
|           | Quer<br>Matc | <br>100.0               | 8                      | 8                      |                        | •                      |                         | •                     | •                    | •                     | •                    | •                    | •                    |                        | •                  | •                | •                  |                  | •           | •           |                 | •              |                |            |          | •              |             |                | •             | ٠              | •              | 12.3         |                | ٠             | ٠                                                     |               |                | ٠                 | ٠                 |                   |                   |                 |                |                   |                    |                    |
|           | COL          | <br>3025                | 2                      | 2                      | 2                      | 8                      | ᆏ                       | 88                    | 88                   | 649.                  | ę.                   | 640.                 | 640.                 | 1156                   | 8                  | 8                | 811                | 811              | 929         | 65          | 16.             | 573.5          | 73.            | 525        | 52       | 80.            | 7.          | 41             |               | ω,             | 80 1           | 371          | ο,             |               |                                                       |               | •              |                   | E.                | 31.               | 30.               | 29.             | 29.            | 26.               | 26.                |                    |
|           | - i          | -                       | 2                      | m                      | 4                      | Ŋ                      | 9                       | 7                     | œ                    | σ                     | 10                   | 11                   | 12                   | 13                     | 14                 | 15               | 16                 | 17               | c 18        | -           | 20              | 21             | 22             | 23         | 24       | c 25           | 56          | 27             | 28            | 29             | 30             | 31           | 3 6            | J C           | # L                                                   | n (           | 9 10           | 3.7               | 38                | 39                | 40                | 41              | 42             | 43                | 4 4                | 45                 |

Sequence 39, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Perman, John A.
APPLICANT: Fekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Ju, Jingfang
APPLICANT: Ju, Jingfang
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Batturajan, Meera
APPLICANT: Edinger: Shlomit R.
APPLICANT: Edinger: Shlomit R. US-10-262-511-39

300

240

80

140 420 480

540

200 9 220

999

240

720

260 780 280 840 300 900

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CAAAGCAAGCAGCTGGAGGAGGAGCAGAAGAAAGCACTGTATGGTTTGGAAGCTGCG 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                         161 PhelleAsnProPheGlyGlyLysGlyGlnGlyLysArglleTyrGluArgLysValAla 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluAspValGluGluTrpGlnValValCySGlyLySPheLeuAla11eAsnAlaThrAsn 420
                                                     241 GAGATCATCGCCGTTGAAAAAAGAAACAGACGTTCACGGGAAACATCAAGGCAGTGGAAAATGG
                                                                                                                                                                                                                                                                          121 ArgTrpLysTrpAlaGlnValThrPheTrpCysProGluGluGlnLeuCysHisLeuTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 IleProAlaGlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 IleIleLysAspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGly
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         APPLICANT: Oct. Tatiana APPLICANT: Schusen, Bryan D. APPLICANT: Schusen, Bryan D. APPLICANT: Catterton, Bryan D. APPLICANT: Catterton, Bryan D. APPLICANT: Catterton, Bryan D. APPLICANT: Catterton, Bryan D. APPLICANT: Willer, Catterton, Bryan D. APPLICANT: School, David J. APPLICANT: Martin D. Martin Catter D.
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 Malyankar, Uriel
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; LOCATION: (76)..(1686)
US-10-262-511-39
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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|                                                                      | 61 181 | Oy                                                                                                                                       | Db         301 CAGAAAATGGAAAAGCCTTACGCTTTTACAGTTCACTGTGTAAAGAGAGACACGACGGCAC           Qy         121 ArgTrpLysTrpAlaGlnValThrPheTrpCysProGluGlnLeuCysHisLeuTrp           Qy | Qy 141 LeuGlnThrLeuArgGluMetLeuGluLysLeuThrSerArgProLysHisLeuLeuVal<br> | OY 161 PhelleAshProPheGlyGlyLysGlyGlnGlyLysArglleTyrGluArgLysValAla                     | Oy 181 ProLeuPheThrLeuAlaSerIleThrThrAspIleIleValThrGluHisAlaAsnGln | Oy 201 AlalysGluThrLeuTyrGluIleAsnIleAsplysTyrAspGlyIleValCysValGly                           | QY         221 GlyAspGlyMetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAla                                                                                  | Oy 241 GlyValAspGlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIle                                             | Qy         261         IlleProAlaGlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGlu           Db         781         ATTCCCGCAGGGTCAACGGAGTGTTACTCCACCGTGGGCACCAGGGAACGCAGAAA | Oy 281 ThrSerAlaLeuHisTleValValGlyAspSerLeuAlaWetAspValSerSerValHis             | Oy 301 HisAsnSerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAsp<br> | Qy         321         IlelleLysAspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGly           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | Oy 341 LeuLysThrPheLeuSerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGln |                                                                                                                              |
|----------------------------------------------------------------------|--------|------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|---------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------|-------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------|
| 401 GluAspValGluGluTrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsn 420 |        | 1381 ATCAGGCACCCAACCAGCAGGACCAGTTTGATCACTTTTGFTGAAGTTTATCGCGTC 1440 481 LysLysDheGlnPheThrSerLysHisMetGluAspGluAspGerAspLeuLysGluGly 500 | 501 GlyLysLysArgPheGlyHis1leCysSerSerHisProSerCysCysCysThrValSer 520                                                                                                         |                                                                         | 1621 CACTGCCAGCTGGTTCGACTCTTTGCACGAGAATTGAAGAGAATCCGAAGCCAGACTCA 1680<br>561 Hisser 562 | Db 1681 CACAGC 1686<br>RESULT 3                                     | 31-958-16<br>action, Application US/10631958<br>cation No. US20040192580A1<br>AL INFORMATION: | AFFLICANT: KOSBAGA, Sophia<br>TITLE OF INVENTION: Regulation of human Sphingosine<br>TITLE OF INVENTION: Kinase-Like Protein<br>FILE REFERENCE: 004974.00594 | CUCRENT APPLICATION NUMBER: US/10/631,958 PRIOR APPLICATION NUMBER: US/09/969,896 PRIOR FILING DATE: 2001-10-04 | LICATION NUMBE<br>ING DATE: 2000<br>LICATION NUMBE<br>ING DATE: 2001                                                                                                           | NUMBER OF SEQ ID NOS: 16 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 4413 | TYPE: DNA<br>ORGANISM: Homo sapiens<br>-10-631-958-16                   |                                                                                                                                    | : 100.00% Mismacches:<br>100.00% Indels:<br>19 Gaps:                | US-10-631-958-11 (1-562) x US-10-631-958-16 (1-4413)<br>Qy 1 HisGluAlaAlaAsnGlyProAlaProLeuGlyValArgAlaProProAlaTrpArgThr 20 |

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| Sequence 1, Application US/10315597A
| Publication No. US2030162206A1
| GENERAL INFORMATION |
| APPLICANT: Sugiura, Masako |
| APPLICANT: Kohama, Takafumi |
| TITLE OF INVENTION: Ceramide Kinase and DNA Encr |
| FILE REFERENCE: 02658CIP/HG |
| CURRENT APPLICATION NUMBER: US/10/315,597A |
| CURRENT FILING DATE: 2000-06-14 |
| PRIOR APPLICATION NUMBER: UP 2000-178039 |
| PRIOR FILING DATE: 2000-06-14 |
| NUMBER OF SEQ ID NOS: 4 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 1 |
| LENGTH: 4463 |
| TYPE: DNA |
| PRATURE: NAM |
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LOCATION: 3371
COTHER INFORMATION:
US-10-315-597A-1
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                                                                                                                                   IleAlaValGluGluThrAspValHisGlyLysHisGlnGlySerGlyLysTrpGlnLys 102
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US-10-631-958-11 (1-562) x US-10-315-597A-1 (1-4463)
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| Score: 2931.50 Matches: 548 Percent Similarity: 98.21\$ Conservative: 2 Best Local Similarity: 97.86\$ Mismatches: 7 Query Match: 17 Gaps: 1 Gaps: 1 | .631-958-11 (1-562) x US-10-120-988-148 (1-4432)                                                                                       | 1135 GGTTCCCGCCCTATAGACAGACAGTCACAGAGAGCTGGCAGGCCTGGCGGACGGCCCG 1  | 1195 GCGCCGAGATGGGGCCGCCGCGCGCGCCCCCTCCAATCCGTGCTGTGGGTGAAG 1 | Qy         43 GlnGlnArgCysAlaValSerLeuGluProAlaArgAlaLeuLeuArgTrpTrpArgSer 62           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII                       | Oy 63 ProGlyProGlyAlaBroGlyAlaAspAlaCysSerValProValSerGluIle 82 | Db 1315 CCGGGCCCGGGCCCCCCCGGGGGGGCCCTGTTTTTTTTT                             | 1375 ATCGCCGTTGAGGAAACAGACGTTCACGGGAAACATCAAGGCAGTGGAAAATGGCAGAAA 1 | DD 1435 ATGGAAAAAGCCTTTTTACAGTTCACTGTAAAAAAGGGCACGCGCGG 1494                                                                                          | Oy 123 LysTrpAlaGlnValThrPheTrpCysProGluGluGlnLeuCysHisLeuTrpLeuGln 142 | Db 1495 AAGTGGGCGCAGGTGACTTCTGGTGTCCAGAGGAGCAGCTGTGTCACTTGTGGCTGCAG 1554  Qy 143 ThrLeuArgGluMetLeuGluLysLeuThrSerArgProLysHisLeuLeuValPheIle 162 | 1555 ACCCTGCGGGAGATGCTGGAGGTGACGTCCAGACCAAAGCATTACTGGTATTATT            | Qy         163 AsnProPheGlyGlyLysGlyGlnGlyLysArglleTyrGluArgLysValAlaProLeu 182 | Qy         183 PheThrLeualaSerIleThrThraspIleIleValThrGluHisalaasnGlnalaLys         202           Db         1675 TTCACCTTAGCCTCCATCACACTGACATCATCGTTACTGAACATGCTAATCAGGCCAAG         1734 | Qy         203 GluThrLeuTyrGluIleAsnIleAsnIleAspLysTyrAspGlyIleValCysValGlyGlyAsp 222           Db         1735 GAGACTCTGTATGAGATTAACATAGACAAATACGACGCCATCGTCTCGTCTCGGCGGAGAT 1794 | Qy         223 GlyMetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyVal 242 | Qy         243 AspGlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIlePro 262 | SerThraspCysvalCysTyrSerThrValGlyThrSerAspAlaGluThrSer 2<br>                                                  | Qy         283 AlaLeuHisIleValValGlyAspSerLeuAlaMetAspValSerSerValHisHisAsn 302           Db         1975 GCGCTGCATATCGTTGGGGACTCGCTGGCCATGGATGTGTCCTCAGTCCACACC 2034 | 303 SerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspllelle | DD 2035 AGCACACTCCTTCGCTACTCCGTGTCCCTGGGCTACGGCTTCTACGGGGACATCATC 2094  323 LysAspSerGluLysLysArgTrDLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLys 342 |
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| Db 1075 ACCTTCCTCTCCACCACTGCTATGAAGGACAGTGTCCTTCCT                                                                                                   | Qy         383 LysGlnGlnLeuGluGluGluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAsp         402           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 403 ValGluGluTrpGlnValValCysGlyLysPheLeuAlaileAsnAlaThrAsnMetSer 1 | 423 CysAlaCysArgArgSerProArgGlyLeuSerProAlaHisLeuGlyAspGlySer | Db 1315 TGTGCTTGTCGCCGGAGCCCCCAGGGCCTCTCCCCGGCTGCCCACTTGGGAGACGGGTCT 1374  Qy 443 SerAspLeulleLeulleArgLysCysSerArgPheAsnPheLeuArgPheLeulleArg 462 |                                                                 | Oy 463 HisThrAsnGlnGlnAspGlnPheAspPheThrPheValGluValTyrArgValLysLys 482<br> | 483 PheGlnPheThrSerLysHisMetGluAspGluAspSerAspLeuLysGluGlyGlyLys 5  | DD 1499 II.C.MGIIIMCGICGAAGGCACAIGGAAGGAAGGGCGACCICAAGGAGGGGGGGAAG 1554<br>Qy 503 IyaargPheGlyHigileCYgSetSetSetHisProSetCygCygCygThrValSetAsnSer 522 | Db 1555 AAGGGTTTGGGCACATTTGCAGCACCCCTCCTGCTGCTGCTGCTGCTCCCAACAGC 1614   | Qy 523 SerTrpAsnCysAspGlyGluValLeuHisSerProAla11eGluValArgValHisCys 542                                                                           | Oy 543 GlnLeuValArgLeuPheAlaArgGlyIleGluGluAsnProLysProAspSerHisSer 562 | 1675 CAGCTGGTTCGACTCTTTGCACGAGAATTGAAGAATCCGAAGCCAGACTCAC<br>SULT 6             |                                                                                                                                                                                            | ; APPLICANT: Tang, Y. Tom ; APPLICANT: Goodrich, Ryle ; APPLICANT: Liu, Chenghua ; APPLICANT: Ren, Feiyan                                                                          |                                                                                 |                                                                                 | PRIOR FILING DATE: 2001-01-30 ; NUMBER OF SEQ ID NOS: 441 ; SOFTWARE: pt_FL_genes Version 2.0 ; SEQ ID NO 148 |                                                                                                                                                                       | ; NAME/KEY: CDS<br>; LOCATION: (1129)(2817)<br>US-10-120-988-148 | Alignment Scores: 4.03e-313 Length: 4432                                                                                                     |

| Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 95.47% Indels: 0 DB: 10 - 31-958-11 (1-562) x US-09-969-896-9 (1-1614) | Qy         26 MetGlyAlaThrGlyAlaAlaGluProLeuGInSerValLeuTrpValLysGlnGlnArg 45 | Qy 46 CysAlaValSerLeuGluProAlaArgAlaLeuLeuArgTrpTrpArgSerProGlyPro 65 | Qy         66 GlyalaGlyalaProGlyalaAspAlaCysSerValProValSerGluIleIleAlaVal 85                                                                                         | Qy         86 GluGluThrAspValHisGlyLysHisGlnGlySerGlyLysTrpGlnLysWetGluLys         105 | Oy 106 ProTyrAlaPheThrValHisCygValLysArgAlaArgAlsArgHisArgTrpLysTrpAla 125  | Qy         126 GlnValThrPheTrpCysProGluGluGlnLeuCysHisLeuTrpLeuGlnThrLeuArg 145 | Qy         146 GluMetLeuGluLysLeuThrSerArgProLysHisLeuLeuValPheileAsnProPhe 165 | Qy         166 GlyGlyLySGlyGlnGlyLySArglleTyrGluArgLySValAlaProLeuPheThrLeu 185                                                                                                               | Qy 186 AlaSerIleThrThrAspIleIleValThrGluHisAlaAsnGlnAlaLysGluThrLeu 205     | Qy         206 TyrGlulleAsnIleAspLySTyrAspGlyIleValCysValGlyGlyAspGlyMerPhe 225 | Qy         226 SerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAspGlnAsn 245 | Qy         246 HisProArgAlaValLeuValProSerSerLeuArgIleG1yIleIleProAlaG1ySer 265 | Qy         266 ThraspCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAlaLeuHis 285                                                                                 | Qy         286 IleValValGlyAspSerLeualaMetAspValSerSerValHisHisHisAsnSerThrLeu 305                                                                           | Qy         306 LeuargTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheTyrGlyBheT | Oy 326 GluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThrPheLeu 345 | 346 SerHisHisHisCosTyrGluGlyThrValSerPheLeuProAlaGlnHisThrValGlySer         |
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|                                                                                                                                                                              | Qy 363 ValGlySerProArgAspArgLysProCysArgAlaGlyCysPheValCysArgGlnSer 382<br>   | Qy       383 LysglnGlnGlnGluGluGluGluGluGluGluBap 402                 | Qy       403 ValGluGluTrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSer 422         Db       2335 GTGGAGGAGTGGCAAGTCGTCTGTGGGAAGTTTCTGGCCATCAATGCCACAAACATGTCC 2394 | Qy 423 CysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySer 442                | Qy 443 SerAspLeuIleLeuIleArgIysCysSerArgPheAsnPheLeuArgPheLeuIleArg 462<br> | Oy 463 HisThrAsnGlnGlnAspGlnPheAspPheThrPheValGluValTyrArgValLysLys 482<br>     | Qy 483 PheGlnPheThrSerLysHisMetGluAspGluAspSerAspLeuLysGluGlyGlyLys 502<br>     | Qy         503 LysargPheGlyHisIleCysSerSerHisProSerCysCysCysThrValSerAsnSer         522           Db         2635 AAGCGTTTGGGGCACATTTGCAGCAGCCACCCCTCCTGCTGCTGCTCCACCACCACCACAGC         2694 | Qy 523 SerTrpAsnCysAspGlyGluValLeuHisSerProAlaIleGluValArgValHisGys 542<br> | Qy 543 GInLeuValargLeuPheAlaArgGlyIleGluGluAsnProLySProAspSerHisSer 562<br>     | RESULT 7<br>US-09-969-896-9<br>; Sequence 9, Application US/09969896            | щО                                                                              | ; TITLE OF INVENTION: KIABSE-LIKE Protein<br>; FILE REFERENCE: 004974.00594<br>; CURRENT APPLICATION NUMBER: US/09/969,896<br>; CURRENT FILING DATE: 2001-10-04 | ; PRIOR APPLICATION NUMBER: US 60/238,005<br>; PRIOR FILING DATE: 2000-10-06<br>; PRIOR APPLICATION NUMBER: US 60/314,113<br>; PRIOR FILING DATE: 2001-08-23 | Ø                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ; TYPE: DNA<br>; ORGANISM: Homo sapiens<br>US-09-969-896-9              | Alignment Scores: 6.05e-309 Length: 1614<br>Pred. No.: 2888.00 Matches: 537 |

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GlnValThrPheTrpCysProGluGluGluGluGluLeuCysHisLeuTrpLeuGlnThrLeuArg 145
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                      US-10-631-958-11 (1-562) x US-10-631-958-9 (1-1614)
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                                                                  ProArgAspArgLysProCysArgAlaGlyCysPheValCysArgGlnSerLysGlnGln
                                    TrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSerCysAlaCys
                                                                                                                             ThrSerLysHisMetGluAspGluAspSerAspLeuLysGluGlyGlyLysLysArgPhe
                                                                                                                                                                                                                                                                                                                                                     GlyHisIleCysSerSerHisProSerCysCysCysThrValSerAsnSerSerTrpAsn
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                                                                                                                                                                                                            446 IleLeulleArgLysCysSerArgPheAsnPheLeuArgPheLeulleArgHisThrAsn
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Sequence 9, Application US/10631958

Publication No. US20040192580A1

GENERAL INFORMATION:
TITLE OF INVENTION: Regulation of human Sphingosine
FILE REFERENCE: 004974.00594

CURRENT APPLICATION NUMBER: US/10/631,958

CURRENT FILING DATE: 2001-10-04

PRIOR PLICH DATE: 2001-10-04

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: US 60/238,005

PRIOR FILING DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 1614

TYPE: DNA

TYPE: DNA

WGANYSM: Homo sapiens
US-10-631-958-9
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Matches:
Conservative:
Mismatches:
Indels:
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|                                                    | Oy         87 GluthraspValHisGlyLysHisGlnGlySerGlyLysTrpGlnLysMetGlULysPro 106 | Oy 107 TyralapheThrValHisCysValLysArgalaArgArgHisArgTrpLysTrpAlaGln 126 | Oy         127 ValThrPheTrpCysProGluGluGlnLeuCysHisLeuTrpLeuGlnThrLeuArgGlu         146 | Oy         147 MetLeudluLysLeuThrSerArgProLysHisLeuLeuValPheileAsnProPheGly 166 | Oy 167 GlytysglyglnGlytysarglleTyrGluarglysValalaProLeuPheThrLeuAla 186 | Qy         187 SerIleThrAspIleIle                                       | Oy 196 GluHisAlaAsnGlnAlaLysGluThrLeuTyrGluIleAsnIleAspLysTyrAspGly 215 | Oy 216 IlevalCysValGlyGlyAspGlyMerPheSerGluValLeuHisGlyLeuIleGlyArg 235 | Qy 236 ThrGlnArgSerAlaGlyValAspGlnAsnHisProArgAlaValLeuValProSerSer 255 | Qy 256 LeuargileGlynleileProAlaGlySerThrAspCysValCysTyrSerThrValGly 275 | Qy         276 ThrSerAspAlaGluThrSerAlaLeuHisIleValValQalGlyAspSerLeuAlaMetAsp 295                                                                  | Oy 296 ValSerSerValHisHisAsnSerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyr 315                                                                      | Oy 316 GlyPheTyrGlyAspIleIleLysAspSerGluLysLysArgTrpLeuGlyLeuAlaArg 335                                                                                | Qy 336 TyraspPheSerGlyLeuLysThrPheLeuSerHisHisHisCysTyrGluGlyThrValSer 355           | Oy 356 PheLeuProAlaGlnHisThrValGlySerProArgAspArgLysProCysArgAlaGly 375 | 376 CysPheValCysArgGlnSerLysGlnGlnLeuGluGluGluGlnLysLysAlaLeuTyr                                                  | Oy 396 GlyLeuGluAlaAlaGluAspValGluGluTrpGlnValValValCysGlyLysPheLeuAla 415 | 416 IleasnalathrasnMetSerCysalaCysargArgSerProArgGlyLeuSerProAla                                                                |
|----------------------------------------------------|--------------------------------------------------------------------------------|-------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|---------------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|
| Db 1021 CCAAGGGATAGGAAAGCCCTGCCGGGCAGGATGCTTTGTTTG | Oy 386 LeugludludludlukysLysAlaLeuTyrdlyLeudluAlaAlaGluAspValGludlu 405        | Oy 406 TrpGlnValValCysGlyLysPheLeuAlalleAsnAlaThrAsnMetSerCysAlaCys 425 | Qy 426 ArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSerAspLeu 445                 | Oy 446 IleLeuIleArgLysCysSerArgPheAsnPheLeuArgPheLeuIleArgHisThrAsn 465         | Oy 466 GINGINASPGINPHeASPPHOTHRPHeVAIGIUVAITYRATGVAILYSLYSPHEGINPHE 485 | Oy 486 ThrSerLysHisMetGluAspGluAspSerAspLeuLysGluGlyGlyLysLysArgPhe 505 | Qy 506 GlyHisIleCysSerSerHisProSerCysCysThrValSerAsnSerSerTrpAsn 525    | Oy 526 CybAspGlyGluValLeuHisSerProAlaIleGluValArgValHisCysGlnLeuVal 545 | Qy 546 ArgLeuPheAlaArgGlyIleGluGluAsnProLysProAspSerHisSer 562<br>      | RESULT 9<br>US-09-784-810A-5<br>; Sequence 5, Application US/09784810A  | ; PAREAL INFORMATION: ; GENERAL INFORMATION: ; APPLICANT: RASTELLI, LUCA ; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING | ; ILILE OF INVENTION: SAME<br>; FILE REFERENCE: 10716-08<br>; CURRENT APPLICATION UNMER: US/09/784,810A<br>; CURRENT FILING DATE: 2001-02-14 | ; PRIOR APPLICATION NUMBER: 60/182,360<br>; PRIOR FILING DATE: 2000-02-14<br>; PRIOR APPLICATION NUMBER: 60/191,261<br>; PRIOR FILING DATE: 2000-03-22 | ; NUMBER OF SEQ ID NOS: 29 ; SOFTWARE Patentin Ver. 2.1 ; SEQ ID NO 5 ; LENGTH: 1840 | ; TYPE: DNA<br>; ORGANISM: Homo sapiens<br>US-09-784-810A-5             | Alignment Scores: 1.9e-282 Length: 1840 Pred. No.: 2649.50 Matches: 495 Excent Similarity: 97.83% Conservative: 1 | : 97.63% Mismatches:<br>87.59% Indels:<br>9 Gaps:                          | US-10-631-958-11 (1-562) x US-09-784-810A-5 (1-1840)<br>, Qy 67 AlaGlyAlaProGlyAlaAspAlaCysSerValProValSerGluIleIleAlaValGlu 86 |

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GlyLysGlyGlyClyLysArglleTyrGluArgLysValAlaBroLeuPheThrLeuAla
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                                                                                      GGAAAAGGACAAGGCAAGCGGATATATGAAAGAAAGTGGCACCACTGTTCACCTTAGCC
                                                                                                         SerileThrThrAspileIle-----ValThr
                                                                                                                 IleasnalaThrasnMetSerCysAlaCysArgArgSerProArgGlyLeuSerProAla
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                                                                 GluValTyrArgValLysPheGlnPheThrSerLysHisMetGluAspSer
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Matches:
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US-10-876-281-5
; Sequence 5, Application US/10876281
; Publication No. US20050123942A1
; GENERAL INFORMATION:
    APPLICANT: RASTELLI, LUCA
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES;
    TITLE OF INVENTION: SAME
; FILE REFERENCE: 10716-08
; CURRENT PELLING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: US/10/876,281
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/182,360
; PRIOR FILING DATE: 2000-02-14
; PRIOR FILING DATE: 2000-02-14
; PRIOR FILING DATE: 2000-03-22
; SOFTWARE: PALENTION NUMBER: 60/191,261
; ROWNERS OF SEQ ID NOS: 29
; SOFTWARE: PALENTION NOWER: 201
; TYPE: DNA
; TYPE: DNA
; TYPE: DNA
; TYPE: DNA
                                                                                                                                                                           1.9e-282
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97.83$
97.63$
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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324 AspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThr 343
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Publication No. US20040192580A1
GENERAL INFORMATION:
APPLICANT: Kossida, Sophia
TITLE OF INVENTION: Kinase-Like Protein
TITLE OF INVENTION: Kinase-Like Protein
FILE REFERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/10/631,958
CURRENT APPLICATION NUMBER: US/09/969,896
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-066
PRIOR FILING DATE: 2001-066
SPIOR APPLICATION NUMBER: US 60/314,113
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
TYPE: DNA
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 CysCysThrValSerAsnSerSerTrpAsnCysAspGlyGluValLeuHisSerProAla 535
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                                        GluValTyrArgValLysLysPheGlnPheThrSerLysHisMetGluAspGluAspSer
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Publication No. US20030125533A1;
GENERAL INFORMATION:
TITLE OF INVENTION: Regulation of human Sphingosine;
FILE REFERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT FILING DATE: 2001-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASELSEQ for Windows Version 4.0
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Mismatches:
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1640.50
96.63%
96.32%
54.23%
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; ORGANISM: Homo sapiens
US-09-969-896-1
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Best Local Similarity:
Query Match:
DB:
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444 AspLeuIleLeuIleArgLysCysSerArgPheAsnPheLeuArgPheLeuIleArgHis 463
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Matches:
Conservative:
Mismatches:
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                                                                                    GENERAL INFORMATION:
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Ren, Feiyan
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Tano, Yong A.
APPLICANT: You, Younghong
APPLICANT: You's You's You's
APPLICANT: You's You's You's
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Porghong T.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 797CON
CURRENT APPLICATION NUMBER: US/10/115,635
CURRENT FILING DATE: 2000-01-17
NUMBER OF SEQ ID NOS: 362
SOFTWARE: PLE_Genes Version 2.0
SEQ ID NO 247
LENGTH: 817
                                                             US-10-115-635-247
Sequence 247, Application US/10115635
Publication No. US20040137434A1
GENERAL INFORMATION:
                           ThrasnGlnGlnAspGln 469
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1156.00
100.00%
100.00%
38.21%
                                   962 ACCAACCAGCAGGACCAG
                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)..(662)
US-10-115-635-247
                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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; ORGANISM: Homo sapiens
US-10-631-958-1
                   Alignment Scores:
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Query Match:
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|------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------|-----------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|
| 103 MetGluLysProTyrAlaPheThrValHisCysValLysArgAlaArgArgHisArgTrp | Qy         163 AsnProPhediyGlyLysGlyClnGlyLysArglleTyrGluArgLysValAlaProLeu 182                                                   | RESULT 14  US-09-969-896-8  Sequence 8, Application US/09969896  Publication No. US20030125533A1  GENERAL INFORMATION:  APPLICANT: KOSSIGA, Sophia  TITLE OF INVENTION: Regulation of human Sphingosine  TITLE OF INVENTION: Robert Sophia  TITLE OF INVENTION: Regulation of human Sphingosine  FILE REFERENCE: 004974.00594  CURRENT APPLICATION NUMBER: US 60/238,005  FRIOR PLING DATE: 2001-10-04  PRIOR FLING DATE: 2001-10-06  FRIOR APPLICATION NUMBER: US 60/314,113  PRIOR FLING DATE: 2001-00-23  NUMBER OF SEQ ID NOS: 16  SEQ ID NO 8  LENGTH: 550  TYPE: DNA  CORGANISM: Home sapiens  US-09-969-896-8                                                                             | Alignment Scores: Pred. No.: Score: Score: 1008.00 Matches: 1008.00 Matches: Best Local Similarity: 100.00\$ Mismatches: 0 Cuery Match: 10 Gaps: 0 US-10-631-958-11 (1-562) x US-09-969-896-8 (1-550) | Qy         1 HisGlualaalaasnGlyProAlaProLeuGlyValArgAlaProProAlaTrpArgThr 20 | ACCCGGCGGCGGAGGCGGCGGCGGGGGCGGCGCGCGCGC                         | Qy 61 ArgSerProGlyPlaGlyAladlyAlaProGlyAlaAspAlaCysSerValProValSer 80                                                                   |

| 181 CGGAGCCCGGGGCCCGGCGCCCCCCGGCGCGGATGCCTGCTCTGTGCCTGTATCT 240 | 81 GluileileAlaValGluGluThrAspValHisGlyLysHisGlnGlySerGlyLysTrp 100 | CCGTTGAGGAAACAGACGTTCACGGGAAACATCAAGGCAGTGGAAAATGG 300 |
|-----------------------------------------------------------------|---------------------------------------------------------------------|--------------------------------------------------------|
| CGGAGCCCGGGGCCCGGAG                                             | GluileileAlaValGluG                                                 | GAGATCATCGCCGTTGAGG                                    |
| 181                                                             | 81                                                                  | 241                                                    |
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| 101 | 101 GlnLysMetGluLysProTyrAlaPheThrValHisCysValLysArgAlaArgArgHis 120 |
|-----|----------------------------------------------------------------------|
| 301 | 301 CAGAAAATGGAAAAGCCTTACGCTTTTACAGTTCACTGTGTAAAGAGAGCACGACGGCAC 360 |
| 121 | 121 ArgTrpLysTrpAlaGlnValThrPheTrpCysProGluGluGluLeuCysHisLeuTrp 140 |

<sup>361</sup> CGCTGGAAGTGGGCGCAGGTGACTTTCTCGTGTCCAGAGGAGCAGCTGTGTCACTTGTGG 420

8 4 8 4 8 4 8 4

<sup>161</sup> PheileasnProPheGlyGlyLysGlyGlnGlyLysArgileTyrGluArgLysValAla 180

<sup>181</sup> ProLeuPhe 183 ||||||||| 541 CCACTGTTC 549

Search completed: September 6, 2005, 10:49:17 Job time : 1646.07 secs

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Scoring table:

Minimum DB Maximum DB

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A6270838 Human Sph
A8877731 DNA encod
AB877731 DNA encod
A6811669 Human cod
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         Abx70921 Novel hum
Aad14426 Human sph
Aaa50510 Human sph
Ads10370 Human the
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antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obselty; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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ABQ99499
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/product= "NOV9a"
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(c) 1993 - 2005 Compugen Ltd.
                                                nucleic search, using frame_plus_p2n model
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22-APR-2002;
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## (CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UW; Ort T, Gorman L, Zerhusen BD, Anderson DM, Zhong M, Carterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36. P-PSDB; ADA05680.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

## Claim 20; Page 134; 586pp; English.

The present line and a carrier; (2) a kit comprising, in one or more described above; (3) an isolated nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for method of identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for show; (10) a method got identifying a potential therapeutic agent for above; (10) a method of a detrivity of the polypeptide; (11) a method for modulating or pathology associated with the polypeptide; (12) method for modulating or pathology associated with the above polypeptide; NoVX ammal; and (14) a method for producing the above polypeptide; NoVX ammal; and (14) a method for producing the above polypeptide; NoVX The present invention describes NOVX proteins, where X can be 1 to 55

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| 180                                                                | 80                                                                 | 240                                                     |
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| 121 GTGAAGCAGCGCTGCGCGTGAGCCTGGAGCCCGCGCGGGGCTCTGCTGCTGCTGGTGG 180 | 61 ArgSerProGlyProGlyAlaGlyAlaProGlyAlaAspAlaCysSerValProValSer 80 | CGGAGCCCGGGGCCCGCCCCCCCCGGTGCTGATGCCTGTCTCTGTGCCTGTATCT |
| 121                                                                | 61                                                                 | 181                                                     |
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| 81 GlullelleAlaValGluGluThrAspValHisGlyLysHisGlnGlySerGlyLysTrp 100 | GAGATCATCGCCGTTGAGGAAACAGACGTTCACGGGAAACATCAAGGCAGTGGAAAATGG | 101 GlnLysMetGluLysProTyrAlaPheThrValHisCysValLysArgAlaArgArgHis 120 |
| 81                                                                  | 241                                                          | 101                                                                  |
| ζ                                                                   | qq                                                           | ò                                                                    |

| 420 | 160                                                          | 480                                                                  |
|-----|--------------------------------------------------------------|----------------------------------------------------------------------|
|     | LeuGlnThrLeuArgGluMetLeuGluLysLeuThrSerArgProLysHisLeuLeuVal | 421 CTGCAGACCCTGCGGGAGATGCTGGAGAAGCTGACGTCCAGACCAAAGCATTTACTGGTA 480 |
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| Db  | δ                                                            | Db                                                                   |

| 180                                                                  | 540                                                           | 200 נ                                                                | 3 600                                                           |
|----------------------------------------------------------------------|---------------------------------------------------------------|----------------------------------------------------------------------|-----------------------------------------------------------------|
| 161 PhelleAsnProPheGlyGlyLysGlyGlnGlyLysArglleTyrGluArgLysValAla 180 | . TITATCAACCCGTITGGAGGAAAAGGACAAGGCAAGCGGATATATGAAAGAAAAGTGGC | 181 ProLeuPheThrLeuAlaSerIleThrThrAspIleIleValThrGluHisAlaAsnGln 200 | . ccacigiticaccitiagcciccatcaccacigacatcatcgitactgaacatgctaatca |
| 161                                                                  | 481                                                           | 181                                                                  | 541                                                             |
| ò                                                                    | ΩÞ                                                            | λ                                                                    | Вb                                                              |

| 201 AlaLysGluThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIleValCysValGly 220 | 601 GCCAAGGAGACTCTGTATGAGATTAACATAGACAATACGACGGCATCGTCTGTGTGGGC 660 |
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| 201 AlaLys                                                           | 601 GCCAAG                                                          |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HisGluAlaAlaAsnGlyProAlaProLeuGlyValArgAlaProProAlaTrpArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerProAlaAlaGluMetGlyAlaThrGlyAlaAlaGluProLeuGlnSerValLeuTrp
                                                               Human sphingosine kinase-like protein; intracellular signalling; ger
cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma;
autoimmune disease; rheumatoid arthritis; Parkinson's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to a human sphingosine kinase-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other;
                                                                                                                                                                                        /product= "sphingosine kinase-like protein"
/note= "see ABB07857"
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                         GGGTCGACCAGAACCACCCCCGGGCTGTGCTCCCCCAGTAGCCTCCGGATTGGAATC
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                                                                                                        ThrSerAlaLeuHisIleValValGlyAspSerLeuAlaMetAspValSerSerValHis
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                                                                                                                                                                                                                                                                                               This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to buman tyrosine and serine/threonine protein kinases (FYK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polynucleotide sequence is a human kinase DNA sequence
                                                                                                                                                                                                             'nucleic acid molecule encoding a kinase polypeptide, useful forparing a composition for treating diseases or disorders, e.g., neurological, immunological or inflammatory disorders.
                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 55; 366pp; English
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                                                     15-JUL-2003; 2003WO-US021730
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P-PSDB; ADJ96664.
                                                                                                              (SUGE-) SUGEN INC
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WO2004006838-A2
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                            22-JAN-2004
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GCGGCGGAGATGGGGGCGACGAGGCGGAGCCGCTGCAATCCGTGCTGTGGAAG 142 GCGCTAACGGTCCGGCGCCCCTCGGCGCGCCCCCAGCCTGGCGGACGACCCC GlnGlnArgCygAlaValSerLeuGluProAlaArgAlaLeuLeuArgTrpTrpArgSer CAGCAGCGCTGCGCCGTGAGCCTGGAGCCCGCGCGGGCTCTGCTGCTGCTGGTGGCGGAGC ProGlyProGlyAlaGlyAlaProGlyAlaAspAlaCysSerValProValSerGluIle CGGGGGCCCGGGGGCCCCCGGCGCGGATGCCTGCTGTTGCTTGTTGTTGTTGAGATC ATCGCCGTTGAGGAAACAGACGTTCACGGGAAACATCAAGGCAGTGGAAAATGGCAGAAA LysTrpAlaGlnValThrPheTrpCysProGluGluGlnLeuCysHisLeuTrpLeuGln AlaAlaAsnGlyProAlaProLeuGlyValArgAlaProProAlaTrpArgThrSerPro AlaAlaGluMetGlyAlaThrGlyAlaAlaGluProLeuGlnSerValLeuTrpValLys IlealaValGluGluThrAspValHisGlyLysHisGlnGlySerGlyLysTrpGlnLys MetGluLysProTyrAlaPheThrValHisCysValLysArgAlaArgArgHisArgTrp Sequence 4429 BP; 1020 A; 1115 C; 1213 G; 1081 T; 0 U; 0 Other; 4429 560 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: (1-4429)US-10-631-958-11 (1-562) x ADJ96598 1.3e-233 3012.00 100.00\$ 100.00\$ 99.57\$ Percent Similarity: Best Local Similarity: Query Match: DB: Scores: 23 23 83 43 143 63 203 83 103 123 ઠે 셤 ò g ઠ 셤 ઠે යි දි ద ઠે 名 8

1342 1402 1522 1042 1462 1162 342 462 182 562 202 622 222 682 242 742 262 802 282 862 302 922 322 982 382 402 442 502 ThrLeuArgGluMetLeuGluLysLeuThrSerArgProLysHisLeuLeuValPheIle AsnProPheGlyGlyLysGlyGlnGlyLysArglleTyrGluArgLysValAlaProLeu TTCACCTTAGCCTCCATCACCACTGACATCATCGTTACTGAACATGCTAATCAGGCCAAG GGTATGTTCAGCGAGGTGCTGCAGCGGTCTGATTGGGAGGACGCAGAGGAGGCCCGGGGTC SerThrLeuLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspIleIle LysAspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLys ThrPheLeuSerHi #Hi #Hi #Cy#TyrGluGlyThrValSerPheLeuProAlaGlnHi #Thr ValGlySerProArgAspArgLysProCysArgAlaGlyCysPheValCysArgGlnSer TGTGCTTGTCGCCGGAGCCCCAGGGGCCTCTCCCCGGCTGCCCACTTGGGAGACGGGTCT CACACCAACCAGCAGGACCAGTTTGACTTCACTTTGTTGAAGTTTATCGCGTCAAGAAA TTCCAGTTTACGTCGAAGCACATGGAGGATGAGGACAGCACCTCAAGGAGGGGGGAAG PheThrLeuAlaSerIleThrThrAspIleIleValThrGluHisAlaAsnGlnAlaLys GluThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIleValCysValGlyGlyAsp GAGACTCTGTATGAGATTAACATAGACAAATACGACGGCATCGTCTGTGTCGCGGGGGAGAT GACCAGAACCACCCCGGGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGAATCATTCCC AlaLeuHisIleValValGlyAspSerLeuAlaMetAspValSerSerValHisHisAsn LysGlnGlnLeuGluGluGluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAsp 1163 AAGCAGCAGCTGGAGGAGGAGAAGAAAAGCACTGTATGGTTTGGAAGCTGCGGAGGAC SerAspLeuIleLeuIleArgLysCysSerArgPheAsnPheLeuArgPheLeuIleArg HisThrAsnGlnGlnAspGlnPheAspPheThrPheValGluValTyrArgValLysLys PheGlnPheThrSerLysHisMetGluAspGluAspSerAspLeuLysGluGlyGlyLys GlyMetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyVal CysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySer 923 343 1343 1403 803 983 1283 1463 503 563 683 743 323 363 383 483 443 163 183 203 623 243 263 283 863 303 423 443 463 143 223 ద ò g g 셤 g 셤 a 셤 g

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The present invention describes an isolated PRO nucleic acid (I). Also described: (I) a vector comprising (I); (2) a host cell comprising the vector of (I); (3) a process for producing a PRO polypeptide; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the polypeptide in combination with a carrier; (8) an article of manufacture comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a matter of (7); (9) a method of determining the presence of a PRO polypeptide in a sample suspected of having the polypeptide; (11) a method of identifying a compound that inhibits or commanal; (12) a method of identifying a compound that inhibits or mimics the activity of or expression of a gene encoding a PRO polypeptide; and (13) a method of stimulating the immune response in a mammal. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                  human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiathmatic; antidabetic; antiallergic; antianemic; antidabetic; antiinflammatory; antipsoriatic; antirhuroid; CNS; dermatological; gastrointestinal; antirheumatic; haptotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; virucide; gene therapy; gene; ss.
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                                                                                                                                                     GlnLeuValArgLeuPheAlaArgGlyIleGluGluAsnProLysProAspSerHisSer
                      SerTrpAsnCysAspGlyGluValLeuHisSerProAlaIleGluValArgValHisCys
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TD;
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PRO sequences have antiallergic, antianaemic, antiarthritic, antidabetic, antinflammatory, antipsoriatic, antitiasthmatic, antitibroid, CNS, dermatological, gastrointestinal, haemostatic, hepatotropic, immunosotimulant, immunosupressive, muscular, nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid (I) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune related disease and in stimulating an immune response. The present sequence represents a human PRO nucleotide sequence from the present invention.
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sequence represents cDNA encoding a human ceramide kinase designated
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 neurological disease; inflammation; human immunodeficiency virus; HIV infection; type 2 diabetes; obesity; sepsis; arteriosclerosis; cancer; neuroprotective; antilflammatory; anti-HIV; antidiabetic; anorectic; antibacterial; antiseptic; anorectic; cytostatic;
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| Qy         443 SerAspLeuIleLeuIleArgLysCysSerArgPheAsnPheLeuArgPheLeuIleArg 462           Db         1375 TCTGACCTCATCCTGAAATGCTCCAAGTTCCAATTTTCTGAGATTTCTCATCAGG 1434           Qy         463 HisThrAsnGlnGlnAspGlnPheAspPheThrPheValGluValTyrArgValLysLys 482           Db         1435 CACACCAACCAGCAGGACCAGTTTGACTTTGTTGAAGTTTATCGCGTCAAGAAA 1494           Qy         483 PheGlnPheThrSerLysHisMetGluAspGluAspSerAspLeuLysGluGlyGlyLys 502           Db         1495 TTCCAGTTTACGTCGAAGCACATGGAGGACAGCGACCTCAAGGAGGGGGGGAAG 1554           Qy         503 LysArgPheGlyHisIleCysSerSerNisProSerCysCysCysCysThrValSerAsnSer 522           Db         1555 AAGCGCTTGGGCACATTGCAGCACCCCCTCCTGCTGCTGCTCCTCCTCCTCCTCCTCCTCCTC | RESULT 6 ADN62844 ID ADN62844 standard; DNA; 1740 BP.  XX AC ADN62844; XX AC ADN62844; XX DT 01-JUL-2004 (first entry) XX KW DE Human NOV9a DNA.  XX KW KW infectious disease; anorexia; cancer-associated cachexia; KW incurodegenerative disorder; Alzheimer's disease; Parkinson's disease; KW metabolic syndrome X; wasting disorder; dyslipidaemia; KW metabolic syndrome X; wasting disorder.  XX XX XX XX NW MC | XX XX XX X6                                                                                                                             |
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| 83 IleAlaValGluGluThrAspValHisGlyLysHisGlnGlySerGlyLysTrpGlnLys 102 295 ATCGCCGTTGAGGAAACATCCAGGGAAACATCAAGGCAGTGGAAAATGGCAGAAA 103 MetGluLysProTyrAlaPheThrValHisCysValLysArgAlaArgArgHisArgTrp 122 1103 MetGluLysProTyrAlaPheThrValHisCysValLysArgAlaArgArgHisArgTrp 122 1123 LysTrpAlaGlnValThrPheThpCysProGluGluGluGluGluCysHisLeuTrpLeuGln 142 1124 LysTrpAlaGlnValThrPheTrpCysProGluGluGluGluGluLeuCysHisLeuTrpLeuGln 142 1125 LysTrpAlaGluMetLeuGluLysErArgGaGGAGCAGCAGTGGTGTCTTGGGCGCAGCGCGGGGGGGGGG                                                                                                                                                                                                                  | SluthrieutyrGluileAsnileAspiysTyrAspGlyileValCysValGlyGlyAsp<br>SluthrieutyrGluileAsnileAspiysTyrAspGlyileValCysValGlyGlyAsp<br>SagaCTCTGTATGGGTTAACATAGACAATACGACGCACGCTCTGTCTG                                                                                                                                                                                                                                                                           | 995 ĠĠĠĊŢĠĠħŶſĠŦŢĠŢĠĠĠĂĊŢĠĠĊĠĸŢĠĠŢĠŢĠŢĠŢĠŢĠŢĠŢĠĸŢĠĸŢĠĸġŢĠĸġ<br>303 SerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyBapileile 322<br> |

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polypeptides and nucleic acids, I treating e.g. cancer, diabetes
                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 39; 395pp; English.
2002US-0381642P.
2002US-0383656P.
2002US-0383831P.
2002US-0391335P.
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PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
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GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                         ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
                                                                                         MALYANKAR U M
                                                                                                                                                                            LEACH M D.
AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                            GUO X.
PATTURAJAN M.
                                                                        SPYTEK K A.
EDINGER S R.
                            SMITHSON G.
MILLET I.
PEYMAN J A.
KEKUDA R.
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                                                                                                                           CATTERTON E.
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RASTELLI
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P-PSDB; ADN62845.
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17-MAY-2002; 28-MAY-2002; 29-MAY-2002; 25-JUN-2002; 2
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                                                                                                                                                                                                                                                                                        Isolated NOVX
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(EDIN/)
(ELLE/)
                                                                                                               (ANDE/)
(ZHON/)
(CATT/)
(JIWW/)
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(PENA/)
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(SHIM/)
(ROTH/)
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(AGEE/)
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(DIPI/)
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(GANG/)
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(JUJJ/)
(LILL/)
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(ORTT/)
(GORM/)
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NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides and cativity of NOVX polypeptides associated with decreased by nucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polymeleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators.

C deponists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide expression and antagonists may also be used to modulate NOVX polypeptide expression and activity of NOVX colypeptides. The anti-NOVX polypeptide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies and antagonists may also be used as a plead as plead to modulate NOVX polypeptide expression and activity of NOVX polypeptides.
Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                     useful for preventing,
and Alzheimer's disease.
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diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polynuclectides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, themaeutopoletic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                 represents DNA encoding a human NOVX protein.
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Novel human cDNA sequence #146.

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This invention relates to the CDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic alasease); neurodegenerative disease, e.g. parkinson's disease, amyotrophic clateral sclerosis, neurodegenerative disease, e.g. parkinson's disease, myotrophic crark-interplant disease (e.g. systemic lupses, rheumatoid arthritis, insulin-dependent diabetes mellitus) erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus); wounds, ulcers, burns; bone disorders (e.g. osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head trauma); lung or luver fibrosis; preperfusion injury in various tissues; bacterial, viral or fungal infections; allergic conditions such as allergic rhinitis, asthma; coagulation disorders (e.g. septic shows); cancer and tumours; and inflammatory diseases (e.g. septic showth, crancer and tumours; and inflammatory diseases (e.g. septic showth, crancer or infection or function of infections agents such as bacteria, fungi, viruses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have

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                                                            Human; gene; ss; nervous system disorder; peripheral neuropathy; huntington's disease; amyotrophic lateral sclerosis; haemophilia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; autoimmune disease; systemic lupus erythematosus; rheumatoid arbritis; insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound; ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke; fibrosis; reperfusion injury; infection; allergic rhinitis; asthma; coagulation disorder; cancer; tumour; inflammatory disease; septic shock crohn's disease; anaphylaxis; prollferation; chemotactic; differentiation; stem cell growth factor; haematopolesis; chemokinetic; haemostatic; antinflammatory; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptide useful for treating neurodegenerative diseases, myo or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.
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Drmanac RT;
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Kue AJ, Yang Y, Wehrman T, Wang J,
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Query Match:

ABX70921 standard; cDNA; 4432 BP.

(first entry)

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                                                                                                                                              The present invention relates to sphingosine kinase (SphK) polypeptides and nucleic acids encoding them. SphK is useful for treating a SphK-associated disorder especially cancers such as leukaemia, lymphoma, ovarian, breast, lung, colon, testicular, stomach and skin, atherosclerosis, restenosis or ischaemia and cell proliferative disease or disorder associated with vascular diseases. SphK gene is used in gene therapy and antisense-therapy. Sphingolipids serving as signalling molecules, have recently emerged as regulators of cell growth, diferentiation, diverse cell phenotypes and cell death. Activation of SphK by tumour necrosis factor (TMF)-alpha inhibits apoptosis in human andothelial cells. The present sequence is human sphingosine kinase
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HisargTrpLysTrpAlaGlnValThrPheTrpCysProGluGluGlnLeuCysHisLeu  ValPheIleAsnProPheGlyGlyLysGlyGlnGlyLysArgIleTyrGluArgLysVal 242 GTATITIATCAACCCGTITGGAGGAAAAGGACAAGGCAAGCGGATATATGAAAGAAAAGTG

160

AlaProLeuPheThrLeuAlaSerIleThrThrAspIleIleValThrGluHisAlaAsn 302 GCACCACTGTTCACCTTAGCCTCCATCACCACTGACATCATCGTTACTGAACATGCTAAT

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GlnAlaLysGluThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIleValCysVal

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of an isolated polynucleotide encoding human sphingosine kinase C (SKC, see AAY96059), an enzyme that phosphorylates sphingosine to form sphingosine 1-phosphate. The polynucleotide was isolated from an Hela cDNA library by PCR amplification. The invention provides polynucleotides (see AAA50808-10) and polypeptides (see AAY96057 c. 59) for the human sphingosine kinase (SK) homologues SKA, SKB and SKC. The polynucleotides may be used as hybridization probes, in the construction of PCR primers for chromosome and gene mapping, in the crecombinant production of SKA, SKB and SKC, and in the generation of associated with abnormal levels of SK expression, or to detect associated with abnormal levels of SK expression, or to detect individuals. Host cells expressing SK can be used in drug screening. Human SK specific antibodies, inhibitors, ligands or their analogues are useful as bioactive agents to treat inflammation or disease including viral, bacterial or fungal infections, allergic responses, mechanical injury associated with trauma, herefatery diseases, lymphoma or here is a conditions with activate the genes of kidney, lung, here is a conditions with activate the genes of kidney, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human sphingosine kinase A, B and C polynucleotides and polypeptides useful in e.g. chromosome and gene mapping, and detecting inflammation or disease associated with abnormal levels of sphingosine kinase expression.
                                                                                            Sphingosine kinase C; SKC; human; drug screening; infection; antiinflammatory; antiallergic; anticancer; inflammation; allergy; cancer; therapy; diagnosis; ds.
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                                                                                                                                                                              Location/Qualifiers
71. .1453
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                                                                   Human sphingosine kinase C cDNA
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                                       (first entry)
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260 IleIleProAlaGlySerThrAgpCygValCysTyrSerThrValGlyThrSerAspAla

ATCATTCCCGCAGGGTCAACGGACTGCGTGTGTACTCCACCGTGGGCACCAGCGACGCA

542 280 602

GCCGGGGTCGACCACCACGACCACCCCCGGGCTGTGCTGGTCCCCCAGTAGCCTCCCGGATTGGA

AlaGlyValAspGlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGly

GluThrSerAlaLeuHisIleValValGlyAspSerLeuAlaMetAspValSerSerVal

GAAACCTCGGCGCTGCATATCGTTGGTTGGGGACTCGCTGGCCATGGATGTGTCCTCAGTC

300 HishisabanSerthrLeuLeuArgTyrSerValSerLeuCeuGlyTyrGlyPheTyrGly CACCACAACAACAGCACACTCCTTCGCTACTCCCGTGTCCCTGCTGGCTTACGGG

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AspilelleLysAspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSer GlyLeuLysThrPheLeuSerHisHisCysTyrGluGlyThrValSerPheLeuProAla GACATCATGAAGGACAGTGAGAAAGGAAACGGTGGTTGGGTTGGCTTTGCCAGATACGACTTTTCA GlnHisThrValGlySerProArgAspArgLysProCysArgAlaGlyCysPheValCys 902 AGGCAAAGCAAGCAGCAGCTGGAGGAGGAGCAGAAAGCACTGTATGGTTTGGAAGCT ArgGlnSerLysGlnGlnLeuGluGluGluGlnLysLysAlaLeuTyrGlyLeuGluAla AsnMetSerCysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGly 320 722 340 782 360 380 420 원 ò ò 셤 셤 ò 66 61 

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Length:
Matches:
Conservative:
Mismatches:
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Gaps:

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Local Similarity: Match:

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| Db 1142 CTCATCAGGCACCACCAGCAGGACCAGTTTGACTTTGACTTTTGTTGAAGTTTATCGC 1201                                                                                                                                                    | Alignment<br>Pred. No.:      | ment Scores:<br>No.:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| Qy       480 VallysEysPheGlnPheThrSerLysHisMetGluAspGluAspSerAspLeuLysGlu 499         Db       1202 GTCAAGAAATTCCAGTTTACGTCGAAGCACATGGAGGATGAGGACGAGCGACCTCAAGGAG 1261                                                     | Score:<br>Percent<br>Best Lo | Score:<br>Percent Similarity:<br>Best Local Similarity:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| Qy 500 GlyGlyLysLysArgPheGlyHisIleCysSerSerHisProSerCysCysThrVal 519                                                                                                                                                       | Query Match<br>DB:           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| מפפפפים אין פין פין די יין יין יין יין פין פין פין פין פין פי                                                                                                                                                              | OT-SO                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| OY 520 SEARBINGSENSETTIANDENCYARABELYGENDALLEGUINGSENSFORMALINGUING 539                                                                                                                                                    | ර් සි                        | 6 GIYProAlaPro<br>   <br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Qy       540 ValHisCysGlnLeuValArgLeuPheAlaArgGlyIleGluGluAsnProLysProAsp 559         Db       1382 GTCCACTGCCAGCTGGTTCGACTCTTTGCACGAGAATTGGAAGAGAATCCGAAGCCAGAC 1441                                                      | & 8                          | 23 AlaAlaGluMet<br>          <br>809 GCGCCGGAGATG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 560 SerHisSer                                                                                                                                                                                                              | ò                            | 43 GlnGlnArgCys                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| DD 1442 TCACACAGC 1450                                                                                                                                                                                                     | g &                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| RESULT 10<br>ADS10370<br>ID ADS10370 standard; DNA; 4702 BP.                                                                                                                                                               | 중 옵                          | 63 FIGGIVERSITY FIGURERS FIGU |
| ADS10370;                                                                                                                                                                                                                  | ò                            | 72                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 16-DEC-2004 (first entry)                                                                                                                                                                                                  | qq                           | 988 GACTCACCTAGO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Human therapeutic DNA - SEQ ID 607.                                                                                                                                                                                        | ò                            | 72                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <pre>KW antinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; KW inflammatory; haematopoiesis; immunity; neurodegenerative;</pre> | q i                          | 1048 CTGTTTAGCTGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|                                                                                                                                                                                                                            | ; 음                          | 1108 CCTGCACCCACC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|                                                                                                                                                                                                                            | ò                            | 72                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 23-SEP-2004.                                                                                                                                                                                                               | q                            | 1168 CCCAGCTCCCAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 30-SEP-2003; 2003WO-US030720.                                                                                                                                                                                              | ò                            | 72                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 02-OCT-2002; 2002US-0416186P.                                                                                                                                                                                              | ପ୍                           | 1228 GGATCTCTGGTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| (NUVE-) NUVELO INC.                                                                                                                                                                                                        | ò                            | 72                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;<br>I wang D Chan B Zhan Oa wang J Ghosh M. Yne al Wang G. Zhou D.                                                                                              | q                            | 1288 ATAGCGGGACGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| waig b, Circli K, allao Kr, mang b, Gilosti M, Aud Ab, meng 6, allou ant. 2004-600007/00                                                                                                                                   | ò                            | 73                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| P-PSI                                                                                                                                                                                                                      | qq                           | 1348 CGGGTGTTCTGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| New polynucleotide, useful in preparing a composition for diagnosing or treating inflammatory, neurodegenerative or stem cell disorders, e.g.,                                                                             | <i>k</i> 1                   | 77 ValProValSer                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|                                                                                                                                                                                                                            | g<br>G                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|                                                                                                                                                                                                                            | ò                            | 97 SerGlyLysTrp<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|                                                                                                                                                                                                                            | gg<br>G                      | 1468 AGTGGAAAATGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating                                                                                  | ò                            | 117 AlaArgArgHis                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|                                                                                                                                                                                                                            | qa                           | 1528 GCACGACC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic DNA of the invention. The current sequence is not shown explicitly within the        | & d                          | 137 CysHisLeuTrp<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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pGlnLysNetGluLysProTyrAlaPheThrValHisCysValLysArg 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGCTGCCCCATAGCTCAGACGTCCCCGAGGCCAGAGGCTGGAGATAAA 1167
                                                                                                                                                                                                                                                                                                                                                                                                  CACTGGTTATTTTGCAGTATGTTCCAAGACTGGGCAGCGTTTACACCTT 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGCTGACTCTGCACGCTGGCCTCCTCCAGCCAGCGGCCTGCTGCTGT 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGGCTGATGCAGGTTTCCCGCGACCTGACAGCATGGAGTGGGGACGG 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isAlaValSerLeuGluProAlaArgAlaLeuLeuArgTrpTrpArgSer 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTTCTCTGGCACTGCTCCAGCAGGGACGGCGCTGGTACTGCCAGGGG 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCCCGGTTCACTGCCTGTTTCTTGTATCTTGTCCAGAGCTATCAGTC 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preuglnThrLeuArgGluMetLeuGluLysLeuThrSerArgProLys 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1PhelleAsnProPheGlyGlyLysGlyGlnGlyLysArgIleTyrGlu 176
                                                                                                                                                                                         t.GlyalaThrGlyalaAlaGluProLeuGlnSerValLeuTrpValLys 42
                                                                                                                                                                                                                                                                                                                           oLeuGly------ValArgAlaProProAlaTrpArgThrSerPro 22
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| diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS44197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the invention and the sequence are sequences. Sequence 2241 BP; 453 A; 627 C; 700 G; 461 T; 0 U; 0 Other; | Alignment Scores:  2.03e-184 Length: 2241 Score: Sc | US-10-631-958-11 (1-562) x AAS77728 (1-2241) | 6 GlyProAlaProLeuGlyValargAlaProProAlaTrpArgThrSerPro 22<br> | 23 AlaAlaGluMetGlyAlaThrGlyAlaAlaGluBroLeuGlnSerValLeuTrpValLys 42<br> | 43 GlnGlnArgCysAlaValSerLeuGluProAlaArgAlaLeuLeuArgTrpTrpArgSer 62<br> | ProGIYProGIYAlaGIYAlaProGIYAla | 72 | 253 GACTCACCTAGCACTGGTTATTTTGCAGTATGTTCCAAGACTGGGCAGCGTTTACACCTT 312 | 72 72 | 313 CTGTTTAGCTGGTTTCTCTGGCACTGCTCCAGCAGGAACGGCGCTGGTACTGCCAGGGG 372 | 72 72 | 373 CCTGCACCCACCCTGCCCCATAGCTCAGACGTCCCCGAGGCCAGAGCTGGAGATAAA 432 | 72 72 | 433 CCCAGCTCCCAGCTGCTGACTCTGCACGCTGGCCTCTCCAGCCAG | 72 72 | 493 GGATCTCTGGTGTCCCCGGTTCACTGCCTGTTTCTTGTATCTTGTCCAGAGCTATCAGTC 552 | 72 72 | 553 ATAGCGGGACGGGAGGCTGATGCAGGTTTCCCGCGACCTGACAGCATGGAGTGGGGACGG 612 | 73 | 613 CGGGTGTTCTGTGTTGAGATGCCAGCTGAAGGACGTGGTGTTTTTACAGATGCCTGCTCT 672 | 77 ValProValSerGluIleIleAlaValGluGluThrAspValHisGlyLyBHisGlnGly 96 | 673 GTGCCTGTATCTCGAGATCGTCGTCGTTGAGGAAACAGACGTTCACGGGAAACATCATCATGGC 732 | 97 SerGlyLysTrpGlnLysMetGluLysProTyrAlaPheThrValHisCysValLysArg 116 | 733 AGTGGAAAATGGCAGAAAATGGAAAAGCCTTACGCTTTTACAGTTCACTGTAAAGAGA 792 |
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| 98999999988                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Align<br>Pred.<br>Score<br>Perce<br>Best<br>Query                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | -SD                                          | දු පු                                                        | \$ B                                                                   | ò 8                                                                    | දි දි                          | ò  | q                                                                    | ò     | qq                                                                  | δ     | g                                                                 | ò     | qq                                                | ઠે    | g                                                                    | ò     | g                                                                    | ઠે | q                                                                    | ò                                                                  | đ                                                                        | ò                                                                   | 원                                                                  |

| ò  | 117 AlaArgArgHisArgTrpLysTrpAlaGlnValThrPheTrpCysProGluGluGlnLeu 136                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| Ob |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| ò  | 137 CysHisLeuTrpLeuGlnThrLeuArgGluMetLeuGluLysLeuThrSerArgProLys 156                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| qq | 853 TGTCACTTGTGGCTGCAGACCCTGCGGGAGATGCTGGAGAAGCTG 897                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| δ  | 157 HisLeuLeuValPhelleAsnProPheGlyGlyLysGlyGlnGlyLysArgIleTyrGlu 176                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| qq | 897                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| ò  | 177 ArgLysValAlaProLeuPheThrLeuAlaSerIleThrThrAspIleIleValThrGlu 196                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| qq | 898ATTACTGAA 906                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| ò  | 197 HisAlaAsnGlnAlaLysGluThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIle 216                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| QQ | / CATGCTAATCAGGCCAAGGAGACTCTGTATGAGATTAACATAGACAAAATACGACGGCATC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| ò  | ValCysValGlyGlyAspGlyMetPheSerGluValLeuHisGlyLeuIleGlyArgThr 236                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| qa | 967 Greneredeseses de la rentación de la contra del la contra |
| ò  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| q  | 1027 cadadadececedederedacedececededererecreerecedaracere 1086                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ò  | 257 ArgileGlylleIleProAla                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| qa | 1087 CGGATTGGAATCCTTCCCGCAGAGCATGTGGGCCCCCGGTGAGAACGCTGGTGGCCTTGGAC 1146                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| ò  | 264 GlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAla 283                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| qq | 1147 GGGTCAACGGACTGCGTGTGTTACTCCCACCGTGGGCACCCACC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| ò  | 284 LeuHisIleValVal 288                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| qq | 1207 CTGCATATCGTTGTTGGCTGCCCCGAGGCTCGGAAACCACCCGCATCCCGCCATACT 1266                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| ò  | 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| qa | 7 GCCTGTGGCAGTGGGCAGCTGTGCCTGGGCTGCCAGCTGTGGAACGCATGCCTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Š  | 9GlyAspSerLeuAlaMetAsp                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| qu | 7 TGTGAGGCCTCGAGGCTTCAGTCCAGGATGCAGAGCCCCGGGGACTCGCTGGCCATGGAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| λõ |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| qq | 7 GIGICCICAGICCACCACACACACACICCITCGCIACTCCGIGICCCIGCIGGGCIAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| λ  | 6 GlyPheTyrGlyAsp1le1leLysAspSerGluLysLysArgTrpLeuGlyLeuAlaArg                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Ωp | 7 GGCTTCTACGGGGACATCATCAAGGACAGTGAGAAAACGGTGGTTGGGTCTTGCCAGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| λ̈ | 336 TyrAspPheSerGlyLeuLysThrPheLeuSerHisHisGysTyrGluGlyThrValSer 355                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| QQ | 1507 TACGACTITICAGGTATAAAGACCTICCTCTCCCACCACTGCTATGAAGGGACAGTGTCC 1566                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| δ  | F PheLeuproAlaGlnHisThrValGlySerProArgAspArgLysFroCysArgAlaGly                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Op | 7 TTCCTCCTGCACACACACGGTGGGATCTCCAAGGAATAGGAAGCCCTGCCGGGCAGGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| ò  | 376 CysPheValCysArgGlnSerLysGlnGlnGluGluGluGluGlnLysLysAlaLeuTyr 395                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| ò  | GlyLeuGluAlaAlaGluAspValGluGluTrpGlnValValCysGlyLysPheLeuAla                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| q  | 87 deringaaderdeedadaacerdeadeadeedadereererdegaagrirereece                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| ò  | 416 IleAsnAlaThrAsnMetSerCysAlaCysArgArgSerProArgGlyLeuSerProAla 435                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |

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useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at the electronic format directly from WIPO at the electronic format directly from WIPO at the sequences.
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                        CGGAGCCCCAGGGGCCTCTCCCCGGCTGCCCACTTGGGGAGACGGGTCTTCTGACCTCATC 900
                                                                                                                                                                                                                                                             HislleCysSerSerHisProSerCysCysCysThrValSerAsnSerSerTrpAsnCys
                                                                                                                                                                  caggaccagriridacircacririgirgaagririarcgcgrcaagaaarrccagriracg
                                                                                                                                                                                                                   CACATTTGCAGCAGCCACCCCTCCTGCTGCTGCACCGTCTCCAACAGGCTCCTGGAACTGC
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                                                                   LeuIleArgLysCysSerArgPheAsnPheLeuArgPheLeuIleArgHisThrAsnGln
                                                                                                                                  GlnAspGlnPheAspPheThrPheValGluValTyrArgValLysLysPheGlnPheThr
                                                                                                                                                                                                 SeriysHisMetGluAspGluAspSerAspLeuLysGluGlyGlyLysLysArgPheGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                 1201 CTCTTTGCACGAGGAATTGAAGAGAATCCGAAGCCAGACTCACACAGC 1248
                                                                                                                                                                                                                                                                                                                                                                                            LeuPheAlaArgGlyIleGluGluAsnProLysProAspSerHisSer 562
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23-AUG-2000; 2000US-00649167.
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P-PSDB; ABG13543.
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New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous system disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g asthma), autoimmune diseases (e.g rheumatoid arthritis) and central and peripheral nervous system disorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein encoding cDNA
                                          Human sphingosine kinase-like protein; intracellular signalling; gene; cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma; autoimmune disease; rheumatoid arthritis; Parkinson's disease; ss.
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/*tag= a
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                                                                                                                                     Location/Qualifiers
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P-PSDB; ABB07854.
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264 ySerThrAspCysValCysTyrSerThrValGlyThrSerAspAla--GluThrSerAla 283
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                                                                       GlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAla 283
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GCTTGTCGCCGGAGCCCCAGGGGCCTCTCCCCCGGCTGCCCACTTGGGAACGGGTCTTCT
                                                             GlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAla
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                           MetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp
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Length: Matches: Conservative: Mismatches:

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Indels: Gaps:

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The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed gene of genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is activity of (II) or to treat disease states involving (II). (II) is cusful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of olypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cand to produce other types of data and products dependent on DNA and amino acid sequences. Assation. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the wint was obtained in the wint was obtained in the way and the invention. The printed specification, but was obtained in the way and the invention. The sequences of the invention are sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 13535; 103pp; English.
                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
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                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
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|-------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|-----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------------------------------------------------------------|
| 284                                                         | 301                                                                  | 321                                                                  | 341                                                                  | 361                                                                  | 381                                                                      | 401                                                                  | 421                                                                  | 441                                                                  | 461                                                                  | 481                                                                   | 501                                                                  | 521                                                                  | 541                                                                                  |
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Search completed: September 6, 2005, 11:26:44 Job time : 944.649 secs

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AB051433 Howo sapi
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CK1386590 Gallus ga
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                      BC067255 H
AX224383 St
BD183468 NA
AB051433 H
CQ730476 St
AB079067 R
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AB079066 Homo sapi
BD102675 Ceramide
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Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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Result No.

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| TOTAL THE STATE OF | Oy 241 GlyValAspGlnAshHisProArgAlaValLeuValProSerSerLeuArgIleGlyIle 260 |
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| - CHICKSH FECCCI VSNOSWICE GENERAL                                                            | s da                                                   | 301 HisbanSerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAsp 320<br>                                                                                                 |
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|                                                                                               | Qy 3                                                   | 361 HisThrvalGlySerProArgAspArgLysProCysArgAlaGlyCysPheValCysArg 380<br>                                                                                                 |
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|                                                                                               | Oy 05                                                  | 441 GlyserSerAspLeulleLeulleArgLysCysSerArgPheAsnPheLeuArgPheLeu 460<br>                                                                                                 |
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|                                                                                               | Oy 15                                                  | 501 GlyLysLysArgPheGlyHisIleCysSerSerHisProSerCysCysCysThrValSer 520<br>                                                                                                 |
|                                                                                               |                                                        | 521 AsnSerSerTrpAsnCysAspGlyGluValLeuHisSerProAlalleGluValArgVal 540<br>                                                                                                 |
| GGATATATGAAAAAGTGGCA 540 1eValThrGluHisAlaAsnGln 200 1fl                                      | Oy 16                                                  | 541 HisCysGlnLeuValArgLeuPheAlaArgGlyIleGluGluAsnProLysProAspSer 560<br>                                                                                                 |
| NYCGITALISAMANISCIAMICAS 800 NYASEGIVILEVALCYSVAIGIY 220 NYGAPGASAMCANTAMICAS 660             | Qy 51                                                  | 561 HisSer 562<br>      <br>1681 CACAGC 1686                                                                                                                             |
|                                                                                               |                                                        | HSA457828 2042 bp mRNA linear PRI 19-APR-2002<br>Homo sapiens mRNA for putative lipid kinase (LK4 gene).                                                                 |
| roserSerLeuArgileGlyile 260<br>                                                               | ACCESSION<br>VERSION<br>KEYWORDS<br>SOURCE<br>ORGANISM | Au457828.1 GI:20269072<br>Au457828.1 GI:20269072<br>Lipid kinase; LK4 gene.<br>Homo sapiens (human)<br>Elwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
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        1 S Van Veldhoven, P. P.
A search for lipid kinases
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S Van Veldhoven, P. P.
Direct Submission
A Submitted (18-APR-2002) Van Veldhoven P. P., Farmakologie,
K. U. Leuven, Herestraat, B-3000 Leuven, BELGIUM
On 12 Submitted (18-APR-2002) Van Veldhoven P. P., Farmakologie,
C. J. Leoven, Merestraat, B-3000 Leuven, BELGIUM
On 12 Submitted (18-APR-2002)
 Eutheria; Primates; Catarrhini; Hominidae; Homo
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                              LysArgPheGlyHisIleCysSerSerHisProSerCysCysThrValSerAsnSer
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Kohama,T.
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Submitted (29-JAN-2002) Masako Sugiura, Sankyo Co., Ltd.,
Parmacology and Molecular Biology Research Laboratories;
Hiromachi 1-chome, Shinagawa-ku, Tokyo 140-8710, Japan
(E-mail:msugiura@shina.sankyo.co.jp, Tel:81-3-3492-3131,
                                                                                                                                                                                                                                                              AB079066 4445 bp mRNA linear PRI Homo sapiens cerk mRNA for ceramide kinase, complete cds AB079066
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Location/Qualifiers
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AlaLeuHisIleValValGlyAspSerLeuAlaMetAspValSerSerValHisHisAsn 302
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E (Dasses 1 to 4463)

Sugiura,M.; Kono,K.

Ceramide kinase and DNA thereof

Patent: WO 0196575-A 1 20-DEC-2001;

SANKYO CO LTD,MASAKO SUGIURA,KEITA KONO,TAKAFUMI KOHAMA

OS Homo sapiens (human)

PN WO 0196575-A/1

PP 11-JUN-2001 WO 2001JP004889

PR 14-JUN-2001 JP 00P 178039

PI MASAKO SUGIURA, KEITA KONO,TAKAFUMI KOHAMA

PC C12N15/54,C12N9/12,C12N1/21,C12Q1/48,C07K16/40,A61K31/7125, PC

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Tang, Y.T., Zhou, P., Goodrich, R., Liu, C., Asundi, V., Ren, F.,
Zhang, Y.T., Zhou, P., Yang, Y., Xue, A.J., Wehrman, T., Wang, J.-R.,
Wang, D. and Drmanac, R.T.
Nucleic acids and polypeptides
Patent: US 6743619-A 148 01-JUN-2004;
Location/Qualifiers
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Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see http://www.sanger.ac.uk/HGP/Chr22/.
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mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1654)
Collins,J.E., Wright,C.L., Edwards,C.A., Davis,M.P., Grinham,J.A., Cole,C.G., Goward,M.E., Aguado,B., Mallya,M., Mokrab,Y.,
Buckle,E.J., Beare,D.M. and Dunham,I.
Direct Submission
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CB10 1SA, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript
Sanger Institute name : pGEM.bK29F11.1
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Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, F.,
Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Soares, M.B., Bonaldo, M.F., Casawant, T.L.,
Stownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Mallahy, S.J., Bosak, S.A., McEwant, P.J.,
Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
ton, E., Ketteman, M., Madan, A., Rodrigues, S.,
hiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Blakesley, R.W., Touchman, J.W., Green, E.D.,
Kodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schein, J.B., Jones, S.J. and Marra, M.A.
See CDNA, sequences
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1772 bp mRNA linear PRI 06-APR-2004 imide kinase, mRNA (cDNA clone IMAGE:6185601),
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nt: Dr. James R. Lupski
paration: Life Technologies, Inc.
ayed by: The I.M.A.G.E. Consortium (LLNL)
y: Genome Sequence Centre,
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TCCATCACCACTGACATCGGTAACAAATTCTATGTTAACTATGTAGAAGTAATTACT 420
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Rastelli,L.
Patent: WO 0160990-A S 23-AUG-2001;
Patent: WO Corporation (US) ; GENENTECH, INC.
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Homo sapiens mRNA for KIAA1646 protein, partial cds.
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                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4171)

2 Ohara,O., Nagase,T. and Nakajima,D.

Novel genes and proteins encoded by the genes

L. Patent: JP 2002345992-A 181 03-DEC-2002;

KAZUSA DNA RESEARCH INSTITUTE
OS Homo aapiens (human)

PN JP 2002345492-A/181

PD 03-DEC-2002

PF 26-FEB-2002

PF 26-FEB-2002

PF 05AMU OHARA,TAKAHIRO NAGASE,DAISUKE NAKAJIMA

PC (12115/09,C07K14/47//A61K31/711,A61K38/00,A61P25/00,PC

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BD183468
BD183468.1 GI:31875668
JP 2002345492-A/181.
Homo sapiens (human)
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Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission

Birect Submission

Birect Submission

Bobartment of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
Fax:81-438-52-3914)
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                                                                                        Hirosawa,M., Nagase,T., Murahashi,Y., Kikuno,R. and Ohara,O. Identification of novel transcribed sequences on human chromosome 2by expressed sequence tag mapping DNA Res. 8 (1), 1-9 (2001) 21156230
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Catarrhini; Hominidae; Homo.
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Homo sapiens
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Mammalia; Eutheria; Primates;
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| 158 LeuLeuValPheIleAsnProPheGlyGly <sup>L</sup> ysGlyGlnGlyLysArglleTyrGluArg 177 | 349 349  178 LysvalhlaProLeuPheThrLeuAlaSerIleThrThrAspIleIleValThrGluHis 197 | ::: | 198 ALAARGIAALELYSGIUTIKIEGUTYGGIULEASBILYSTYTASBGIYITEVAL 217<br> | 218 CysvalGlyGlyAspGlyMetPheSerGluValLeuHisGlyLeuIleGlyArgThrGln 237                                  | 238 ArgSerAlaGlyValAspGlnAsnHisProArgAlaValLeuValProSerSerLeuArg 257 |   | 542 ATTGGAATCATTCCCGCAGGGTCAACGGACTGCGTGTTACTCCACCGTGGGCACCAGC 601 278 AppalaGluThrSerAlaLeuHisIleValValGlyAppSerLeuAlaMetAppValSer 297                                                          | 602 GACGCAGAAACCTCGGCGCTGCATATCGTTGGGGACTCGCTCG                                         | 298 SerValHisHisAsnSerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPhe 317 | 318 TyrGlyaspileileLysaspSerGluLysLysargTrpLeuGlyLeualaargTyrAsp 337 | PheserGlyLeuLysThrPheLeuSerHisHisCysTyrGluGlyThrValSerPheLeu<br>                                                    | 358 ProAlaGlnHisThrValGlySerProArgAspArgLysProCysArgAlaGlyCysPhe 377 | ValCysArgGlnSerLysGlnGlnLeuGluGluGluGlnLysLysAlaLeuTyrGlyLeu                                                          | GTTTGCAGGCAAAGCAAGCAGCTGGAGGAGGAGCAGAAGAAAGCACTGTATGGTTTG GluAlaAlaGluAspValGluGluTxpGlnValValCysGlyLySPheLeuAlaIleAsn                 | 962 GAAGCTGCGGAGGACGTGGAGGGGAGTCGTCTGTGGGAAGTTTCTGGCCATCAAT 1021 418 AlaThrAsnMetSerCysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHis 437 | 1022 GCCACAAACATGTCCTGTGCTTGTCGCCGGAGCCCCAGGGGCCTCCCCGGCTGCCCAC 1081 | TIGGGAGACGGGTCTTCTGACCTCATCCTCATCCGGAAATGCTCCAGGTTCAATTTTCTG                                                                                                     | 458 ArgPheLeulleArgHisThrAsnGlnGlnAspGlnPheAspPheThrPheValGluVal 477 | 478 TyrargvallysDheGlnDheThrSerLysHisMetGluAspGluAspSerAspLeu 497 | 498 LysgludlyglybysbysArgPhedlyHislleCysSerSerHisProSerCysCysCys 517<br> |
|-----------------------------------------------------------------------------------|-------------------------------------------------------------------------------|-----|--------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|---|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------------|--------------------------------------------------------------------------|
| ò                                                                                 | 요 &                                                                           | ପ୍ର | <b>ĕ</b> 8                                                         | è a                                                                                                   | S G                                                                  | ò | a &                                                                                                                                                                                              | qq                                                                                      | S S                                                                  | ò 8                                                                  | 8 8                                                                                                                 | 8 8                                                                  | ò                                                                                                                     | 名 &<br>8                                                                                                                               | 8 B                                                                                                                                   | 음 중                                                                  | S q                                                                                                                                                              | S G                                                                  | λο qα                                                             | S G                                                                      |
|                                                                                   | Qy 542 CysGlnLeuValArgLeuPheAlaArgGlyIleGluGluAsnProLysProAspSerHis 561<br>   | 562 | UD 1442 AGC 1444<br>RESULT 11                                      | CQ730476 LCCUS LCCUS DEFINITION Sequence 16410 from Patent WO02068579. VERSION CQ730476.1 G1.42304409 | Homo sapiens (human)                                                 |   | AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses | Thereof<br>JOURNAL Patent: WO 02068579-A 16410 06-SEP-2002;<br>PE Corporation (NY) (US) | FEATURES Location/Qualifiers source 1. 1459 /organism="Homo sapiens" | /mol_cype="unassigned_bnA<br>/db_xref="taxon:9606"                   | Alignment Scores: 3.17e-164 Length: 1459 Pred. No.: 2510.00 Matches: 478 Percent Similarity: 87.89% Conservative: 1 | ty: 87.71% Mismatches:<br>82.98% Indels:<br>6 Gaps:                  | US-10-631-958-11 (1-562) x CQ730476 (1-1459)<br>Qy 18 TrpArgThrSerProAlaAlaGluMetGlyAlaThrGlyAlaAlaGluProLeuGlnSer 37 | Db 3 TGGCGGACCAGCGGCGGCGGACATGGGGGCGACGGGCGGCGGCGCGCTGCAATCC 62  Qy 38 ValleuTrpValLy8GlnGlnAxgCy8AlaValSerLeuGluProAlaArgAlaLeuLeu 57 | Db 63 GTGCTGTGGGTGAAGCAGCAGCGCTACCAA                                                                                                  | 95GGACGTGTTTTTACAGATGCTCTGTG                                         | Qy       78 ProValSerCluIleIleAlaValGluGluThrAspValHisGlyLysHisGlnGlySer 97         Db       128 CCTGTATCTGAGATCATCGCCGTTGAGGAAACAGACGTCACGGGAAACATCAAGGCAGT 187 | GlyLysTrpGlnLysMetGluLysProTyrAlaPheThrValHisCysValLysArgAla         | 118 ArgargHisArgTrpLysTrpAlaGlnValThrPhFTrpCysProGluGluGlnLeuCys  | 138<br>308                                                               |

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                                                            GTCAGAGTCCACTGCCAGCTGGTTCGACTCTTTGCACGAATTGAAGAATTGAAGAAATTGAAGAATCCGAAG 1441
                                                                                                                                                                      2830 bp mRNA linear ROD 27-JUN-2002 for ceramide kinases, complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                            538 ValArgValHisCysGlnLeuValArgLeuPheAlaArgGlyIleGluGluAsnProLys
ThrValSerAsnSerTrpAsnCysAspGlyGluValLeuHisSerProAlaIleGlu
                                                                                                                                                                                                                                                                                          Sugiura, M., Kono, K., Liu, H., Shimizugawa, T., Minekura, H., Spiegel, S. and Kohama, T.
Ceramide Kinase, a Novel Lipid Kinase. MOLECULAR CLONING AND FUNCTIONAL CHARACTERIZATION J. Blod. Chem. 277 (26), 23294-23300 (2002)
                                                                                                                                                                                                                                                                                                                                                                               Sugiura,M., Kono,K., Shimizugawa,T., Minekura,H., Spiegel,S.
Kohama,T.
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Submitted (29-JAN-2002) Masako Sugiura, Sankyo Co., Ltd.,
Pharmacology and Molecular Biology Research Laboratories;
Hiromachi 1-chome, Shinagawa-ku, Tokyo 140-8710, Japan
(E-mail:msugiura@shina.sankyo.co.jp, Tel:81-3-3492-3131,
Fax:81-3-5436-8565)
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Mismatches:
Indels:
Gaps:
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Mus musculus cerk mRNA
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                                             GluGluThrAapValHisGlyysHisGlnGlySerGlyLysTrpGlnLysMetGluLys 105
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961 TCTCATCAGTACTATGAAGGGACACTGTCCTTCCCAGCACAGCACACGGTGGGATCT
                                                                                                                                                                                                                                                     IleValValGlyAspSerLeuAlaMetAspValSerSerValHisHisAsnSerThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysAlaValSerLeuGluProAlaArgAlaLeuLeuArgTrpTrpArgSerProGlyPro
                                                                                                                                                                                 GlnValThrPheTrpCysProGluGluGlnGeuCysHisLeuTrpLeuGlnThrLeuArg
                                                                                                                                                                                         186 AlaSerIleThrThrAspIleIleValThrGluHisAlaAsnGlnAlaLysGluThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                  HisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAlaGlySer
MetGlyAlaThrGlyAlaAlaGluProLeuGlnSerValLeuTrpValLysGlnGlnArg
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Start codon is not identified."

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is not identified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 TATGATGGCATCGTGTGGGTAGGTGGGGACGGCATGTTCAGCGAGGTGCTGCATGGGGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 AlaMetAspValSerSerValHisHisAsnSerThrLeuLeuArgTyrSerValSerLeu
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Conservative:
Mismatches:
Indels:
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1912.50
92.49%
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Prediction of the coding sequences of mouse homologues of KIAA gene: III. the complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries 22977043
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Direct Submission

Submitted (13-JUL-2003) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7

Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mail:mouse@kazusa.or.jp, Tel:81-418-52-3919, Pax:81-438-52-3918)

The CREATE program supported by Japan science and technology
corporation; cDNA full insert sequencing: Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
IleLeulleArgLysCysSerArgPheAsnPheLeuArgPheLeulleArgHisThrAsn
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                                                          TrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSerCysAlaCys
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protein.
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/mol_type="mRNA"
/db_xref="taxon:10090"
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Mus musculus mRNA for mKIAA1646
AK129416
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Mus_musculus (house mouse)
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ECORI-NotI cut cDNA was then ligated into the vector. Vector:
pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia
coli DH10B.
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72
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Conservative:
Mismatches:
Indels:
Gaps:
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/ organism="gallus gallus"

/ mol type="mENA"

/ strain="White Leghorn, Hisex"

/db xref="raxon:9031"

/ clone="ChEST29119"

/ clone lib="CSEQCHV2"

/ dev_stage="stage 22"
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                            ThrValSerPheLeuProAlaGlnHisThrValGlySerProArgAspArgLysProCys 372
                                                                                 AlaLeuTyrGlyLeuGluAlaAlaGluAspValGluGluTrpGlnValValCysGlyLys 412
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Tickle, C. and Wilson, S.A.

Direct Submission

Submitted (05-APR-2004) Sanger Institute, Hinxton, Cambridgeshire, CBIO 18A, UK. E-mail enquiries: chickeet@bms.umist.ac.uk

BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
  Gallus gallus (chicken)
Gallus gallus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing project.
This sequence is from the BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from heads, normalised, and poly A-trimmed.
                                                                                                                                                                                                                TTCCTGGCCATCAATGCCACCAACATGTCCTGTGCTTGTCCTCGGAGCCCTGGGGGCCTG
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CR386590.1 GI:46239349
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|1217 GAGGAAGAGTCATAAGCAAGAACCCCAAAGCCCAGGAGC 1255
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.Ac.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergen, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skallska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Mazra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-JUN-2004) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4801, Rockville, MD 20892-7510, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QHICKPRAFTVRYVQRVRKHRWRCKEVTFWCSDEQLFYQWLQAFHDLLEQQTHRPKNL
LVYINPYGGKKRGKQIYENKVAPLFSAAGICADVIVTEYANHARDHLYDANLEKYDGV
VCVGGDGMFSEVLHGLIVRWQKDSDVDHNNPSAQLSRCNMRIGIIPAGSTDCICYATV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RERSRPGICLTRVLHQTRGLVNRFTRQFPSGGVTVPVTE1VSVGEAEIDEKYYNSMKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 161 Row: a Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/clone lib="NICHD XGC_Brn1"
/lab_host="DH10B"
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/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="MGC:84197 IMAGE:6954181"
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/db_xref="LocusID:444656"
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/protein_id="AAH74350.1"
/db_xref="GI:49257665"
                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project
Contact: XGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement:
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Klein, S. and Gerhard, D.S.
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Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,
Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
Hopkins, F., Jordan, H., Moore, T., Max, S. I., Wang, J., Heish, F.,
Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
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Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W.
and Richardson,P.
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                                                                                           Thr Val SerPhe Leu Pro Ala Glu His Thr Val Gly Ser Pro Arg Asp Arg Lys Pro Cys
                                                                                                                         ArgAlaGlyCysPheValCysArgGlnSerLysGlnGlnLeuGluGluGluGlnLysLys
                                                                                                                                                                                                                                                                                                                         393 AlaLeuTyrGlyLeuGluAlaAlaGluAspValGluGluTrpGlnValValCysGlyLys
                                                                                                                                                                                                                                                                                                                                                                                                                                               PheLeuAlaIleAsnAlaThrAsnMetSerCysAlaCysArgArgSerProArgGlyLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgPheAsnPheLeuArgPheLeuIleArgHisThrAsnGlnGlnAspGlnPheAspPhe
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Xenopus laevis MGC84197 protein, mRNA (cDNA clone MGC:84197
MACB:6954181), complete cds.
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GINDPETSALHIILGDCQPLDVCSVHYKRTFLKYSVSLLGYGFYGDVLKGSEKNRWLG
PARYDVSGFKTFLTHHCYEGSVSFQPAKWVLGSPRDQTTCTSGCYICRQSSKQLDEQE
QTQACGSEHREQDDDWTTIKGRFWAINAVSWSCACPRSPNGISPAHLADGSADLIIV
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NPSKVF"

116 499 156 HisLeuLeuValPheIleAsnProPheGlyGlyLysGlyGlnGlyLysArgIleTyrGlu 176 619 196 619 216 739 236 919 559 CACCAAACAAGAGGCCTAGTAAACCGTTTCACTCGGCAATTCCCTTCAGGTGGTGTTACC 319 CTGAGGCCCCGACACGGAAGAGAACGGAGCCGGCCCGGAATCTGCTTGACAAGAGTGCTC 259 71 ------AlaAspAlaCysSer 76 96 GinginArgCysAlaValSerLeuGluProAlaArgAlaLeuLeuArgTrpTrpArgSer ValProValSerGluIleIleAlaValGluGluThrAspValHisGlyLysHisGlnGly HisAlaAsnGlnAlaLysGluThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIle SerGlyLygsTrpGlnLysMetGluLysProTyrAlaPheThrValHisCysValLysArg AlaArgArgHisArgTrpLysTrpAlaGlnValThrPheTrpCysProGluGluGlnLeu CysHisLeuTrpLeuGlnThrLeuArgGluMetLeuGluLysLeuThrSerArgProLys 177 ArglysValAlaProLeuPheThrLeuAlaSerIleThrThrAspIleIleValThrGlu ValCysValGlyGlyAspGlyMetPheSerGluValLeuHisGlyLeuIleGlyArgThr GTTTGTGTTGGTGGGATGGATGTTCAGCGAAGTGCTGCATGGCCTCATTGTCAGAATG nArgSerAlaGlyValAspGlnAsnHisProArgAlaValLeuValProSerSerLeu AlaAlaGluMetGlyAlaThrGlyAlaAlaGluProLeuGlnSerValLeuTrpValLys ProGlyProGlyAlaGly-----AlaProGly------2494 322 83 125 30 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: (1-2494)US-10-631-958-11 (1-562) x BC074350 6.16e-109 1714.00 72.32% 57.50% 56.66% Percent Similarity: Best Local Similarity: Query Match: DB: Scores: ជ 260 63 200 320 380 440 200 157 960 217 300 960 43 143 72 77 97 117 137 620 197 680 740 237 . No. . Alignment

1159 1219 1399 1039 1099 1339 1459 TIAAGGCACCITATCAGGCACACAAGCAATAAAGACCAGTTTGACTTTCCATTTGTTGAA 1519 1759 376 396 416 476 GTTTATCGAGTAAAGAATTTTCAGTTTACTCCAAAACACTTTGAAGATGAAGACAATGAA 1579 533 316 336 436 456 494 AspPheSerGlyLeuLysThrPheLeuSerHisHisCysTyrGluGlyThrValSerPhe SerCysCysCysThrValSerAsnSerSerTrpAsnCysAspGlyGluValLeuHisSer LeudrgPheLeulleArgHisThrAsnGlnGlnAspGlnPheAspPheThrPheValGlu ---SeraspLeuLysGluGlyGlyLysLysArgPheGlyHisIleCysSerSerHisPro SeraspalaGluThrSeralaLeuHisIleValValGlyAspSerLeuAlaMetAspVal PheTyrGlyAspileIleLysAspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyr rrrrargeagargrraaagggagrgaaaaaaarcgrrggrragrccrgcragarar PheValCysArgGlnSerLysGlnGlnLeuGluGluGluGlnLysLysAlaLeuTyrGly LeuGluAlaAlaGluAspValGluGluTrpGlnValValCysGlyLysPheLeuAlaIle HisLeuGlyAspGlySerSerAspLeulleLeulleArgLysCysSerArgPheAsnPhe ValTyrArgValLysLysPheGlnPheThrSerLysHisMetGluAspGluAsp-----1220 1340 1640 277 920 297 980 317 1040 337 1100 377 397 417 437 1400 457 1460 477 495 357 g & 6 6 6 6 6 6 B 6 B 6 B 6 B 6 B 6 6 6 6 ద 상 음 ò 셤 ò

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Sequence 46720, A
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-817-6768-12
US-09-817-6768-12
US-09-817-6768-12
US-09-949-016-7026
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| Sequence 264, App<br>Sequence 3319, A<br>Sequence 53119, A<br>Sequence 5319, A<br>Sequence 328, App<br>Sequence 516, Ap<br>Sequence 513, Ap<br>Sequence 513, Ap<br>Sequence 62139, A<br>Sequence 62139, A<br>Sequence 374, Ap<br>Sequence 3121, Ap<br>Sequence 378, Appl<br>Sequence 45, Appl<br>Sequence 1350, Ap | of Drosophila melanogaster                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 26.5%;   Score 801.5;   DB 4;   Length 687;                                                                    |
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| 4 US-09-603-208A-264<br>4 US-09-270-767-53119<br>4 US-09-270-767-53119<br>4 US-09-134-000C-5366<br>4 US-09-134-000C-5366<br>4 US-09-134-000C-5366<br>4 US-09-270-767-62339<br>4 US-09-270-767-62339<br>4 US-09-270-767-62339<br>4 US-09-134-000C-3813<br>3 US-09-134-001C-4774<br>4 US-09-959-897-45<br>4 US-09-959-897-37<br>4 US-09-959-897-37<br>4 US-09-252-991A-2614;<br>4 US-09-252-991A-2614;                                             | ALIGNMENTS tion US/09270767 t al. cletc acids and proteins eference: 7326-094 MBER: US/09/270,767 62517 . 2.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 5%; Score 801.5; DB 3%; Pred. No. 9.7e-74 97; Mismatches 20 EPARALLEWWRSPGRGAGAP :           CGNEAKAPLPPDSPAGA |
| 64 4 4 8 3 3 7 2 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9                                                                                                                                                                                                                                                                                                                                                                                           | 874, Applica<br>6703491<br>GRMATION:<br>DRMATION:<br>DRWENTION: NU<br>ENCE: File R<br>ENCE: File R<br>ENC: File R<br>ENCE: File R<br>ENCE: File R<br>ENCE: File R<br>ENCE: File R<br>ENC |                                                                                                                |
| 28 146<br>29 144<br>30 126.5<br>32 123.5<br>33 119.5<br>35 116.5<br>36 116.5<br>39 116.5<br>40 107.5<br>41 104.5<br>42 104.5<br>45 103.5                                                                                                                                                                                                                                                                                                         | RESULT 1 US-09-270-767-45874 US-09-270-767-45874 Patent No. 6703491 GENERAL INFORMATION: APPLICANT: Homburge; TITLE OF INVENTION: CURRENT FILICATION: CURRENT FILICATION: CURRENT FILICATION: CURRENT FILICATION: CURRENT FILING DATE SEQ ID NO 45874 LENGTH: 687 LENGTH: 687 CREATH: 687                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Ouery Match Best Local S Matches 197  Oy 36  Db 59  Oy 112  Oy 127  Db 172  Oy 184  Db 172                     |

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TITLE OF INVENTION: METHODS OF USE THEREFOR
                                                                                                                                  ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-053-510-19
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Best Local Similarity
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                               467 RNQQVETEDSHLAASEAALLRPRPRPGNLRLPTGSISSMRNLGNDQWKVVRGNFFMICGA 526
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                                                                                                                                                                                                                                                                                                            Sequence 46720, Application US/09270767

Fatent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburer et al.
TITLE OF INVENTION:
FILE REFERENCE: File Reference: 7226-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46720
LENGTH: 359
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; APPLICANT: Saba, Julie D.; APPLICANT: Fyrst, Henrik; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 19.4%; Score 585.5; DB 4; Length 359; Best Local Similarity 35.5%; Pred. No. 8.7e-52; Matches 125; Conservative 55; Mismatches 103; Indels 69
                                                                                                                                                                                                    530 VLHSPAIEVRVHCQLVRLFARGIEENPKP 558
                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Drosophila melanogaster
399 AAEDVE-
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US-09-270-767-46720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REPERENCE: FILE REFERENCE: FILE REPERENCE: FILE REPERENCE: FILE REPERENCE: VS/09/270, 767
CURRENT APPLICATION NUMBER: US/09/270, 767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 64405
LENGTH: 299
                                                                                                                                                                                                                                                                                                                                     Query Match 10.1%; Score 306; DB 4; Length 490;
Best Local Similarity 24.6%; Pred. No. 1.4e-22;
Matches 119; Conservative 68; Mismatches 165; Indels 132; Gaps
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FILE REPERENCE: 200116 402C2
CURRENT APPLICATION NUMBER: US/10/053,510
CURRENT FILING DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-270-767-61405
, Sequence 61405, Application US/09270767
, Patent No. 6703491
, GENERAL INFORMATION:
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9.0%; Score 271.5; DB 4; llarity 30.0%; Pred. No. 7.5e-19; Conservative 44; Mismatches 111;
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US-09-817-676A-14
Sequence 14, Application US/09817676A
Parent No. 6800470
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                        US-09-970-516-4; Sequence 4, Application US/09970516; Patent No. 6610534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 14
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US-09-970-516-4
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US-09-817-676A-14
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Matches 78; Conserval
                                                                                                                                                                                                                                                                                                                                                               ; GENERAL INFORMATION:
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                                                                                                   -----EWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFL
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      Gaps
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APPLICANT: Saba, Julie D.
APPLICANT: Saba, Julie D.
APPLICANT: Saba, Julie D.
APPLICANT: Fyreat, Henrik
TITLE OF INVENTION: SPHINGSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
TITLE OF INVENTION: POLYNCLEOTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 --SSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKP
      Indels
   82;
   Mismatches
                                                                                                                                                                                 380 ---RQSKQQLEEEQKKALYGLEAAEDVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Drosophila melanogaster
   35;
                                                           342 KTFLSHHCYEGTVSFL-
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Matches 121, Conservative
   Conservative
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   85;
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   Matches
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APPLICANT: No. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REPERENCE: 4-316.7
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                    116 RARRHRWKWAQVTFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 CRGGGHPLDLLSVTLASGSRCFSFLSVAMGFVSDVDIQSERFRALGSARFTLGTVLGLAT 332
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APPLICANT: Kohama, Takafumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
PRIOR APPLICATION NUMBER: US 60/194,318
PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 ERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGR
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453 RFNFLRFLIR---HTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSD---LKEGGKKRFG
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Sequence 2, Application US/09970516

Patent No. 6610534

GENERAL INFORMATION:

APPLICANT: No. 6610534artis AG

TITLE OF INVENTION: Induction of blood vessel formation through administration of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NHYAGYEQVTNEDLLINCTLLLCRRLLSPMNLLSLHTASGLRLFSVLLSAWGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 RPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 QLEEEQKKALYGLEAAEDV-EEWQVVCGK----FLAINATNMSCACRRSPRGLSPAAHLG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GVMHLFYVRACVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFR-----LEPKD--- 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 KEGGKKRFGHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENP- 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----YSTVGTSDAETSALHIVVGDSLA-MDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQ 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 DGSSDLILIRK-CSRFNFLR-FLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDL 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 RPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSBELGRW 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 DAH-----LVPLE--EPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 DGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVC---
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25.3%; Pred. No. 1.2e-18;
tive 68; Mismatches 169;
                                                                           GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT: Brian, WATTENBERG W
APPLICANT: Brian, WATTENBERG W
APPLICANT: Pu, XIA
APPLICANT: Richard, D'ANDRA J
APPLICANT: Mathew, VADAS A
APPLICANT: MATHER: 2000-11-13
CURRENT APPLICATION NUMBER: US/09/959,897
CURRENT APPLICATION NUMBER: PCT/AU00/00457
PRIOR APPLICATION NUMBER: AU PQ 0339
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PATENTIN VERSION 3.1
FENDIN OF SEQ ID NOS: 20
                     Sequence 2, Application US/09959897
Patent No. 6730480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.3*
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-959-897-2
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                                                                      GENERAL INFORMATION:
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                                                                                                                          236 TQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYS-----TVGTSDAETSALHI 286
                                                                                                                                                                                                                                                                                                                                                                                287 VVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLS 346
                                                                                                                                                                                                                                                                                                                                                                                                              273 CRGGGHPLDLLSVTLASGSRCFSFLSVAWGFVSDVDIQSERFRALGSARFTLGTVLGLAT 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 TSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINID 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Takafumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expession and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 12
                                                Gaps
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Length 618;
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9.0%; Score 271.5; DB 4; Length 30.0%; Pred. No. 7.5e-19; Live 44; Mismatches 111; Indels
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28.5%; Pred. No. 1.9e-18;
tive 49; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09817676A
Patent No. 6800470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 HHCYEGTVSFLPAQHTVGSP 366
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Best Local Similarity 20...
Rest Toy Conservative
                                              Conservative
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ORGANISM: Mus musculus
US-09-817-676A-12
Query Match
Best Local Similarity
Matches 78; Conserv
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154 RPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKY 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----YSTVGTSDAETSALHIVVGDSLA-MDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VDGELMVSEAVQGQVHPNYFWMVSGCVEPPPS 371
                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 384
TAPE. ...
                                                                                                                                                                                                                                                                                                                                      68; Mismatches 169;
                                                                                                                                                                                                                                                                                                    8.7%; Score 264.5; DB 4
25.3%; Pred. No. 1.9e-18;
   7 09:36:39 2005
                                                                                                                                                                                                                                                                                                                    al Similarity 25.3
107; Conservative
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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Matches 10
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79;

DB 4; Length 384;

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Sequence 7026, Application US/09949016
Patent No. 6812339
WKP 374
            RESULT 11
US-09-949-016-7026
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; TYPE: PRT ; ORGANISM: Human US-09-949-016-7026

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NAME/KEY: MISC_FEATURE
LOCATION: (1): (184)
COURT INFORMATION: SEQ ID NO 3 is the peptide sequence of hSPHK1 in Fig. 3, correspondence in the sequence of hSPHK1 in Fig. 3, correspondence in the sequence of homo sapiens SPHK-1 of General INFORMATION: nding to amino acid residue 1 to 384 of Homo sapiens SPHK-1 of General INFORMATION: nbank sequence Accession Number AAF73423.

AUTHORS: Nava et al.
TITLE: Functional characterization of human spingosine kinase-1
VOLUME: 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Spiegel, Sarah

TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
FILE REPERENCE: 07320001aa (2033957-0001)

CURRENT APPLICATION NUMBER: US/09/796,487

CURRENT FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: US 60/186,532

PRIOR PILING DATE: 2000-03-03

PRIOR PILING DATE: 2000-03-03

PRIOR PILING DATE: 2000-03-03

PRIOR PILING DATE: 2000-03-03

SOFTWARE: PALCATION NUMBER: US 09/530,868

PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3
                                                                                                                                                                                                                                   73 DALVVMSGDGLMHEVVNGLMERPDWETAIQK------PLCSLPAGSGNALAASL 120
                                                                                                                                                                                                                                                                                                      ----YSTVGTSDAETSALHIVVGDSLA-MDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD 324
                                                                                                                                                                                                                                                                                                                                   SEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQ 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440 DGSSDLILIRK-CSRFNFLRFLI-----RHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDE 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 -GVMHLFYVRAGVSRAMLIRFFLAMEKGRHM----EYECPYLVYVPVVAFR-----LEPK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 D-----GKGVFA-------VDGELMVSEAVQGQVHPNY FWMVSGCVE 367
                                                                                                    154 RPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKY
                                                                                                                                 214 DGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVC---
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                                                   Gaps
                                                   87;
                                                   Indels
8.7%; Score 263.5; DB 4;
25.1%; Pred. No. 2.4e-18;
ative 69; Mismatches 164;
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DATE: 2000
DATABASE ACCESSION NUMBER: AAF73423
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Patent No. 6830916
                         Best Local Similarity 25.19
Matches 107; Conservative
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ORGANISM: Homo sapiens
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     Query Match
Best Local (
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; DATABASE ENTR)
US-09-817-676A-15
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Patent No. 6800470

GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT PILING DATE: 2001-03-26
PRIOR PILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 15
LENGTH: 388
                                                                                                                                                                                                                                                                                                                                      154 RPKHLLVFINPFGGKGGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKY 213
                                                                                                                                                                                                                                                      214 DGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVC--- 270
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                                                                                                                            Length 384;
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PUBLICATION INFORMATION:
TITLE: Molecular cloning and functional characterization of
TITLE: murine sphingosine kinase
JOHENBAL: J. Biol. Chem.
                                                                                                                            8.7%; Score 263.5; DB 4; Length
25.1%; Pred. No. 2.4e-18;
cive 69; Mismatches 164; Indels
; DATABASE ENTRY DATE: 2000-06-01
; RELEVANT RESIDUES: (1)..(384)
; PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AFF73423
; DATABASE ENTRY DATE: 2000-06-01
; RELEVANT RESIDUES: (1)..(384)
US-09-796-487-3
                                                                                                                           Query Match
Best Local Similarity 25.1:
Matches 107; Conservative
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PAGES: 23722-23728
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US-09-817-676A-15
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FEATURE:
NAME/KEY: MISC_PEATURE
LOCATION: (1).7(388)
COTHER INFORMATION: SEQ ID NO 2 is the peptide sequence of SPHKIb in Fig. 1, correspondence INFORMATION: ACCESSION Number AAC61698.
OTHER INFORMATION: Accession Number AAC61698.
PUBLICATION INFORMATION:
AUTHORS: Kohama et al.
TITLE: Molecular cloning and fuctional characteriation of murine sphingosine
TITLE: kinase
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Patent No. 6830916

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use TIER ERFERCE: 07320001aa (2033957-0001)
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use FILE REPRENCE: 07320001aa (2033957-0001)
FILE REPRENCE: 07320001aa (2033957-0001)
FILE OF INTERING DATE: 2000-03-03
FRIOR PRILING DATE: 2000-03-03
FRIOR APPLICATION NUMBER: US 60/186,532
FRIOR PILING DATE: 2000-05-05
FRIOR FILING DATE: 2000-05-05
FRIOR FILING DATE: 2000-03-05
FRIOR FRIOR FILING DATE: 2000-03-05
FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIO
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                                                                                                                                                                                                                                                                                                                                             Length 388;
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DATABASE ACCESSION NUMBER: AAC61698
DATABASE ENTRY DATE: 1998-09-26
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Best Local Similarity 23.3%
Matches 100; Conservative
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352 CEAVQGQVH 360
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Musculus
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APPLICANT: Saba, Julie D.
APPLICANT: Strt, Henrik
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
CURRENT APPLICATION NUMBER: US/10/053,510
CURRENT PILING DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASELSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                    8.6%; Score 260; DB 4; Length 388;
23.3%; Pred. No. 5.6e-18;
trive 70; Mismatches 173; Indels
                          DATE: 1998
DATABASE ACCESSION NUMBER: AAC61698
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (1). (388)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC61698
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (1). (388)
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Patent No. 6830881
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ORGANISM: Homo sapiens
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8; Search time 114.766 Seconds (without alignments) 1893.930 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-631-958-11 3025 1 HEAANGPAPLGVRAPPAWRT......QLVRLFARGIEENPKPDSHS 562 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s: geneseqp1990s: geneseqp2001s: geneseqp2001s: geneseqp2002s: geneseqp2003bs: geneseqp2003bs: A\_Geneseq\_16Dec04:\* 4.0.0 / 8 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description                   | Abb07857 Human sph | Abb07856 Human sph | Human    | Adj96664 Human lip | Human    | Aam49115 Human cer | Abr56302 Human Sph | Aay96059 Human sph | Aae07884 Human sph | Human    | Human    | Abg13541 Novel hum | Abr56301 Human Sph |          | •        |          | Ads12267 Human the | Aab41822 Human ORF | Abp64913 Human pro | Human    | Abb69669 Drosophil | Abg13540 Novel hum | Aae07885 Partial r | Abg13542 Novel hum |          |
|-------------------------------|--------------------|--------------------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|----------|----------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|----------|
| ID                            | ABB07857           | ABB07856           | ADA05680 | ADJ96664           | ADN62845 | AAM49115           | ABR56302           | AAY96059           | AAE07884           | ADP55248 | ADS11054 | ABG13541           | ABR56301           | ABG13543 | ABB07854 | ABG13544 | ADS12267           | AAB41822           | ABP64913           | AAB42383 | ABB69669           | ABG13540           | AAE07885           | ABG13542           | ADQ88891 |
| DB                            | ß                  | 'n                 | 9        | œ                  | æ        | ß                  | v                  | ٣                  | 4                  | 8        | æ        | 4                  | 9                  | 4        | ß        | 4        | æ                  | ო                  | ς.                 | ო        | 4                  | 4                  | 4                  | 4                  | 8        |
| %<br>Query<br>Match Length DB | 562                | 537                | 537      | 537                | 537      | 537                | 481                | 460                | 471                | 531      | 536      | 746                | 416                | 727      | 326      | 454      | 255                | 228                | 190                | 182      | 296                | 136                | 144                | 136                | 532      |
| Query<br>Match                | 100.0              | 95.5               | 95.5     | 95.5               | 95.5     | 95.2               | 85.6               | 81.4               | 81.2               | 80.3     | 77.7     | 73.2               | 73.1               | 56.7     | 54.2     | 45.0     | 38.3               | 34.9               | 34.1               | 32.6     | 22.3               | 22.0               | 21.4               | 20.8               | 19.8     |
| Score                         | 0                  | 2888               | 2888     | 2888               | 2888     | 2880               | 2588               | 2463               | 2456.5             | 2428     | 2350     | 2215               | 2210               | 1714.5   | 1640.5   | 1361.5   | 1159               | 1055               | 1032               | 986      | 675                | 664                | 647                | 628                | 900      |
| Result<br>No.                 |                    | 7                  | c        | 4                  | S        | 9                  | 7                  | æ                  | σ                  | 10       | 11       | 12                 | 13                 | 14       | 15       | 16       | 17                 | 18                 | 19                 | 20       | 21                 | 22                 | 23                 | 24                 | 25       |

The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g. asthma), autoimmune diseases (e.g. rheumatoid arthritis) and central and peripheral nervous system disorders (e.g. parkinson's disease). The present sequence represents the human sphingosine kinase-like protein

Claim 25; Fig 11; 120pp; English.

| Partia<br>Drosop<br>D. mel<br>D. mel<br>D. mel<br>Drosop<br>D. mel<br>Novel<br>Human<br>Ruman<br>Human<br>Human<br>Human<br>Human<br>Human<br>Human | Adf28783 Human sph<br>Aab18659 A human r |
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## ALIGNMENTS

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New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous system
                                                                                                        Human sphingosine kinase-like protein; intracellular signalling; cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma; autoimmune disease; rheumatoid arthritis; Parkinson's disease.
                                                                                     Human sphingosine kinase-like protein.
                     ABB07857 standard; protein; 562 AA.
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23-AUG-2001; 2001US-0314113P.
                                                                03-JUL-2002 (first entry)
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Mismatches 0;
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Sequence 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKKRWIGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILIRKCSRFNFLRFLIRHTNQQDQFDFTFVEVYRVKXFQFTSKHMEDEDSDLKEGGKKRF 505
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and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         537
                                                                                                                                                                                                                                                                 The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (eathman, autoimmune diseases (e.g. rheumatoid arthritis) and central an peripheral nervous system disorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMLEKLISRPKHLLVFINPFGGKGGCKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGATGAAEPLQSVLWVKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMLEKLTSRPKHLLVFINPFGGKGOGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                           New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.5%; Score 2888; DB 5; L
llarity 100.0%; Pred. No. 1.3e-269;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                    Claim 25; Fig 10; 120pp; English.
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Local Similarity
thes 537; Conserva
WPI; 2002-340094/37
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                         N-PSDB; ABL40828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 537 AA;
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protein SEQ ID NO:40
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immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. antibacterial; virucide; human; NOVX; antidiabetic; anorectic;

Homo sapiens

WO2003029424-A2

10-APR-2003

02-OCT-2002; 2002WO-US031373

09-0CT-2001; 2001US-0377475. 09-0CT-2001; 2001US-0379170. 09-0CT-2001; 2001US-0328044P. 09-0CT-2001; 2001US-0328044P. 12-0CT-2001; 2001US-0328044P. 15-0CT-2001; 2001US-0328044P. 16-0CT-2001; 2001US-0330109P. 22-0CT-2001; 2001US-0330309P. 24-0CT-2001; 2001US-0341058P. 24-0CT-2001; 2001US-0341658P. 24-0CT-2001; 2001US-0341658P. 29-0CT-2001; 2001US-034955P. 01-NOV-2001; 2001US-034955P. 2002US-0373260P. 2002US-0373815P. 17-APR-2002;

2002US-0373817P. 2002US-0373826P. 2002US-0373884P. 2002US-0374977P 2002US-0381038P. 2002US-0381037P 19-APR-2002; 22-APR-2002; 16-MAY-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002; 16-MAY-2002;

2002US-0381642P. 2002US-0383656P. 2002US-0381042P. 29-MAY-2002; 2002US-0383831P, 25-JUN-2002; 2002US-0391335P. 16-MAY-2002; 17-MAY-2002;

2002US-00262511 (CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

2003-381626/36.

N-PSDB; ADA05679

obesity, or New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing pharmacogenomics

Claim 1; Page 135; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell

comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above colypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a cor preventing a pathology associated with the above polypeptide; NOVX sequences have antidiabetic, anoredicit, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian conditions associated with a human disease. The polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease immune disorders, because immune disorders, because of pathons, in chromosome mapping, tissue typing, preventive medicine and corposer, in chromosome mapping, tissue typing, preventive medicine and corposer, in chromosome mapping, tissue typing, preventive methodicine. ö 120 420 145 205 265 240 325 300 385 360 445 82 9 61 EETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLR 181 YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS EKKRWLGLARYDFSGLKTFLSHHCYBGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQ MGATGAAEPLOSVIWVKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV 1 MGATGAAEPLÓSVLWVKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS TDCVCYSTVGTSDAETSALH1VVGDSLAMDVSSVHHNSTLLRYSVSLLGYGYGFYGD11KDS TDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDS EKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQ LEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDL **EETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLR** EMLEKLTSR PKHLLVFINP FGGKGQGKR I Y ERKVA PLFTLAS I TTD I I VTEHANQAKETL Gaps . 0 Length 537; Indels 95.5%; Score 2888; DB 6; L 100.0%; Pred. No. 1.3e-269; ive 0; Mismatches 0; Best Local Similarity 100. Matches 537; Conservative present invention. Sequence 537 AA; 56 907 266 326 146 241 386 Query Match Best Local ( 98 301 셤 셤 a ద a 셤 ઠે ò ઠે 8 à à ò

505 562 ILIRKCSRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRF ILIRKCSRFNFLRFLIRHTNQQDQFDFTFVBVYRVKKFQFTSKHMEDEDSDLKEGGKKRF GHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEBNPKPDSHS 446 421 361 206 481 셤 요 Š 8

445

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human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
                                                                                                                            1LIRKCSRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDBDSDLKEGGKKRF 480
181 YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS 240
                                                                                                                                                                                                                 LEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDL 420
                                                                                                                                                                                                                                                      ILIRKCSRFNFLRFLIRHTWQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRF 505
                                                                                                                                                                                                                                                                                                                              CHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS 562
                                   EKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQ
                                                                                                                                                                                  LEBEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDL
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2001US-0328029P.
2001US-0328029P.
2001US-0328054P.
2001US-0328044P.
2001US-033843P.
2001US-033843P.
2001US-033843P.
2001US-033832844P.
2001US-03382843P.
2001US-034382P.
2001US-034383P.
2001US-034383P.
2001US-034383P.
2001US-034383P.
2001US-034383P.
2002US-0373815P.
2002US-0373815P.
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2002US-0373815P.
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09-OCT-2001;
12-OCT-2001;
15-OCT-2001;
17-OCT-2001;
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22-OCT-2001;
24-OCT-2001;
24-OCT-2001;
29-OCT-2001;
01-NOV-2001;
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09-OCT-2001;
09-OCT-2001;
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17-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NOV9a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (FTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polypeptide sequence is a human kinase protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMLEKLTSRPKHLLVFINPFGGKCGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule encoding a kinase polypeptide, useful for preparing a composition for treating diseases or disorders, e.g., cancer, or neurological, immunological or inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                              kinase; human; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease; cardiovascular disease; brain; neuronal associated disease; metabolic; inflammatory disorder; cytostatic; neuroprotective; immunomodulator; antiinflammatory; enzyme; lipid kinse; KIAA1646.
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100.0%; Pred. No. 1.3e-269;
.ive 0; Mismatches 0;
                                                                                                                              Human lipid kinse KIAA1646 protein SeqID 121.
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                    ADJ96664 standard; protein; 537 AA
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                                                                                            (first entry)
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537; Conservative
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                                                                                                                                                                                                                                                                                                                                WO2004006838-A2.
                                                                                                                                                                                                                                                                               sapiens
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                                                                                            06-MAY-2004
                                                          ADJ96664;
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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abstrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The cused to modulate NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polypeptide antibodies and antagonists may also be used to modulate NOVX polypeptide antibodies and in a says to identify of NOVX cused to modulate NOVX polypeptide antibodies and antagonists may also be used to modulate NOVX polypeptide antibodies and in a says a say also be used to modulate for detecting the presence of NOVX in samples. NOVX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 40; 395pp; English.
28-MAY-2002; 2002US-0383656P.
29-MAY-2002; 2002US-0383831P.
25-JUN-2002; 2002US-0391335P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EISEN A.
GANGOLLI E A.
RIEGER D K.
                                                                                                                                                                                                             ELLERMAN K.
MALYANKAR U M.
ORT T.
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ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
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SHENOY S G.
SHIMKETS R A.
ROTHENBERG M I
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BERGHS C.
DIPIPPO V A.
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PATTURAJAN M.
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EDINGER S R.
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                                                                        MILLET I.
PEYMAN J P
KEKUDA R.
                                                             SMITHSON
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(JUJJ/)
(LILL/)
(GUOX/)
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(MALY/)
(ORTT/)
(GORM/)
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(CATT/)
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polypeptides and polynucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
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                                                                                                                                                                                                                                                                          26 MGATGAAEPLQSVLWVKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV
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                                                                                                                                                                                                     95.5%; Score 2888; DB 8; Length 537; 100.0%; Pred. No. 1.3e-269; ive 0; Mismatches 0; Indels (
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Matches 537; Conservative
                                                                                                                                                                         Sequence 537 AA;
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Best Local S
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Matches
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                                                                                                                                                                                                                                                              This sequence represents a human ceramide kinase designated hCERKI. The invention relates to hCERKI, nucleic acids encoding it, expression vectors and host cells containing hCERKI nucleic acids, the recombinant production of hCERKI and antibodies specific for hCERKI. The invention also encompasses methods of isolating hCERKI from samples, the use of hCERKI indig screening, and the use of hCERKI nucleic acid sequences in gene therapy. hCERKI mediates the ATP-dependent 1-phosphorylation of carmides and can be used to screen for therapeutic and preventive agents for a wide range of disorders. Such disorders include neurological disease, inflammation, human immunodeficiency virus (HIV) infection, type 2 diabetes, obesity, sepsis, arteriosclerosis and cancer
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                                                                                                                                                                                           Human ceramide kinase gene and the enzyme encoded by it for screening substances as drugs for neurological, inflammatory and other disorders
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Pred. No. 7.7e-269;
1; Mismatches 1;
                                                                                                                                                                                                                                      Claim 1; Page 54-57; 61pp; Japanese.
                                                                                                                    Kohama T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.2%;
                             11-JUN-2001; 2001WO-JP004889
                                                          14-JUN-2000; 2000JP-00178039
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Matches 535; Conservative
                                                                                                                    Sugiura M, Kono K,
                                                                                                                                                 2002-179513/23
                                                                                      (SANY ) SANKYO CO
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20-DEC-2001
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241 IKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IIAVEETDVHGKHQGSGKHQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to human sphingosine kinase 4 (SPHK4; ABR56301). The kinase can be used for the diagnosis and treatment of sphingosine related disorders. The kinase can also be potentially used for controlling toxicity of platelet transfusion and as a platelet stabiliser. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Platelet derived polypeptides with sphingosine kinase activity treatment of sphingosine related disorders.
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                                                                                                                                                                                                                                                      Human, enzyme, haemostatic, sphingosine kinase 4; SPHK4; platelet transfusion; platelet stabiliser.
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                                                                                                                                                                                                   Human Sphingosine kinase 4-related protein.
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standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of human sphingosine kinase C (SKC), an enzyme that phosphorylates sphingosine to form sphingosine 1-phosphate. The sequence was deduced from that of a polymucleotide (see AAASOIO) isolated from an Hela cDNA library. The invention provides polymucleotides (see AAASOSO8-10) and polypeptides (see AAYSOSO-10) for the human sphingosine kinase (SK) homologues SKA, SKB and SKC. The polymeptides can be obtained using recombinant DNA methods, and host cells containing expression vectors including SK polymucleotides are used in a claimed method of screening for compounds that inhibit or activate human SK activity. Human SK specific antibodies, inhibit or activate their analogues can be used as bioactive agents to treat inflammation or disease including viral, bacterial or fungal infections, allergic responses, mechanical injury associated with trauma, hereditary diseases, lymphoma or carcinoma, and other conditions with activate the genes of kidney, lung, heart, lymphoid or tissues of the nervous system
                                                                      480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human sphingosine kinase A, B and C polynucleotides and polypeptides useful in e.g. chromosome and gene mapping, and detecting inflammation or disease associated with abnormal levels of sphingosine kinase expression.
                                           561
                                       Sphingosine kinase C; SKC; human; drug screening; infection; antiinfilammatory; antiallergic; anticancer; inflammation; allergy; cancer; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 460;
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Pred. No. 1.2e-228;
1; Mismatches 1;
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                                                                                                                                                                                           AAY96059 standard; protein; 460
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                                                                                                                                                                                                                                                                          Human sphingosine kinase C.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    WO200052173-A2.
                                                                                               S 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, sphingosine kinase; SphK; restenosis; ischaemia; gene therapy; antisense therapy; cancer; sphingolipid; signalling molecule; apoptosis; cytostatic; tumour necrosis factor-alpha; TNF; atherosclerosis; lymphoma; leukaemia; vasctropic; cell proliferative disorder; vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated Sphingosine Kinase polypeptide useful for treating a SphK-
associated disorder especially cancer, restenosis or ischemia in a human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to sphingosine kinase (SphK) polypeptides and nucleic acids encoding them. SphK is useful for treating a SphK-associated disorder especially cancers such as leukaemia, lymphoma,
                                                                                                                                                                             241 TFLSHHCYEGTVSFLPAOHTVGSPRDRKPCRAGCFVCROSKQSLEEEQKKALYGLEAAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 VEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 HTNQQDQFDFTFVEVYRVKKPQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNS
                                         NPFGGKGOGKRIYERKVAPLFTLASITTDIIVTEHANOAKETLYEINIDKYDGIVCVGGD
                                                                                                                                           GMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETS
                                                                                                                                                                                                                                                                                          ALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLK
                                                                                                                                                                                                                                                                                                                                                          181 ALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTNQQDQPDFTFVEVYRVKKPQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNS
NPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                     TFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE07884 standard; protein; 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2000; 2000US-0182360P.
22-MAR-2000; 2000US-0191261P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKC 451
               atherosclerosis, restenosis or ischaemia and cell proliferative disease or disorder associated with vascular diseases. SphK gene is used in gene therapy and antisense-therapy. Sphingolipids serving as signalling molecules, have recently emerged as regulators of cell growth, diverse cell phenotypes and cell death. Activation of SphK by tumour necrosis factor (TNR) -alpha inhibits apoptosis in human endothelial cells. The present sequence is human sphingosine kinase
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                                                                                                                                                                                                                                                                                                               1 MEKPYAFTVHCVKRARRHRWKWAQVTFWCPESQLCHLWLQTLREMLEKLTSRPKHLLVFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWL
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                         4; Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS
 ovarian, breast, lung, colon, testicular, stomach and skin,
                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                     Score 2456.5; DB 4
Pred. No. 5.4e-228;
1; Mismatches 0;
                                                                                                                                                                                                                     tch 81.2%;
al Similarity 97.5%;
459; Conservative
                                                                                                                                                                                    Sequence 471 AA;
                                                                                                                                                 (SphK) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     512
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                                                                                                                                                                                                                       Query Match
Best Local
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human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiatehmatic; antidibbetic; antilinflammatory; antipsoriatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; lammunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
                                                                                                                    Human PRO protein sequence SEQ ID NO:1224.
                             ADP55248 standard; protein; 531 AA
                                                                                        (first entry)
                                                                                                                                                                                                                                      virucide; gene therapy
                                                                                                                                                                                                                                                                                                WO2004039956-A2
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                        18-NOV-2004
                                                          ADP55248
RESULT 10
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13-MAY-2004

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265

205

YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS

206 181 566 241

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TDCVCYSTVGTNDAETSALHIIIGDSLAIDVSSVHYHNTLLRYSVSLLGYGFYGDLIKDS 300

TDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDS 325

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The present invention describes an isolated PRO nucleic acid (1). Also described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the cisolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) fused to a heterologous amino acid sequence; (6) an tibody which specifically binds to a polypeptide of (4); an agonist or composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the comparising a container, a label on the container and a composition of marmal; (10) a method of treating an immune related disease in a marmal; (10) a method for determining the presence of a PRO polypeptide or an asample suspected of having the polypeptide; (11) a method of container and a composition of container and a composition of a marmal; (12) a method of identifying a compound that inhibits or comparisons an immune related disease or an inflammatory immune response in a mammal; (12) a method of stimulating the immune response in a mammal. The container have antializeristic, antialmatory, antipsociatic, antialmatory, antispociatic, antialmatory, antispociatic, antialmatory, antispociatic, antialmatory, antispociatic, antialmatory, antispociatic, antialmatory, and the encoded polypeptides, compositions, kits and methods are conspectation personal and treating an immune response and methods are cuseful in diagnosing and treating an immune response and methods are cuseful in diagnosing and immune response. The present sequence represents a human construction from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO polynucleotides and polypeptides, useful in useful in diagnosing treating an immune related disease, e.g. systemic lumis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMLEKLISRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITIDIIVTEHANQAKETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 MGATGAAEPLOSVLWVKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEBQLCHLWLQTLR
                                                                                                                                                                                                                                                                            nimmune related disease, e.g. systemic lupus rheumatoid arthritis, diabetes mellitus or asthma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                        Williams PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.3%; Score 2428; DB 8;
85.1%; Pred. No. 3.7e-225;
iive 33; Mismatches 46;
                                                                                                                        Schoenfeld J,
                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1224; 3009pp; English
                                                                                                                           Gurney AL,
                                                                                                                                                                                                                                                                                                                   stimulating an immune response.
28-OCT-2003; 2003WO-US034381
                                         29-OCT-2002; 2002US-0422472P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 85.1
Matches 450; Conservative
                                                                                 (GETH ) GENENTECH INC
                                                                                                                        Clark H,
                                                                                                                                                                                          2004-376182/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                              N-PSDB; ADP55247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 531 AA;
                                                                                                                                              Wu TD;
                                                                                                                                                                                                                                                                                                erythematosus,
                                                                                                                        Aggarwal S,
Wood WI, Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
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The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinfilammatory, neuropercetive, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic protein of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
                                                          445
                                                                                    420
                                                                                                                                 ILIRKCSRPNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRP 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z, Ma Y;
Weng G, Zhou P;
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                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy.
            EKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQ
                                                         LEBEQKKALYGLEAAEDVEEWQVVCGKPLAINATNMSCACRRSPRGLSPAAHLGDGSSDL
                                                                        New polynucleotide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
                                                                                                                                                                                            GKICKDRPSCTCSASRSSWNCDGEVMHSPAIEVRVHCQLVRLFARGIEE 529
                                                                                                                                                                           GHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEE 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2350; DB 8; Length 536;
Pred. No. 1.3e-217;
2; Mismatches 9; Indels 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang
AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J, Wehrman
, Ghosh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 1291; 718pp; English
                                                                                                                                                                                                                                                                                                                                                                      Human therapeutic protein - SEQ ID 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang J,
Wang J,
                                                                                                                                                                                                                                                                                 ADS11054 standard; protein; 536 AA
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78.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asundi V, Ren F,
Chen R, Zhao QA,
                                                                                                                                                                                                                                                                                                                                          (first entry)
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N-PSDB; ADS10370.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Wang D,
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                                                                                                                                                                                                TNQQDQFDFTFVEVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNSS
HITTINIANE MEMORRANG COMBANDA SETTANG 
                                                                                                                                                                                                                                                                                                                                                                                                                198 HTFTLVTALGCEHRSHPHFMDEDRRTGEHVGPGENAGGLDGSTDCVCYSTVGTSDAETSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKT
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                                                                                                                                                                          GKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRH
                                                                                                                                                                                                                                                                                                                                                                      ----GSTDCVCYSTVGTSDAETSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder.
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                                                                                                              60 VHCVKRARRHRWKWAQVTFWCPEBQLCHLWLQTLREMLBKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WNCDGEVLHSPAIEVRYHCOLVRLFARGIEENPKPDSHS
                                                                                                                                                                                                                                                                    GLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA---
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2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome
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23-AUG-2000;
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Gaps

Indels 116;

452; Conservative

Best Loca Matches

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LRWWR-----SPGPGAGAPGADACSVPVSEIIAVEETDVHGKHQGSGKWQKMEKPYAFT 110

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stabiliser
                            678
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                                                                 The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for generation expression or blodycal activity. The polypeptide and polynuclectide sequences for other traits to assess biodiversity and to acid sequences. Asgono10-48030377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at (II) with very manual directly from WIPO at (II) at the printed specification, but was obtained in the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPAPTLL---PHSSDVPEARAGDKPSSQLLTLHAGLSSQRACCCGSLVSPVHCLFLVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ITEHANQAKETLYEINID 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRW 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 WNACLCEASRLOSRMOSPGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRW 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRK 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLREMLEKL 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LRWWR-----SPGPGAGAPGADACSVPVSEIIAVEETDVH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 ELSVIAGREADAGFPRPDSMEWGRRVFCVEMPAEGRGV-FTDACSVPVSEIIAVEETDVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 GPAPLGVRAPPAWRTSPAAEMGATGAAEPLQSVLWVKQQR----CAVSLEPARAL----
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    assess
                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                   73.2%; Score 2215; DB 4; Length 746; 68.7%; Pred. No. 2.3e-204;
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  or other traits and
                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Mismatches
                                         SEQ ID NO 43900; 103pp; English
responsible for genetic disorders biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 MLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Platelet derived polypeptides with sphingosine kinase activity for treatment of sphingosine related disorders.
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  556
                                                                                                                                                                                                                                                                                                                                                                                     Human, enzyme; haemostatic; sphingosine kinase 4; SPHK4; platelet transfusion; platelet stabiliser.
511 SHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENP
                          SHPSCCCTVSNSSWNCDGEVLHSPAIEVR----AVWARGCRKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HOKK-) HOKKAIDO TECHNOLOGY LICENSING OFFICE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 29-30; 39pp; Japanese.
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                                                                                                                                                                                      416
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                                                                                                                                                                                 ABR56301 standard; protein;
                                                                                                                                                                                                                                                                                                                                          Human Sphingosine kinase 4.
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Best Local Similarity 100.
Matches 416; Conservative
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               LIRKCSRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFG
                                                                       HICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy, forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 43902; 103pp; English.
                                                                                                                                                                                                                                                 Novel human diagnostic protein #13534.
                                                                                                                                                            ABG13543 standard; protein; 727 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT;
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Best Local Similarity
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                                                                                                                                                                                                                                                         241 IVVGCCPEARKPPASRHTACGSGHGOLCLGCOLWNACLCEASRLOSRMOSPGDSLAMDVS 300
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                                                                         61 GPKQMPAKGQVCRLPLLKLEASGLLRSEGRTCRSPDRLCSSCSIVCVGGDGMFSEVLHGL
                                                                                                                                                                                      181 FTLVTALGCEHRSHPHFMDEDRRTGEHVGPGENAGGLDGSTDCVCYSTVGTSDAETSALH
                                                                                                                                                                                                                                                                                                                                                                478 YRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNSSWNCDGEVLHSPAIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 IVV------GDSLAMDVS
                                                                                                                                                                                                                                                                                       SVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFL
                                                                                                                                                                                                                                                                                                                                              358 PAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAIN
                                                                                                                                                                                                                                                                                                                                                                                                      418 ATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHTNQQDQFDFTFVEV
                IGRIORSAGVDONHPRAVLVPSSLRIGIIPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human aphingosine kinase-like protein; intracellular signalling; cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma; autoimmune disease; rheumatoid arthritis; Parkinson's disease.
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195 TEHANQAKETLYEINIDKYDG-
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23-AUG-2001; 2001US-0314113P.
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N-PSDB; ABL40822

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New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynuclectide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous system
                                                                                                                                                                                                                 The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g. asthma), autoimmune diseases (e.g. rheumatoid arthritis) and central and peripheral nervous system discorders (e.g. parkinson's disease). The present sequence represents the human sphingosine kinase-like protein
                                                                                                                                                                     Claim 25; Fig 2; 120pp; English.
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ä TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120 GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 323 GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180 ------VTEHANQAKE 203 204 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 263 DSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK 383 QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 443 1 PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE 60 11; Gaps Score 1640.5; DB 5; Length 326; Pred. No. 2.3e-149; 1; Mismatches 0; Indels 11; PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDII DLILIRKCSRFNFLRFLIRHTNQQDQ 469 54.2%; Query Match Best Local Similarity 96.3 Matches 314; Conservative 155 324 181 444 384 61 264 121 QQ ઠ g ò g ò g ઠે ò 셤 ò

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Search completed: September 3, 2005, 04:37:42 Job time : 116.766 secs

DLILIRKCSRFNFLRFLIRHTNQQDQ 326

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12 ; Search time 111.217 Seconds (without alignments) 1990.064 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*

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4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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3025
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Sequence 11, Appl | Sequence 11, Appl | Sequence 10, Appl | Sequence 40, Appl | Sequence 10, Appl | Sequence 121, App | "                | Sequence 6, Appli | Sequence 6, Appli | Sequence 11, Appl | Sequence 2, Appli |
|-------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|
| SUMMARIES                     | US-09-969-896-11  | US-10-631-958-11  | US-09-969-896-10  | US-10-262-511-40  | US-10-631-958-10  | US-10-618-941-121 | US-10-315-597A-2 | US-09-784-810A-6  | US-10-876-281-6   | US-09-784-810A-11 | US-09-969-896-2   |
| DB                            | 10                | 16                | 10                | 15                | 16                |                   |                  | σ                 | 18                | თ                 | 10                |
| %<br>Query<br>Match Length DB | 562               | 562               | 537               | 537               | 537               | 537               | 537              | 471               | 471               | 326               | 326               |
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| Score                         | 3025              | 3025              | 2888              | 2888              | 2888              | 2888              | 2880             | 2456.5            | 2456.5            | 1640.5            | 1640.5            |
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                                                                   481 KKFQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRV 540
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121 RWKWAQVTFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVA 180
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TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Kinase-Like Protein
FILE REFERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-06-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 537
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US-09-969-896-10
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Publication No. US20040192580A1

GENERAL INFORMATION:
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Rinase-Like Protein
FILE REFERENCE: 004974.00594
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US/09/969,896
PRIOR APPLICATION NUMBER: US/09/969,896
PRIOR FILING DATE: 2000-10-06
SPIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
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100.0%; Pred. No. 5.2e-281;
tive 0; Mismatches 0;
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ORGANISM: Homo sapiens
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US-10-631-958-11
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Query Match
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US-10-262-511-40
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US-10-631-958-10
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                                                                                    ILIRKCSRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRF 505
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                                                                   EKKRWIGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQ 385
                                                                                                                                       LEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDL 445
                                                                                                                                                                                                                                                                               GHICSSHPSCCCTVSNSSWNCDGEVLASPAIEVRVHCQLVRLFARGIEENPKPDSHS 562
TDCVCYSTVGTSDAETSALH1VVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGD11KDS
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APPLICANT: Miller, Charles E.
APPLICANT: Matelii, Luca
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenberg, Mark E.
APPLICANT: Rochenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
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CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR PLING DATE: 2001-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2001-10-09
PRIOR PLING DATE: 2001-10-09
PRIOR PLING DATE: 2001-10-09
PRIOR PLING DATE: 2002-05-17
PRIOR PLING DATE: 2002-06-17
PRIOR PLING DATE: 2002-10-09
PRIOR PLING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR PLING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR PLING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR PLING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
Gorman, Linda
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Peyman, John A.
Kekuda, Ramesh
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Anderson, David W.
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Catterton, Elina
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Li, Li
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PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-09
PRIOR PAPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFWARE: CuraSeqList version 0.1
SEQ ID NO 40
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Publication No. US20040192580A1
GENERAL INFORMATION:
APPLICANT: Kossida, Sophia
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Rinase-Like Protein
FILE REFERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/10/631,958
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US/09/969,896
PRIOR PILING DATE: 2001-10-04
PRIOR PLILING DATE: 2000-10-06
PRIOR PLILING DATE: 2000-10-06
PRIOR PLILING DATE: 2000-10-06
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100.0%; Pred. No. 6.9e-268;
ative 0; Mismatches 0;
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Best Local Similarity
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                                                                                                                                                                                                     1 MGATGAAEPLQSVLWYKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV
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                                                                                                                               Length 537;
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                                                                                                                            95.5%; Score 2888; DB 16;
100.0%; Pred. No. 6.9e-268;
ive 0; Mismatches 0;
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APPLICANT: WANNING, GERARD
APPLICANT: CARENEPEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT PILING DATE: 2003-07-15
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.2
LENGTH: 537
           NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 537
TYPE: PRT
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PRIOR FILING DATE: 2001-08-23
                                                                                                                                                         Conservative
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US-10-618-941-121
                                                                                   ORGANISM: Homo sapiens
                                                                                                                            Query Match
Best Local Similarity
Matches 537; Conserv
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US-10-631-958-10
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95.5%; Score 2888; DB 16; Length 537;

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                                                                         26 MGATGAAEPLOSVLWVKOORCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV
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95.2%; Score 2880; DB 14;
Best Local Similarity 99.6%; Pred. No. 4.1e-267;
Matches 535; Conservative 1; Mismatches 1;
Pred. No. 6.9e-268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2. Application US/10315597A
Fublication No. US20030162206A1
GENERAL INFORMATION:
APPLICANT: Sugiura, Masako
APPLICANT: Kono, Keita
APPLICANT: Kohama, Takafumi
TITLE OF INVENTION: Ceramide Kinase and DNA Enc.
FILE REFERENCE: 02658CIP/R:
CURRENT APPLICATION NUMBER: US/10/315,597A
CURRENT FILING DATE: 2002-12-10
FRIOR APPLICATION NUMBER: JP 2000-178039
PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
                       0; Mismatches
100.0%;
                       537; Conservative
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ORGANISM: Homo sapiens
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US-10-876-281-6

i Sequence 6, Application US/10876281

i Publication No. US20030123942A1

i GENERAL INFORMATION:

i APPLICANT: RASTELLI, LUCA

i TITLE OF INVENTION: SAME

i TITLE OF INVENTION: SAME

i TITLE OF INVENTION: SAME

i CURRENT APPLICATION WUMBER: US/10/876,281

i CURRENT APPLICATION WUMBER: US/09/784,810

i PRIOR APPLICATION WUMBER: 60/182,360

i PRIOR PILING DATE: 2001-02-14

i PRIOR PILING DATE: 2000-02-14

i PRIOR PILING DATE: 2000-03-14

i PRIOR PILING DATE: 2000-03-22

i NUMBER OF SEQ ID NOS: 29

i SOFTWARE: Patentin Ver. 2.1

i SEQ ID NO 6
                                                                                     301 KALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILITRKC 360
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Pred. No. 1.6e-226;
1; Mismatches 0; Indels
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ilarity 97.5%;
Conservative 1
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US-10-876-281-6
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Best Local 3
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TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
FILE REFERENCE: 10716-09
CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT APPLICATION NUMBER: 60/192,360
PRIOR APPLICATION NUMBER: 60/192,360
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                           GHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPRPDSHS 537
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Pred. No. 1.6e-226;
1; Mismatches 0; Indels 11;
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Patent No. US20020082203A1
GENERAL INFORMATION:
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Best Local Similarity 97.59
Matches 459; Conservative
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ORGANISM: Homo sapiens
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US-09-784-810A-6
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CRGANISM: Homo sapiens
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US-10-631-958-2
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US-10-631-958-2
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                                                                                                              Sequence 11, Application US/09784810A

Sequence 11, Application US/09784810A

Patent No. US20020082203A1

GENERAL INFORMATION:

APPLICANT: RASTELL: LUCA

TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING

TITLE OF INVENTION: SAME

FILE REFERENCE: 10716-08

CURRENT APPLICATION NUMBER: US/09/784,810A

CURRENT APPLICATION NUMBER: 60/182,360

PRIOR APPLICATION NUMBER: 60/182,360

PRIOR APPLICATION NUMBER: 60/182,261

PRIOR FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 11

LENGTH: 326
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                     421 HPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 326;
512 HPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS
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Publication No. US20030125533A1
GENERAL INPORMATION:
APPLICANT: KOSSIGA, Sophia
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Kinase-Like Protein
FILE OF INVENTION: Kinase-Like Protein
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT APPLICATION NUMBER: US 60/238,005
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/314,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
54.2%; Score 1640.5; DB 9
Best Local Similarity 96.3%; Pred. No. 2.1e-148;
Matches 314; Conservative 1; Mismatches 0;
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CORGANISM: Homo sapiens
US-09-784-810A-11
                                                                                                         US-09-784-810A-11
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US-09-969-896-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384 QOLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 443
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Publication No. US20040192580A1
GENERAL INFORMATION:
APPLICANT: Kossida, Sophia
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Masse-Like Protein
FILE REPRENCE: 004974.00594;
CURRENT APPLICATION NUMBER: US/10/91969;
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: US 60/314,113
PRIOR APPLICATION NUMBER: US 60/314,113
PRIOR APPLICATION NUMBER: US 60/314,113
NUMBER OF SEQ ID NOS: 16
SSOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 96.3%; Pred. No. 2.1e-148;
Matches 314; Conservative 1; Mismatches 0;
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Best Local Similarity 96.3%; Pred. No. 2.1e-148;
Matches 314; Conservative 1; Mismatches 0;
; NUMBER OF SEQ ID NOS: 16
; SCFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 326
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Sequence 29, Application US/09784810A
Patent No. US20020082203A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
TITLE OF INVENTION: SAME
FILE REPERENCE: 10716-08
CURRENT PILING DATE: 2004-66-24
CURRENT PILING DATE: 2001-02-14
FRICH APPLICATION NUMBER: US/09/784,810
FRICH APPLICATION NUMBER: 06/182,360
FRICH APPLICATION NUMBER: 60/182,360
FRICH APPLICATION NUMBER: 60/181,261
FRICH APPLICATION NUMBER: 60/181,261
FRICH APPLICATION NUMBER: 60/181,261
FRICH FILING DATE: 2000-02-14
FRICH FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PARCENTIN Ver. 2.1
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                                                                                                                                                                          241 QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 300
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Pred. No. 2.1e-148;
1; Mismatches 0; Indels 11;
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Publication No. US20050123942A1
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Best Local Similarity 96.3
Matches 314; Conservative
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ORGANISM: Homo sapiens
US-10-876-281-11
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US-10-876-281-11
264
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US-10-876-281-29

Sequence 29, Application US/10876281

Publication No. US2005012394241

GENERAL INFORMATION:

APPLICATION: NASTELLI, LUCA

TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING

TITLE OF INVENTION: SAME

FILE REFRENCE: 10716-08

CURRENT FILING DATE: 2004-06-24

PRIOR FULING DATE: 2001-02-14

PRIOR FILING DATE: 2000-02-14

PRIOR PRILING DATE: 2000-02-14

PRIOR PRILING DATE: 2000-02-14

PRIOR PRILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTIN UNIVER: 60/191,261

PRIOR PRILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTIN VEV. 2.1

LENGTH: 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VTFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGGGKRIYERKVAPLFTLA 120
APPLICANT: RASTELLI, LUCA
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
FILE REFERENCE: 10716-09
CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT FILING DATE: 2001-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PACENTIN VET: 2.1
SEQ ID NO 29
LENGTH: 182
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; OTHER INFORMATION: Description of Unknown Organism: 80432911
US-10-876-281-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Unknown Organism: 80432911
US-09-784-810A-29
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ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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67 AGAPGADACSVPVSEIIAVEETDVHGKHQGSGKWQKWEKPYAFTVHCVKRARRHKWKWAQ 126
                                      0; Gaps
Best Local Similarity 100.0%; Pred. No. 6.4e-86; Matches 182; Conservative 0; Mismatches 0; Indels
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September 3, 2005, 04:08:02; Search time 106.269 Seconds (without alignments) 1990.064 Million cell updates/sec
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20: /cgn2_6/ptodata/2/pubpaa/USIOB_NEW PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/USIOB_NEW PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/USIOB_NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                         OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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2888
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                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                      | Sequence 10, Appl | Sequence 40, Appl | Sequence 10, Appl | Sequence 121, App | 11,              | Sequence 11, Appl | . 7              | Sequence 6, Appli | Sequence 6, Appli | Sequence 11, Appl | Sequence 2, Appli |
|----------------------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|
| SUMMARIES                        | US-09-969-896-10  | US-10-262-511-40  | US-10-631-958-10  | US-10-618-941-121 | US-09-969-896-11 | US-10-631-958-11  | US-10-315-597A-2 | US-09-784-810A-6  | US-10-876-281-6   | US-09-784-810A-11 | US-09-969-896-2   |
| 08                               | 2                 | 15                | 16                | 16                | 10               | 16                | 14               | 6                 | 18                | 0                 | 10                |
| %<br>Query<br>Match Length DB ID | 537               | 537               | 537               | 537               | 262              | 562               | 537              | 471               | 471               | 326               | 326               |
| %<br>Query<br>Match              | 100.0             | 100.0             | 100.0             | 100.0             | 100.0            | 100.0             | 7.66             | 85.1              | 85.1              | 56.8              | 56.8              |
| Score                            | 2888              | 2888              | 2888              | 2888              | 2888             | 2888              | 2880             | 2456.5            | 2456.5            | 1640.5            | 1640.5            |
| Result<br>No.                    | 1                 | C                 | ን                 | 4                 | Ŋ                | 9                 |                  | <b>\</b>          | σ                 | 10                | 11                |

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| Sequence 2, Appli<br>Sequence 29, Appl<br>Sequence 29, Appl<br>Sequence 8, Appli<br>Sequence 8, Appli<br>Sequence 361076,<br>Sequence 195284,<br>Sequence 195284,<br>Sequence 190233,<br>Sequence 190233,<br>Sequence 202261,<br>Sequence 202261,<br>Sequence 202261,<br>Sequence 202261,<br>Sequence 202261,<br>Sequence 202261,<br>Sequence 197631,<br>Sequence 197631,<br>Sequence 187631,<br>Sequence 284221,<br>Sequence 284221,<br>Sequence 284221,<br>Sequence 284221,<br>Sequence 284321,<br>Sequence 284321,<br>Sequence 284321,<br>Sequence 284321,<br>Sequence 28, Appl<br>Sequence 28, Appl<br>Sequence 29, Appl<br>Sequence 19, Appl<br>Sequence 19, Appl<br>Sequence 20, Appl<br>Sequence 20, Appl                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
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| US-10-631-958-2<br>US-10-876-281-11<br>US-09-784-810A-29<br>US-10-876-281-8<br>US-10-876-281-8<br>US-10-876-281-8<br>US-10-876-281-8<br>US-10-425-115-21076<br>US-10-425-115-21076<br>US-10-425-115-21365<br>US-10-425-115-21365<br>US-10-425-115-24955<br>US-10-425-115-24955<br>US-10-425-115-24955<br>US-10-425-115-24955<br>US-10-425-115-24955<br>US-10-425-115-24955<br>US-10-425-115-24955<br>US-10-425-115-24955<br>US-10-425-115-24955<br>US-10-425-114-53957<br>US-10-425-115-264987<br>US-10-437-963-161184<br>US-10-425-115-264987<br>US-10-425-115-264987<br>US-10-425-115-264987<br>US-10-425-115-264987<br>US-10-425-115-264987<br>US-10-425-115-264987<br>US-10-625-101-9<br>US-10-622-011-9<br>US-10-622-011-9<br>US-10-622-011-10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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| 1326<br>1326<br>1326<br>1326<br>1441<br>1444<br>1444<br>1446<br>1446<br>1446<br>1446<br>14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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## ALIGNMENTS

01-968-696-60-SD

61 BETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLR 120 EETDVHGKHQGSGKWQKMEKPYAPTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLR 120 1 MGATGAAEPLQSVLWVKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV 1 MGATGAAEPLOSVLWVKQORCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV Gaps ö 100.0%; Score 2888; DB 10; Length 537; 100.0%; Pred. No. 38-278; tive 0; Mismatches 0; Indels 0; Sequence 10, Application US/0996986

Publication No. US20030125533A1

GENERAL INFORMATION:

APPLICANT: KOSSIGA

TITLE OF INVENTION: Regulation of human Sphingosine

TITLE OF INVENTION: Rinase-Like Protein

FILE REFERENCE: 004974.00594

CURRENT APPLICATION NUMBER: US/09/969,896

CURRENT FILING DATE: 2001-10-04

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2001-06

PRIOR FILING DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0 Query Match
Best Local Similarity 100.
Matches 537; Conservative TYPE: PRT ORGANISM: Homo sapiens ) US-09-969-896-10 61

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EMLEKLTSRPKHLLVFINPFGGKGOKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
                                                            YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mastell, Luca APPLICANT: Stone, David J. APPLICANT: Stone, David J. APPLICANT: Shenoy, Barcol B. A. APPLICANT: Shenoy, Suresh G. APPLICANT: Shenoy, Mark E. APPLICANT: Rothenberg, Mark E. APPLICANT: Leach, Martin D. APPLICANT: Agee, Michele L. APPLICANT: Agee, Michele L. APPLICANT: Berghs, Constance TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/313,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/313,917
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Publication No. US20040038223A1
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
Gort, Tatiana
Zerhusen, Bryan D.
Anderson, David W.
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Catterton, Elina
Ji, Weizhen
Miller, Charles E.
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APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
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US-10-262-511-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDS 300
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PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-10-05-17
PRIOR PILING DATE: 2002-10-038,029
PRIOR FILING DATE: 2002-10-09
PRIOR PILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR PELING DATE: 2001-10-09
PRIOR PELING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR APPLICATION NUMBER: 60/373,426
PRIOR APPLICATION NUMBER: 60/373,426
PRIOR APPLICATION NUMBER: 60/373,436
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Publication No. US20040192580A1
GENERAL INFORMATION:
APPLICANT: KOSSIGA:
TITLE OF INVENTION: Regulation of human Sphingosine; TITLE OF INVENTION: Kinase-Like Protein
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Best Local Similarity 100.0%;
Matches 537; Conservative 0
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ORGANISM: Homo sapiens
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US-10-631-958-10
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FILE REFERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/10/631,958
CURRENT FILING DATE: 2003-08-01
FRIOR APPLICATION NUMBER: US/09/969,896
FRIOR PILING DATE: 2001-004
FRIOR FILING DATE: 2000-10-06
FRIOR PAPLICATION NUMBER: US 60/238,005
FRIOR FILING DATE: 2000-10-06
FRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 537
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Publication No. US20040197792A1
GENERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: WANNING, GERAND:
TILLE OF INVENTION: NOVEL KINASES
FILE REPERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT FILING DATE: 2003-07-15
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 537; Conservative
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; ORGANISM: Homo sapiens
US-10-631-958-10
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US-10-618-941-121
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Pred. No. 3.2e-278;
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; Publication No. US20030125533A1
; GENERAL INFORMATION:
    APPLICANT: Kossida, Sophia
; TITLE OF INVENTION: Regulation of human Sphingosine
    TITLE OF INVENTION: Regulation of human Sphingosine
; TITLE OF INVENTION: Kinase-Like Protein
; FILE REPERENCE: 004974.00594
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/238,005
; PRIOR FILING DATE: 2001-00-10-06
; PRIOR FILING DATE: 2001-00-10-06
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 562
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Best Local Similarity 100.0%;
Matches 537; Conservative 0
SOFTWARE: Patentin version 3.2
SEQ ID NO 121
LENGTH: 537
TYPE: PRT
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                                                                     ORGANISM: Homo
US-10-618-941-121
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Pred. No. 1.9e-277,
1; Mismatches 1;
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APPLICANT: Kono, Keita
APPLICANT: Kono, Keita
Tarafuni: Konoma, Takafuui
TITLE OF INVENTION: Ceranide Kinase and DNA Enc
FILE REFERENCE: 0.2658CIP/HG
CURRENT APPLICATION NUMBER: US/10/315,597A
CURRENT APPLICATION NUMBER: 2002-12-10
PRIOR PILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 4
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Best Local Similarity 99.6%;
Matches 535; Conservative
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US-10-315-597A-2
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LENGTH: 537
TYPE: PRT
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100.0%; Pred. No. 3.2e-278;
.ive 0; Mismatches 0; Indels 0;
    0; Indels
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GENERAL INFORMATION:
FULL OF INVENTION: Regulation of human Sphingosine;
TITLE OF INVENTION: Ranae-Like Protein;
FILE REPERENCE: 004974,00594
CURRENT PILING DATE: 2003-00-01
FRICH APPLICATION NUMBER: US/09/969,896
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
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PRIOR FILIN
  Mismatches
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Sequence 11, Application US/10631958
Publication No. US20040192580A1
GENERAL INFORMATION:
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Matches 537; Conservative
  Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-876-281-6
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US-09-784-810A-11
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Sequence 6, Application US/09784810A

Patent No. US20020082203A1

GENERAL INFORMATION:
APPLICANT: RASTELLI, LUCA

TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING

TITLE OF INVENTION: SAME

TITLE OF INVENTION: SAME

TITLE OF INVENTION: SAME

CURRENT PELLORATION NUMBER: US/09/784,810A

CURRENT PILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/182,360

PRIOR APPLICATION NUMBER: 60/191,261

PRIOR FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTIN VET. 2.1

SEQ ID NO 6

LENGTH: 471
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        1 MEKPYAFTVHCVKRARRHRWKWAQVTFWCPEGLCHLWLQTLREMLEKLTSRPKHLLVFI
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                                                      EKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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RESULT 9

US-10-676-281-6

i Sequence 6, Application US/10876281

i Sequence 6, Application No. US20050123942A1

i GENERAL INFORMATION:

i TITLE OF INVENTION:

TITLE OF INVENTION: SAME

TITLE OF INVENTION: SAME

CURRENT APPLICATION NUMBER: US/10/876,281

CURRENT FILING DATE: 2004-06-24

PRIOR PEPLICATION NUMBER: US/09/784,810

PRIOR PEPLICATION NUMBER: US/09/784,810

PRIOR PELLING DATE: 2001-02-14

PRIOR PELLING DATE: 2000-02-14

PRIOR PELLING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTING OF 21

LENGTH: 471 120 306 240 366 426 360 420 420 138 NPFGGKGQGKRIYERKVAPLFTLASITTDII-------VTEHANQAKETLYEINID 186 246 180 241 GLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQK 300 486 9 61 NPFGGKGGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKETLYEINID 301 KALYGLEAAEDVEEWQVVCGKFLAINATNWSCACRRSPRGLSPAAHLGDGSSDLILIRKC 361 SRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSS 1 MEKPYAFTVHCVKAARRHRWKWAQVIFWCPEEQLCHIMLQTLREMLEKLTSRPKHLLVFI 307 GLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQK KALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKC 78 MEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFI 427 SRFNFLRFLIRHTWQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSS 537 471 Query Match 85.1%; Score 2456.5; DB 18; Length 471; Best Local Similarity 97.5%; Pred. No. 2.4e-235; Matches 459; Conservative 1; Mismatches 0; Indels 11; 421 HPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS HPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS

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LENGTH: 326
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                                             APPLICANT: RASTELLI, LUCA
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
FILE REFERENCE: 10716-08
CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT APPLICATION NUMBER: 60/182,360
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 11
LENGTH: 326
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Pred. No. 2.9e-154;
1; Mismatches 0; Indels 11;
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Publication No. US20030125533A1
GENERAL INFORMATION:
APPLICANT: Kossida, Sophia
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Rinase-Like Protein
FILE REFERENCE: 004974-00594
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT APPLICATION NUMBER: US 60/238,005
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US 60/234,113
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 326
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Application US/09784810A
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96.3%;
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Best Local Similarity 96.3
Matches 314; Conservative
               Patent No. US20020082203A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-969-896-2
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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US-09-969-896-2
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  Length 326;
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                                                       0; Indels
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Publication No. US20040192580A1

GENERAL INFORMATION:

APPLICART: KOSSIGA SOPHIA

TITLE OF INVENTION: Regulation of human Sphingosine

TITLE OF INVENTION: ENGINEER: US/10/631,958

CURRENT FILING DATE: 2003-08-01

PRIOR FILING DATE: 2001-10-04

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FREEEE FREEEE FOOT WINDOWS VETSION 4.0
     DB 10;
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96.3%; Pred. No. 2.9e-154;
tive 1; Mismatches 0;
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  Score 1640.5; DB 10
Pred. No. 2.9e-154;
1; Mismatches 0;
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     56.8%;
                            96.38;
Query Match
Best Local Similarity 96.33
Matches 314; Conservative
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APPLICANT: RASTELL, LUCA
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
FILE REFERENCE: 10716-08
CURRENT APPLICATION NUMBER: US/10/876,281
CURRENT APPLICATION NUMBER: US/09/784,810
PRIOR APPLICATION NUMBER: 60/182,360
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Unknown Organism: 80432911
US-09-784-810A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 34.1%; Score 986; DB 9; Length 182;
Best Local Similarity 100.0%; Pred. No. 2e-89;
Matches 182; Conservative 0; Mismatches 0; Indels
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US-10-876-281-29
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CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT FILING DATE: 2001-02-14
FRIOR APPLICATION NUMBER: 60/182,360
FRIOR FILING DATE: 2000-02-14
FRIOR PELING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO SEQ ID NOS: 4
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; Sequence 29, Application US/10876281
; Publication No. US20050123942A1
; GENERAL INFORWATION:
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Unknown Organism
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/10876281
| Publication No. US20050123942A1 |
| Publication No. US20050123942A1 |
| GENERAL INFORMATION: |
| TITLE OF INVENTION: SAME |
| TITLE OF INVENTION: SAME |
| TITLE OF INVENTION: SAME |
| TITLE OF INVENTION: SAME |
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| FRICK FILING DATE: 2004-02-14 |
| PRIOR APPLICATION NUMBER: 60/191,261 |
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                                           418
                                                                            241 QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIK 180
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Batent No. US20020082203A1

GENERAL INFORMATION:
APPLICANT: RASTELLI, LUCA
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: NOAPE
FILE REFERENCE: 10716-08
                                           QQLEBEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --VTEHANQAKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 18; Length 326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1640.5; DB 1
Pred. No. 2.9e-154;
1; Mismatches 0;
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                                                                                                                                                                          419 DLILIRKCSRFNFLRFLIRHTNOODO 444
                                                                                                                                                                                                              301 DLILIRKCSRFNFLRFLIRHTNQQDQ 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.3%;
Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-10-876-281-11
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US-09-784-810A-29
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| 162 SITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNH | 121 SITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNH 180 |
| 162                                                              | 121                                                                  |
|                                                                  |                                                                      |

<sup>222</sup> PR 223 || |181 PR 182

Search completed: September 3, 2005, 04:32:35 Job time : 115.269 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 3, 2005, 04:25:44; Search time 99.8632 Seconds (without alignments) 2753.633 Million cell updates/sec Run on:

US-10-631-958-10 2888 1 MGATGAAEFLQSVLWVKQQR......QLVRLFARGIEENPKPDSHS 537 Title: Perfect score: Sequence:

Scoring table:

1612378 seqs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1612378 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|           | Description           | 28tct0 homo sapien | Q8k4q7 mus musculu | Q6zpk5 mus musculu | Q6nx59 homo sapien |        |        |        |        | Q7pra8 anopheles g | Q6usk2 arabidopsis | _      | Q9lu45 arabidopsis | Q6uzf6 homo sapien | Q9tzil caenorhabdi |        |        |        |        |        | Q9fhl3 arabidopsis |        |        | -      | Q7xcs9 oryza sativ | Q7qip4 anopheles g | xn57 oryza sativ | Q9vyy8 drosophila | -      |        | Q9nra0 homo sapien | Q6ayb2 rattus norv |
|-----------|-----------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------|--------------------|--------|--------|--------|--------------------|--------------------|------------------|-------------------|--------|--------|--------------------|--------------------|
|           | De                    | 8                  | ő                  | ğ                  | 90                 | 9ŏ     | 8      | 8      | 8      | 0                  | 8                  | ğ      | 8                  | 8                  | 8                  | 8      | 80     | 90     | 8      | 8      | 8                  | 8      | 8      | 8      | 0                  | 0                  | 0                | 8                 | 60     | 6      | 60                 | 8                  |
| SUMMARIES | н                     | CEK1 HUMAN         | CEK1_MOUSE         | Q62PK5             | Q6NX59             | Q6GLV1 | Q6GMF3 | Q9VNA6 | Q95S15 | Q7PRA8             | Q6USK2             | Фенен1 | Q9LU45             | QGUZF6             | Q9TZI1             | Q949C3 | Q8L7L1 | 065419 | Q9LRB0 | Q8H350 | Q9FHL3             | Q6ZP59 | Q84S01 | Q94HY9 | Q7XCS9             | Q7QIP4             | Q7XN57           | Q9VYY8            | 0MZA6O | 014159 | SPH2_HUMAN         | Q6AYB2             |
|           | В                     | -                  | Н                  | ~                  | ~                  | ~      | ~      | ~      | ~      | ~                  | ~                  | 7      | ~                  | 7                  | 0                  | ~      | 0      | N      | ~      | N      | 7                  | ~      | 7      | 7      | 7                  | ~                  | N                | ~                 | ~      | N      | ۲                  | ~                  |
|           | Query<br>Match Length | 537                | 531                | 409                | 339                | 572    | 485    | 687    | 487    | 410                | 909                | 700    | 533                | 532                | 549                | 586    | 485    | 1240   | 763    | 480    | 732                | 280    | 446    | 757    | 757                | 685                | 748              | 641               | 199    | 458    | 654                | 616                |
| do        | Query                 | 100.0              | 84.1               | 62.9               | 62.7               | 59.3   | 51.8   | 27.8   | 26.4   | 23.1               | 22.4               | 21.4   | 20.5               | 20.0               | 19.7               | 16.6   | 14.8   | 14.5   | 12.8   | 12.8   | 12.1               | 11.9   | 11.5   | 11.4   | 11.4               | 11.2               | 10.9             | 10.8              | 10.3   | 10.1   | 9.4                | 9.3                |
|           | Score                 | 2888               | 2428               | 1904               | 1811               | 1713   | 1495   | 801.5  | 763    | 666.5              | 648                | 619    | 583.5              | 576.5              | 567.5              | 480    | 428    | 417.5  | 369.5  | 368.5  | 349                | 343    | 331.5  | 330.5  | 330.5              | 323                | 314.5            | 310.5             | 298.5  | 291.5  | 271.5              | 267.5              |
|           | Result<br>No.         | -                  | 7                  | n                  | 4,                 | S      | 9      | 7      | 89     | σ                  | 10                 | 11     | 12                 | 13                 | 14                 | 15     | 16     | 17     | 18     | 19     | 20                 | 21     | 22     | 23     | 24                 | 25                 | 56               | 27                | 28     | 29     | 30                 | 31                 |

| Ogjia7 mus musculu |            |        |        | Q8n632 homo sapien | O88886 mus musculu | Q86kf9 dictyosteli | Q91zn3 mus musculu | -      |        | Q74ze3 ashbya goss |        | Q642f6 rattus norv | Q7jm91 caenorhabdi |
|--------------------|------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------|--------------------|--------------------|
| SPH2_MOUSE         | SPHI HUMAN | Q96HV8 | Q96GK1 | Q8N632             | 088886             | Q86KF9             | Q91 ZN3            | Q8C115 | 088885 | Q74ZE3             | 006147 | Q642F6             | Q7JM91             |
| н.                 | ٠,         | 7      | 0      | N                  | 0                  | N                  | N                  | N      | N      | 0                  | ~      | N                  | N                  |
| 617                | 384        | 384    | 398    | 470                | 388                | 624                | 381                | 382    | 504    | 579                | 687    | 383                | 423                |
| 6.0                | 7.         | 2.2    | 9.5    | 9.5                | 9.0                | 8.9                | 8.8                | 8.8    | 8.8    | 8.8                | 9.8    | 8.5                | 8.5                |
| 267.5              | 264.5      | 264.5  | 264.5  | 264.5              | 260                | 257.5              | 254                | 254    | 254    | 253.5              | 248.5  | 245.5              | 245.5              |
| 32                 |            | 34     | 32     | 36                 | 37                 | 38                 | 39                 | 40     | 41     | 42                 | 43     | 44                 | 45                 |

## ALIGNMENTS

| (Lipid                                                                                                                                                          | ;<br>s                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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  |
| (hcerk)                                                                                                                                                         | Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. TERIZATION. 206; DOI=10.1074/jbc.M201535200; himizugawa T., Minekura H., Spiegel d kinase. Molecular cloning and                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ∑<br>⊆<br>9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Bagquley C., Bailey J., Barlow K.F., Bates K.N., Beaaley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conroy D., Corby N.E., Coville G.J., Cox A.V., Davis J., Dawson E., Bhan P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Gilbert J.G.R., Goward M.E., Grafham D.V., Gariffiths M.N.D., Hall C. Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Laird G.K., Langlord C.F., Leversha M.A., LLOyd C., LLOyd D.M., Martyn I.D., Mashreghi-Mohammadi M., Mathews L.H., McCann O.T., McCalay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T., Odell C.N., Plumb R.W., Ramsey Y., Rogers L., Rose B.J.C.T., Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M., Vaudin M., Walli M., Wallis J.W., Willeley M.N., Willey D.L., Williams S.A., Williamson H., Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., Winoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., |
| kinase)                                                                                                                                                         | ta; Buté<br>dae; Hom<br>bc.M2015<br>ekura H                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | tabases<br>90031;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Babbage Beasley Burgess Chen Y. Connor Bavis J. I. M. Ellii ner A.A. iths M.N.I. Holmes A.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | C., LLO) H., Mortin Phillim Rogers Smith M. J.E., Sv Willey I r T.E., Rogers , Kudoh                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| RT; 537 AA.<br>ence update)<br>tation update)<br>(Acylsphingosine kinase)                                                                                       | Homo sapiens (Human).  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Bukarnalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TAXID=9606;  113  TISSUE FROM N.A., AND CHARACTERIZATION.  TISSUE-Leukemia;  MEDLINE=22075121; Pubmed=11956206; DOI=10.1074/jbc.M201535200;  Suguiram M., Kono K., Liu H., Shimizugawa T., Minekura H., Spie  "Ceramide kinase, a novel lipid kinase. Molecular cloning and "ceramide kinase, a novel lipid kinase. Molecular cloning and                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Tunctional characterization."; J. Biol. Chem. 277:23294-23300(2002). [2] SEQUENCE FROM N.A. SEQUENCE FROM N.P.; "A search for lipid kinases."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. [3] SEQUENCE FROM N.A. SEQUENCE FROM N.A. THINF 2.0057165; PubMed=10591208; DOI=10.1038/990031; Punham 1 Hunt & P. Colling I R. Brinskiewich R. 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| 537<br>upda<br>on up                                                                                                                                            | ata;<br>rhini<br>ATION<br>DOI=1<br>ugawa                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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|                                                                                                                                                                 | Homo sapiens (Human). Bukaryota, Metazoa; Chordata; Craniata; V Maumalia; Butheria; Primates; Catarrhini; NCBI_TaxID=9606, NCBI_TaxID=9606, TISSUE=Leukemia; MEDLINE=22075121; Pubmed=11956206; DOI=10 Sugiura M., Kono K., Liu H., Shimizugawa Kohama T.; Ale Eramia (Rohama T.) Erezmaide kinase, a novel lipid kinase. M                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | tunctional Characterization.";  12) Biol. 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| eat<br>st<br>1.1                                                                                                                                                | Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Bukarwalia; Butheria; Primates; NCBL_TaxID=9606; [1] TSSUE-Eukemia; MEDLINE-Eukemia; MEDLINE-2075121; PubMed=1195 Suguira M., Kono K., Liu H., Kohama T., Kohama T., Kohama T., Rohama T., Roh | functional characterization."; J. Biol. Chem. 277:23294-23300 [2] Biol. Chem. 277:23294-23300 [2] SEQUENCE FROW N.A. 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EEY V.E., N.R., N.R., J.M., Goward                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | itord Chreshineshineshineshineshineshineshineshin                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| T 1  HUMAN CEK1 HUMAN S  OSTCTO: Q98123; 10-OCT-2003 (Rel 10-OCT-2003 (Rel 05-JUL-2004 (Rel 05-JUL-2004 (Rel ceramide kinase kinase 4) (LK4). Name=CERK; Synon: | Eukaryota, Metazoa;<br>Mammalia; Eutheria;<br>Mammalia; Eutheria;<br>NCBL_TaxID=9606;<br>NCBL_TaxID=9606;<br>SEQUENCE FROM N.A.,<br>TISSUE=Leukemia;<br>MEDLINE=22075121; P.<br>Medama T.;<br>Kohama T.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | tunctional charact J. 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HABELINES-20057165; Mincham T Hunt A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 116 C.P.,<br>C.P.,<br>Ill W.<br>J. S. M.<br>J. P. D.,<br>I. P. D.,<br>S. K. L.,<br>S. K. E.,<br>S. K. E.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Laird G.K., Langford<br>Martyn I.D., Mashregl<br>McClay J., Mclaren S.<br>Odell C.N., Pavitt R.<br>Phillips S.H., Plumb<br>Scott C.E., Sehra H.<br>Soderlund C., Spragor<br>Vaudin M., Wall M.,<br>Williams L., William<br>Wright C.L., Hubbard<br>Minoshima S., Kawasah                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|                                                                                                                                                                 | Homo<br>Eukar<br>Mamme<br>NCBI<br>[1]<br>SEQUE<br>TISSE<br>MEDLI<br>Sugit<br>Koham                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | runct<br>J. 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Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
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Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
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A Khan A.S., Lane L., Tilahun Y., Wright H.;
A Khan A.S., Lane L., Tilahun Y., Wright H.;
A The DNA sequence of human chromosome 22.";
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Hirosawa M., Nagase T., Murahashi Y., Kikuno R., Ohara O.;
Hirosawa M., Nagase T., Murahashi Y., Kikuno R., Ohara O.;
Hirosawa M., Nagase T., Murahashi Y., Kikuno R., Ohara O.;
Hirosawa M., Nagase T., Murahashi Y., Kikuno R., Ohara O.;
Hirosawa M., Nagase T., Murahashi Y., Kikuno R., Ohara O.;

"Identification of novel transcribed sequences on human chromosome 22
DNA Res. 8:1-9(2001).

"Identification of novel transcribed sequences on human chromosome 22
Cofficiently on natural and analog ceramides (76, 68, C16 ceramides, and C8-dihydroceramide),
Cofficiently on natural and analog ceramides (76, 68, C16 ceramides and C8-dihydroceramide),
Cofficiently on natural and con the Ilpids, such as various sphingosines.

Cofficiently on natural and con the a various sphingosines.
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Cofficiently ACTIVITY: ATP + ceramide = ADP + ceramide 1-phosphate.
Cofficiently ACTIVITY: ATP + ceramide = ADP + ceramide 1-phosphate.
Cofficiently ACTIVITY: High level expression in heart, brain, skeletal muscle, kidney and liver; moderate in peripheral blood placenta and thymus; very low in spleen, small intestine, placenta and thymus; very low in spleen, small intestine, placenta and lung.

"SMELLANEOUS: Optimal pH is 6.0-7.5.
"SMILLANEOUS: Optimal pH is 6.0-7.5.
"SMILLANEOUS: Optimal and identifican exon may exist between amino acid positions 168 and 169.
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Go, GO:0000299; C:integral to membrane of membrane fraction; IDA.

GO; GO:0000289; F:calcium/calmodulin-dependent protein kinase. . .; IDA.

GO; GO:0001299; F:caramide kinase activity; IDA.

GO; GO:0000287; F:magnesium ion binding; IDA.

GO; GO:0006672; P:ceramide metabolism; TAS.

InterPro; IPR001206; DAGKc.

InterPro; IPR001849; PH related.

Pfam; PP00781; DAGK cat; 1.

ProDom; PD005043; DAGK cat; 1.

SWART; SM00248; DAGKC; 1.
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EMBL; A4457828; CAD29884.1; -.
EMBL; AL0967766; CAB62977.1; ALT SEQ.
EMBL; AL118516; -; NOT ANNOTATE CDS.
EMBL; AB051433; BAB33316.1; -.
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Calcium; Kinase; Magnesium; Transferase.

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MEDLINE=22354683; PubMed=124668B1; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22075121; PubMed=11956206; DOI=10.1074/jbc.M201535200;
Sugiura M., Kono K., Liu H., Shimizugawa T., Minekura H., Spiegel
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last amnotation update)
Ceramide kinase (EC 2.7.1.138) (Acylsphingosine kinase) (mCERK)
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                                        Length 537;
                                                                   Indels
          59977 MW; 3DBFC0ED8D679F7F CRC64;
                                        DB 1;
                                                                   0
                                       100.0%; Score 2888; DB 1 100.0%; Pred. No. 5e-233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     531 AA.
                                                 100.0%; Preq. ...
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DAGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   functional characterization."
                                                      Best Local Similarity 100. Matches 537; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
            537 AA;
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            SEQUENCE
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                                          Query Match
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DOMAIN
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CEK1_MOUSE
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Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brutsic V., Chothia C., Corbani L.E., Cousins S.,
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Marinond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Kanaga A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Maglott D.R., Maltais L., Pontius J.U., Qi D., Ramachandran S.,
Bardelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Wilming L.G., Wynshaw-Boris A., Yanagiswa M., Yang I., Yang I.,
Yuan Z., Zavolan M., Zimmer A., Carninci P., Hayatsu N.,
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
Milwiaz A., Hashizume W., Imetani K., Ishii Y., Itch M., Kagawa I.,
Milyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Malunishi A., Yoshino M., Waterston R., Lander E.S., Shination S.,
Malus L.,
Malus L
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EMBL; AK042077; BAC31157.1; --
EMBL; AK042077; BAC31157.1; --
EMBL; AK052269; BAC34908.1; --
MGD; MGI:2386052; Cerk.
GO; GO:0000299; C:integral to membrane of membrane fraction; ISS.
GO; GO:0004685; F:calcium/calmodulin-dependent protein kinase. .; ISS.
GO; GO:0001299; F:ceramide kinase activity; ISS.
GO; GO:0001299; F:ceramide kinase activity; ISS.
GO; GO:0000287; F:magnesium ion binding; ISS.
GO; GO:0006729; F:ceramide metabolism; ISS.
InterPro; IPR011036; PH_related.
PFam; PF00781; DAGK_cat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
TISSUE SPECIFICITY: High level expression in heart, brain and
testis; low expression in spleen, liver and lung; not detected in
skeletal muscle.
DEVELOPMENTAL STAGE: Highly expressed at 7 dpc and decreases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to form ceramide 1-phosphate. Acts efficiently on natural and analog ceramides (C6, C8, C16 ceramides, and C8-dihydroceramide), to a lesser extent on C2-ceramide and C6-dihydroceramide, but not on other lipids, such as various sphingosines (By similarity). CATALYTIC ACTIVITY: ATP + ceramide = ADP + ceramide 1-phosphate. COFACTOR: Calcium and magnesium (By similarity). SUBCELLUIAR LOCATION: Cytoplesmic and membrane-associated (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ceramide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.1%; Score 2428; DB 1; Length 531;
85.1%; Pred. No. 1.7e-194;
ive 33; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Catalyzes specifically the phosphorylation of
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167 D -> Y (in Ref. 2; BAC34908).
59811 MW; 31FEC534C348AAOA CRC64;
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Calcium, Kinase, Magnesium, Transferase.
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Gaps

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Matches 450; Conservative

Best Local Similarity

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TDCVCYSTVGTNDAETSALHIIIGDSLAIDVSSVHYHNTLLRYSVSLLGYGFYGDLIKDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 EKKRWMGLVRYDFSGLKTFLSHQYYEGTLSFLPAQHTVGSPRDNKPCRAGCPVCRQSKQO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 ILIRKCSRENFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRF
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                                                                                                                                                                                                                                                                                                                                                       181 YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS
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                                                                                                                       EETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryonic tail;
PubMed=14621295;
Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Nagase T., Ohara O., Koga H.;
"Prediction of the coding sequences of mouse homologues of KIAA gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            III. the complete nucleotide sequences of 500 mouse KIAA-homologus cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";

BMBL, AK129416; BAC98226.1; -.

EMBL, AK129416; BAC98226.1; -.

GO; GO:0004143; F:diacylglycerol kinase activity; IEA.

GO; GO:0007205; P:protein kinase C activation; IEA.

Pfam; PF00781; DAGK_Cat; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
65-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
MXIAA1646 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.9%; Score 1904; DB 2;
87.6%; Pred. No. 9.2e-151;
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ProDom; PD005043; DAGKc; 1.
SMART; SM00046; DAGKc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=mKIAA1646;
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SEQUENCE
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TISSUB-Peripheral Nervous System;

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MEDLINE-2238257; PubMed-12477932; DOI=10.1073/pnas.242603899;

Attausher R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Attachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhata N.K.,

Attachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhata N.K.,

Mopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haith F.,

Attachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhata N.K.,

Mopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haith F.,

Attachul S., Morase M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wokernan R.J., Markey J.A., Gunzartne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Hale S., Garcia S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakestey R.W., Touchman J.W., Green E.D., Dickson M.C.,

And Mulinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

And Mouse S.J., Marine M.N., Senderstion and Initial analysis of more than 15,000 full-length human
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                                                                                               YDGIVCVGGDGMFSEVLHGVIGRTQQSAGIDPNHPRAVLVPSTLRIGIIPAGSTDCVCYS 125
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                                                                                                                                                                                                                                                                                                                  SRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDK 187
                                                                                                                                     TVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLG 307
                                                                                                                                                                                                                  LVRYDFSGLKTFLSHQYYEGTLSFLPAQHTVGSPRDNKPCRAGCFVCRQSKQQLEEEEKK 245
                                                                                                                                                                                                                                                                                                   RFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSSH 487
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                                           SRPXHLLVFINPFGGKGGKRIYEKTVAPLFTLASITTEIIITEHANQAKETLYEINTDS
                                                                                 YDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYS
                                                                                                                                                                                         LARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQKK
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  Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  24; Indels
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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  Mismatches
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TISSUE=Peripheral Nervous System;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Name=CERK;
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RA Stransberg N.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Stransberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altasner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hishe F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wordin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
A Jones S.J., Marra M.A.;
RA Jones S.J., Marra M.A.;
Ra deneration and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                    Score 1811; DB 2; Length 339;
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EMBL, BC067255; AAH67255.1; -. GO; GO:0004143; F:diacylglycerol kinase activity; IEA. GO; GO:0007205; P:protein kinase C activation; IEA. InterPro; IPR001206; DAGKC.
ProDom; PD005043; DAGKC; 1. SEQUENCE 339 AA; 37780 MW; A4C2ACHFF7FKF710 CPACA.
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Best Local Similarity 100.
Matches 339; Conservative
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Name=MGC84197;
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                                              MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                    "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                 / Match 59.3%; Score 1713; DB 2; Length 572; Local Similarity 58.4%; Pred. No. 1.4e-134; nes 320; Conservative 81; Mismatches 117; Indels 3:
                                                                                                                                SEQUENCE FROM N.A.
TISSUB-Brain;
TISSUB-Brain;
Klain S., Gerhard D.S.;
Klain S., Gerhard S., Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC074350; AAH74350.1; -.
GO; GO:00004143; Fidiacylglycerol kinase activity; IEA.
GO; GO:0001205; P:protein kinase C activation; IEA.
InterPro; IPR001206; Poggkc.
Pfam; PF00781; DGKC at; 1.
FroDom; PD005043; DAGKC, 1.
SMART; SM00046; DAGKC; 1.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                           Dev. Dyn. 225:384-391(2002)
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                         SEQUENCE FROM N.A.
                                                                                                initiative.'
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PRELIMINARY;

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RESULT 6

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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
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TISSUE-Embryo;

Ridin S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; BC074110; AAH74110.1; -.

GO; GO:0007205; P:protein kinase activity; IEA.

GO; GO:0007205; P:protein kinase C activation; IEA.

InterPro; IPR001206; DAGKc.

Pfam; PPR0981; DAGK cat; 1.
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TEMBLrel. 27, Last annotation update)
MGC81777 protein.
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                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Gocayne J.D., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X., Banatatides P.G., Batter E.G., Helt G., Nelson C.R., Galden R.D., Randarid J.F., Agbayani A., An H.J., Andrews Pfannoch C.R., Galdwin D., Bander J. S., Barnew R.A., Basu A., Baxandal J., Bayakaroglu L., Beasley E.B., Abril J.F., Agbayani A., An H.J., Andrews Pfannoch C.R., Galdwin D., Ballew R.M., Banos P.V., Barman B.P., Bhandari D., Boltshavov S., Borkova D., Botchan M.R., Bouck J., Barcketein P., Brottier P., Brotcher A., Deuck J., Bernostor K.Y., Bernos P.V., Bernan B.P., Bhandari D., Boltshavov S., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., R.A., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Acher J. M. B., Davies P., Brotchies P., Boctonian M.R., Bouck J., Bernostort E.B., Davies P., Brotchier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier A., Deng Z., Mays A.D., Dew I., Diecz S.M., Acher R.A., Dedon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rodier C., Gabriellian A.B., Garg N.S., Galbart W.M., Glasser K., Alloch R., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Kathor M., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Millin M., Mandel B.E., Kodirac C.D., Kraft C., Kravitz S., Kulp D., Lai S., Kodirac C.D., Kraft C., Kravitz S., Kulp D., Lai S., Mount E.B., McIntosh T.C., McLeol M.P., Marry D.M., Muskern D.R., Millin N.V., Mattei B. M., Millin N.V., Muskern D.R., Millin N.V., Muskern D.R., Nelson K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., Sunder K., 
                                                                                                                                                                                                                        SVSLLGYGFYGDVLKGTEKNRMLGPARYDVSGCKTFLTHHCYEGSVSFQPAKWVLGSPRD 370
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                                                                                                                                                                                                 SVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRD 343
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164 TIDIIVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRIQRSAGVDQNHPR 223
                                                                                              224 AVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRY 283
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                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ebhydroidea, Drosophilidae, Drosophila.
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MEDIJNE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin: QSVLWVKQQRCAVSLE--PARALLRWWRSPGPGAGAPGADACSVPVSEIIAVEETDVHGK VTFWCPEEQLCHLWLQTLREMLEKLT - - - SRPKHLLVFINPFGGKGQGKRIYERKVAPLF Indels 129; Gaps MEDINE=22426069; PubMed=12537572; Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J. Kusso S., Schroder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., MEDINE-22426065, PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A. Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shorgun. Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002). "Annotation of the Drosophila melanogaster euchromatic genome:  ${\it systematic}$  review."; Length 687; FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases Premi; PF00781; DAGK.cat; 1. SMART; SM00046; DAGKc; 1. SEQUENCE 687 AA; 75690 MW; AAE081230A939412 CRC64; Drosophila melanogaster."; Query Match 27.8%; Score 801.5; DB 2; Best Local Similarity 31.3%; Pred. No. 4.1e-58; Matches 197; Conservative 97; Mismatches 206; Rubin G.M., Venter J.C.; a genomics perspective."; Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002). Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002) GDELL, AE0035603, AAF52040.2; -. FlyBase, FBgn0037315; CG16708. GO; GO:0048102; P:autophagic cell death; IEP. GO; GO:0035071; P:salivary gland cell death; Science 287:2185-2195(2000). InterPro; IPR001206; DAGKC Myers E.W., R SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. Gibbs R.A., The genor systemati 11 59 102 FlyBase,

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KCSRFNFLRFLIRHTNQQ-DQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHI 483
                                                                                                                                                                                                                                                TQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMD 270
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                                                                                                                                                                                                                                                                                                          COPITPPEEMTAHSS---STEFSSWNCDGEVVTDLDITMRSHCQLIEVFMRGPHSYSKP 464
                                                                            | :: | |: | |: | | ORCSFASSIQEQRSSLFIQEESKEA----ERNQQVETEDSHLAASEAALLRPRPRPGNLR
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                                                                                                                                                                         -------EWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 KVAPLFTLASITTDIIVTEHANQAKE--TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGR
VGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 RRHRWKWAQVIFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                           ----SSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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                                                                                                                352 FVC------RQSKQQLEEEQKKALYGLEAAEDVE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.

EMBL, AAABO1008859; BAA07556.2; ...

EQO; GO:0001413; F:diacylglycerol kinase activity; IEA.

GO; GO:0007205; P:protein kinase C activation; IEA.

Interpro; IRR001206; DoGKc.

Pfam; PF00781; DAGK cat; 1.

ProDom; PD005043; DĀGKc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.1%; Score 666.5; DB 2; 38.9%; Pred. No. 4.2e-47; ive 59; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                410 AA
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                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=ENSANGG000000008356;
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                                                                       QNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNS
                                                        279 TLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFL----
                                                                                                               333 ---PAQHTVGSPRD------RKPCRAGCFVC------RQSKQQLEEEQKKALYGLE
                                                                                                                                                                                                    467 RNQQVETEDSHLAASEAALLRPRPRPGNLRLPTGSISSMRNLGNDQWKVVRGNFFMICGA
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A Champae I., Agbayani A., Carlson J.,
STRAIN=Berkeley;
A champae M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
A champae M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
A Champae M., Chavez C., Dorsett V., Parfan D., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY061001; AAL2849.1; -.
FlyBase; FBgn0037315; CG16708.
R GO; GO:0048102; P:autophagic cell death; IEP.
R GO; GO:0055071; P:salivary gland cell death; IEP.
R InterPro; IPR00126; DAGK_cat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 RPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKY
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
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35.5%; Pred. No. 4.4e-55;
ive 73; Mismatches 146; Indels
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Last annotation update)
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                                                                                                                                                                         374 AAEDVE-----
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Matches 170; Conservative
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----HGLIGRIORSA 215
                            SFLPAQ-----HT-----VGSPRDRK-PCRAGCFVCRQSKQQLEEEQKKALYGLE 373
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                                                                                                                                                                                                                                                                      FLIRHTNQ-QDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCC 492
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                                                                                     427 MFEEÄESENSKASLHTRSKTWPFRNTTRSEKILCRÄNCKICNS-----KVGWNSÄSTTLN 481
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                                                                                                                                                 374 AAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLR
                                                                                                                                                                                                                                                                                                         542 HLTELAKRGGEPLNFEFVEYHKTRAFTFTS-------FG------FG
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28.3%; Pred. No. 8.2e-43;
Live 86; Mismatches 192; Indels 206; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative ceramide kinase.

Name=P0519E06.23; Synonyms=OJ1003_B06.39;
Oryza sativa (japonica cultivar-group).

Bukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 --EESVWNLDGEIFEAHQLSAQVLRGLIPLFASGPE 607
                                                                                                                                                                                                                                                                                                                                                                                              TVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIE 528
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Best Local Similarity
Matches 191; Conserv
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                             ----NSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARY 311
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ISAVYSADAAAKCDEGASPAGTGRPRPOLLKLFASALSYGYLGDIAYDSEKYRWMGPKRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurobids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.4%; Score 648; DB 2; Length 608;
31.6%; Pred. No. 2.5e-45;
ive 68; Mismatches 188; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-2595668; PubMed=14563678; DOI=10.1101/gad.1140503; Liang H., Yao N., Song J.T., Luo S., Lu H., Greenberg J.T.; Cramides modulate programmed cell death in plants."; Genes Dov. 17:2636-2641(2003).

EMBL; AX362552; AAQ62904.1; -. GO; GO:0004143; F:diacylglycerol kinase activity; IEA. GO; GO:000205; P:protein kinase C activation; IEA. Pfam; PF00781; DAGK cat; 1. Probom; PD005043; DAGK cat; 1.
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Last annotation update)
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395 LRLLTMTSK 404
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VSSVHH---
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                                                                                                                     312
                                                        219
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                                                                                                                                                                                                                                         307 FSSERPRFGLIPAGSTDAIVMCTTGARDPVTSALHIILGRKLFLDAMQVVRWKTASTSTI 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HT-----VGSPRDRK-PCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEW
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                                                                                      ------RSAG-----VDQ--NHPRAVLVPSSL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 QVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFL 432
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PubMed=14681825;
Tuson M., Marfany G., Gonzalez-Duarte R.;
Tuson of CERKL, a novel human ceramide kinase gene autosomal recessive retinitis pigmentosa (RP26).";
Am. J. Hum. Genet. 74:128-138(2004).
EMBL, AX357073; ARX13670.1; -.
GO; GO:0004143; F:dlacylglycerol kinase activity; IEA.
GO; GO:0002205; P:protein kinase C activation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    532 AA; 59602 MW; C73E590F7C25EED1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Ceramide kinase-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
20.0%; Score 576.5; DB 2;
Best Local Similarity 27.6%; Pred. No. 2.1e-39;
Matches 149; Conservative 102; Mismatches 195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=CERKL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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SGHKSMLIFYCFIINNMKCQEHRNNDLSNSELTGDDANAISGSSNTPDDHEPLLSTTRST 343
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v Pl and TAC
                                                                                                                                                                                                                                                                                                                            463 PARYDFSGTMVFLKHRSYEAKVAFLENGNTHSLTASAENNANGVQTLQYHQNRHRKTICR
                                                        GVD------VCYSTVGTSDAE
                                                                                            256 TSALHIVVGDSLAMDVSSV-----HHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLG
                                                                                                                                                                                                        LARYDFSGLKTFLSHHCYEGTVSFLPAQHT------VGSPRDRKP-CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SVWNLDGELLQACEVSVQAFRGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHTNQ-----QDQFDFTFVEVYRVKKFQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 TSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 WAQVTFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 TLASITTDIIVTEHANQAKETLYEI---NIDKYDGIVCVGGDGMFSEVLHG-LIGRTQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity to unknown protein.
Arabidopsis thaliana (Wouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Abamizu B., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. X. Se
features of the regions of 3,076,755 bp covered by sixty Pl and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               teatur...
clones.";
DNA Res. 7:31-63(2000).
DNA Res. 7:31-63(2000).
EMBL; AB023044; BAA97392.1; -.
GO; GO:0004143; F:diacylglycerol kinase activity; IEA.
GO; GO:0007205; P:protein kinase C activation; IEA.
tnterPro; IPR001206; DAGKc.
tnterPro; IPR001206; DAGKc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9LU45;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 AA.
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Q9LU45
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12

Pred. No. 1.2e-38

30.8%;

Local Similarity

STDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD 299

275 300 359 373 419

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490 ASE

RESULT 14

01-MAY-2000

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21;
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                                                              301 IGSECHVDVCTVHQHQKIIRISANAISYGWLGDVLRDSEEYRCLGDIRYQWSALRTTIRH 360
                                                                                                                                              203 VIHGLIGRIORSAGVDONHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIV 262
                                                                                                                                                                                                                          411
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                                                                                                                       KRIYERKVAPLFTLA-SITTDIIVTEHANQAKETLYEINIDKY---DGIVCVGGDGMFSE 202
                                                                                                                                                                                                                                                                                  263 VGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                382 QVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHT-- 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 HCYEGTVSFLPAQHTVGSPRDR-KPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEW 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --NQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNS 497
                                       VKRARRHRWKWAQ---VTFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQG
                                                                                                                                                                                                                                                                                                                                                                                       361 PIYRGMVQFSLSHKENVNPKDQLPPCLPPCPVCMK----PQGNDKYDYHWHA----EFT
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21329048; PubMed=11435398; DOI=10.1101/gr.GR-1617R; Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.D., Terryn N., Lemcke K., Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W., Bevan M., Bancroft I.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 26, Last annotation update)
Hyporhetical protein C875ERIPDS.
Name=C875ERIPDS;
Oryza sativa (Rice).
Bukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Manoliophyta, Liliopsida; Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Conservation of microstructure bewtween a sequenced region of the genome of rice and multiple segments of the genome of Arabidopsis
61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.6%; Score 480; DB 2; Length 586; 26.8%; Pred. No. 2.8e-31; ive 81; Mismatches 173; Indels 162;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gramene; 0949C3; -
60:0004143; F:diacylglycerol kinase activity; IEA.
60; 60:0004143; F:diacylglycerol kinase activity; IEA.
60; 60:0007205; P:protein kinase C activation; IEA.
InterPro; IPR001206; DAGKC.
Probom; PD005043; DAGKC; 1.
Prypothetical protein.
SEQUENCE 586 AA; 64892 MW; IC45DFBB670EIE22 CRC64;
91; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 GGKÓLYELD-PSLNCÝRVTKWSY-----OPDADOEDPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 VWNLDGEILEOPKDEPLHFKLHPOLISFFGR 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 11:1167-1174(2001).
EMBL; AJ307662; CAC39069.1; -.
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  Conservative
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139;
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Matches
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  SEKKRWLG-LARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK 358
                                                                                                334 AEKYRWMSPNORRDFAVVKALAKLKAEDCEISFLPPNSS------- 372
                                                                                                                                          QQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSS 418
                                                                                                                                                                 DLILIRKCSRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKH------MEDEDSD 471
                                                                                                                                                                                                                                                                                                     472 LKEGGKKRFGHICSSHPSCCCTVSNSSWNCDGEVLH-SPAIEVRVHCOLVRLFARGIEE 529
                                                                                                                                                                                                                                                                                                                                             528
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Minx P., Kemp K.,
"The sequence of C. elegans cosmid T10B11.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MXY-2000 (TrEMBLrel. 13, Last sequence update) 01-UNN-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein T10B11.2. Name=T10B11.2. Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                549 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.7%; Score 567.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2004) to the EMBL/Ge
EMBL; AF09893; AAC67466.1; -.
PIR; T33517.
Wormbase; WEGene0002039; T10B11.2.
WormPep; T10B11.2; CE18241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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MEDLINE=99069613; PubMed=9851916;
WormBase Consortium;
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Pfam; PF00781; DAGK_cat; 1.
Hypothetical protein.
SEQUENCE 549 AA; 62425 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Wilson R.;
Submitted (JUN-2003)
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Waterston R.;
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Query Match

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311 SSDEPCNGDQVPLVSFPNNWFRLGIIPSGSTDAIVLRRISLDIAQV----VRWKSSPSAE 366
              105 WCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASIT 164
                                                                  132 GHXDQQTCKTWVEHIKTCINKEQDRPKSLMVFVHPLCGKGRGCKGWE-TVAPLFERAKVK 190
                                                                                                                                                             ----- 218
                                                                                                                                                                                     251 GFGYFRNNMKCQEHRNNDLSNSELTGDDANAISGSSNTPDDHEPLLSTTRSTGLDISSSD 310
                                                                                                                                                                                                              ----QNHPRAVLV--PSS-LRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMD 270
                                                                                                                                                                                                                                                                    271 VSSVHHNSTLLRYSVSLLG-YGFYGDIIXDSEXKRWLGLARYDFSGLKTFLSHHCYEGTV 329
                                                                                                                                                                                                                                                                                  367 VSPT-----VRYAASFAGSYEAKVAFLENGNTHSLTASAENNANGVQT-LQYH----- 413
                                                                                                                                                                                                                                                                                                                        330 SPLPAQHIVGSPRDRKP-CRAGCFVCR---QSKQQLEEEQKKALYGLEAAEDVEEWQVVC 385
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SEIIAVEETDV-----HGKHQGSGKWQ-KMEKPYAFTVHCVKRARRHRWKW--AQVTF 104
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Search completed: September 3, 2005, 04:43:16 Job time : 101.863 secs

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AK042077

Mus musculus 3 days neonate thymus CDNA, RIKEN full-length enriched library, clone:A630056D11 worduct:D59918.2 (NOVEL PROTEIN SIMILAR TO HUMAN, MOUSE, YEAST, WORM AND PLANT (PREDICTED) PROTEINS)

(FRAGMENT) homolog (Homo sapiens), full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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-Q=/cgn2_1/USPTO_spool/US10631958/runat_02092005_165816_4562/app_query.fasta_1.1941
-DB=EST -QFNT=fastap -SUFFTX=rst -MINATCH=0.1 -LOOPEXT=0
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-USER=US10631958 @CGN 1 1 9235 @runat 02022005_165816_4562 -NCPU=6 - ICPU=3
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Analysis of the mouse transcriptome based on functional annotation of 60,710 full-length cDNAs
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/db_xref="taxon:10090"
/clone="x630056D11"
/tissue type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-UL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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                          Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.
Okazaki,Y., Muzamatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
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Ohara, E.,
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   Inoue, K., Togawa, Y., Izawa, M.,
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/dev_stage="3 days neonate"
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/protein_id="BAC31157.1"
/db_xref="G1:26334913"
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/strain="C57BL/6J"
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PSTTTEITITEHANQAKETLYEINTDSYDGIYCVGGDGMFSEYLHGYIGRTQQSAGID
PNHPRAVLVPSTLRIGIIPAGSTDCVCYSTVGTNDAETSALHIIGBDSLAIDVSSVHY
HNTLLRXSVSLLGYPYGDLIKDSEKKRWMGLINRYDFSGLKYFLSHQYYEGTLISFLPA
QHTVGSPRDNKPCRAGCFVCRQSKQQLEBEEKKAMYGLNYGLENAEMEWQYTCGKFLAIN
ATMWSCARPRSPGGLSPFAHLGDGSSDLILIRKCSRPNFLRFLIRHYQEDQPDFTFV
BVYRVKKFHFTSKYPEDENNDSKEQEKQKFGKICKDRPSCTCSASRSSWNCGEVWHS
PAIEVRVKGHFTSKYPEBENNDSKEGEKQKFGKICKDRPSCTCSASRSSWNCGEVWHS
PGADARSVLVSEIIAVEEKDDCEKHASSGRWHKMENPFAFTVHRVKRVRHHRWKWARV
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         Length:
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

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Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hayashida,K., Mayatsu,N., Hiramoto,K., Konno,H., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Nakami,J., Nomita,K., Nomazaki,R., Ohno,M., Ohaza,N., Nakami,J., Satio,R., Satio
                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                             Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Hatsunch,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details
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High-efficiency full-length cDNA cloning
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ASITTEIIITEHANQAKETLYEINTDSYGOLGCKGGGGKRIYGYGGTQGSAGID
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ATNMSCACPRS PGGLSPFAHLGDGSSDLILIRKCSRPNFLRFLIRHTNQEDQFDFTFV
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Matches:
Conservative:
Mismatches:
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Gaps:
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         /dev_stage="13 days embryo
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AGENCOURT 6771237 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5803668
5, mRNA sequence.
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1 (Bases 1 to 1059)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 601.
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                                                                                                                                                                                                                                                 ArgGlnSerLygGlnGlnLeuGluGluGluGlnLygLygAlaLeuTyrGlyLeuGluAla
                                                                                                                                                                                                                                                                                      AGGCAAAGCAAGCAGCTGGAGGAGGAGCAGAAAAAAAACCACTGTATGGTTTGGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                              AsnMetSerCysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 AspGlySerSerAspLeuIleLeuIleArgLysCysSerArgPheAsnPheLeuArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 ArgValLysLysPhe-GlnPheThrSerLysHisMetGluAsp-----GluAspSerAs
                                    AspileileiysAspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSer
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961 CCTCCAAGGGGGGGGGGGAAAAAAAACGCCCTTTTGGG 1000
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B 1 (bases 1 to 1063)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation. Life Technologies, Inc.

CDNA Library Preparation. Life Technologies (ILML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
/the Sall; Cloned unidirectionally. Primer: Oligo dT.
/rechnologies."
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BM479389
BM479389.1 GI:18528431
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92.22%
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/db_refe="Law.
/db_refe="Law.
/db_refe="Law.
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/gcAcGAG(G). Size-selected >500bp for average insert size into EcoRI/Xhol sites using the following 5' adaptor:
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                                                                                                                                                                                                                                                                                                                                                     OCUOS/38 AGENCOURT 6873251 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:592538257, mRNA Requence.
                  GluAlaAlaGluAspValGluGluTrpGlnValValCys-GlyLysPhereuAlaIleAs 392
                                          nAlaThr-AsnMetSerCysAla---CysArgArgSerProArgGlyLeuSerProAlaA 411
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                           411 la-----HisLeuGly---AspGlySerSerAspLeuIleLeuIle-----ArgLysC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MG clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2096 row: p column: 23
High quality sequence stop: 640.
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into EcoRI/XhoI sites using the following 5' adaptor:
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1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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//done="InhiOB TonA"
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//clone="Organ: mixed; Vector: pVX-Asc; Site 1: EcoRI;
//note="Organ: mixed; Vector: Average insert size directionally into pvx-Asc; Vector: Average insert size 4-5K). Adaptors 5'(AATTCGGCACGAGG)3' and 5'd
//cTCGTGCG3)3' 3' 1. Linker sequence - GCGGCCGTGAGAGCC T18.
//organ: mixed 3' end: T3 promoter primer 5'd
//ATTACGCTCACTAAAGGG3)3' 1. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC
Library"
NH-MGC http://mgc.nci.nih.gov/.

NHI-MGC http://mgc.nci.nih.gov/.

NAtional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm.0A07 Betheada, MD 20892

Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin, University of Iowa

CDNA Library Preparation: M. Bento Soares, University of Iowa

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://imaga.llnl.gov

Plate: NDAM1073 row: C column: 20

High quality sequence stop: 656.
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AGENCOURT 16363467 NIH MGC_221 Homo sapiens cDNA clone
IMAGE:30707875 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
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/do_type="mRNA"
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/tissue_type="lymphoma, cell line"
/tissue_type="lymphoma, cell line"
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ECRI; cDNA made by oligo-dT priming. Directionally cloned
into EccRI/AnoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
I.8kb. Library constructed by Ling Hong in the laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 1047)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cONA Library Preparation: Rubin Laboratory
cONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2662 row: I column: 15
High quality sequence stop: 535.

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AGENCOURT 6769595 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5812382
5', mRNA sequence.
BQ057191
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                                                    AsnAlaThrAsnMetSerCysAlaCysArgArgSerProArgGlyLeuSerProAlaAla
                                                                                                                                                             AspPheSerGlyLeuLysThrPheLeuSerHisHisGysTyrGluGlyThrValSerPhe
                                                                                                                                                                             GACTITICAGGITITAAAGACCTICCTCCCCACCACCACGCTAIGAAGGGACAGIGICCCTIC
                                                                                                                                                                                                                                   CTCCCTGCACAACACACGGTGGGATCTCCAAGGGATAGGAAGCCCTGCCGGGCAGGATGC
                                                                                                                                                                                                                                                                    PheValCysArgGlnSerLysGlnGlnLeuGluGluGluGluGlnLysLysAlaLeuTyrGly
 SerAspAlaGluThrSerAlaLeuHisIleValValGlyAspSerLeuAlaMetAspVal
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ThrValGlySerProArgAspArgLy8ProCysArgAlaGlyCysPheValCysArgGln 356
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                                                                                                                                      AGCAAGCAGCAGCAGCAGAGGAGGAGCAGAAGGAAGCACTGTATGGTTTGGAAGCTGCGGAG 308
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Tochtacir Daniela S. Gerhalth, Mammalian Gene Collection (MGC)

Office of Cancer Institute / NIH

National Cancer Institute / NIH

Bldg. 31 RmloADV Betheada, MD 20892

Email: cgapba-r@mail.nih.gov

Tissue Procurement: James Martin, University of Iowa

CDNA Library Prarayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be

thtp://imago.lln.gov

Plate: NDANJOTS row: a column: 22

High quality sequence stop: 689.

I. 713

Hold guality sequence stop: 689.

Abb host="MARS: 1070859"

Aclone lib-"NIH MGC 221"

Anote-"Organ: mixed-Vector: prx.Asc; Site I: ECORI;

Site 2: Not1; Library is oligo-dT primed with holigo-dT

primer containing a Not I site. Double strand cDNA was give fractionated on a 1% agarcse

gel. First strand cDNA synthesis was primed with holigo-dT

primer containing a Not I site. Double strand cDNA was give fractionally cloned

directionally into prX.Asc vector. Average insert size

4-5KD. Adaptors 5'(AATTGGGCAGAGGA)3': 3' Lihrary was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC

Library"
                                                                                                                                                CK000525 713 bp mRNA linear EST 26-NOV-2003 AGENCOURT 16369000 NIH MGC 221 Homo sapiens cDNA clone IMAGE:30708597 5', mRNĀ sequence.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 713)
NIH-WGC http://mgc.nci.nih.gov/.
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FEATURES

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
I (bases 1 to 820)
II (bases 1 to 820)
INIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
IL Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bidg. 31 RM10AD7 Betheeda, MD 20892
Email: Cgapbs-r@mail.nih.gov
CDNA Library Preparation: Vilan Piao and Minoru Ko
cDNA Library Arrayed by: The I.M.A.G.E Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC c CD655311 820 bp mRNA linear EST 18-JUN-2003 AGENCOURT\_14552675 NIA Human H1 Embryonic Stem Cell cDNA Library (Long) Homo sapiens cDNA clone IMAGE:30426593 5', mRNA sequence.

ORIGIN

Score:

611

728

us-10-631-958-10.rst

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CF135528 T10-0-UI.rl NIH MGC_50 Homo sapiens cDNA clone CF13528, mRNA sequence.
                GlyThrValSerPheLeuProAlaGlnHisThrValGlySerProArgAspArgLysPro 346
                                                                    CysArgAlaGlyCysPheValCysArgGlnSerLysGlnGlnLeuGluGluGluGlnLys 366
                                                                                                                             LysAlaLeuTyrGlyLeuGluAlaAlaGluAspValGluGluTrpGlnValValCysGly 386
                                                                                                                                                                                   447 PheThrPheValGluValTyrArgValLysLysPheGlnPheThrSerLysHisMetGlu 466
                                                                                                                                                                                                                                                                                                                                                                                                                467 AspGluAspSerAspLeuLysGluGlyGlyLysLysArgPheGlyHisIleCysSerSer 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487 HisProSerCysCysCysThrValSerAsnSerSerTrpAsnCysAspGlyGluValLeu 506
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University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
781 Saylon Road , 4156 MEBRF, Iowa City, IA 52242, USA
781 19 315 9565
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9565
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html
                                SerArgPheAsnPheLeuArgPheLeulleArgHisThrAsnGlnGlnAspGlnPheAsp 446
                                                                                                                                                                                                                                                                                                                                                                           ---ACCCTCTGCTGCTGCACGC---TCTCACAGCTCTG---GACTGCGACGGAGTCTG--- 777
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                  LeuSerProAlaAlaHisLeuGlyAspGlySerSerAspLeuIleLeuIleArgLysCys
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
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can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDAM512 row: k column: 18 High quality sequence stop: 673. Location/Qualifiers
                                                                     1. 820
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/db_xref="taxon:9606"
/clone="TMAGE:30426593"
/tissue_type="Embryonic Stem cells"
/cell_line="WAO1"
/lab_host="DH10B (TI phage-resistant)"
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/tissue type="whole brain"
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Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
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primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA is
cAGCCACGAC. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
                                                                                                                  CB246749 11near EST 09-JUL-2003
UI-M-FIO-cdx-b-10-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone
IMAGE:6835595 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 758)
11H-MG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 GlyMetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyVal 217
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Matches:
Conservative:
Mismatches:
US-10-631-958-10 (1-537) x CB246749 (1-758)
                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                              CB246749.1 GI:28368393
EST.
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                                                                                                                                     DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                              CB246749
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(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuSerProAlaAlaHisLeuGlyAspGlySerAspLeuIleLeuIleArgLysCys 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 GlyThrValSerPheLeuProAlaGlnHisThrValGlySerProArgAspArglysPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 AAGTTTCTGGCCATCAATGCCACAAACATGTCCTGTGCTTGTGCCCGGAGCCCCAGGGGC
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231
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Seq primer: pYX-5.
Location/Qualifiers
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99.57%
43.07%
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                                                                                                                                                                                                                                                                                                                                                                                                                                            61
consortium of the German Genome Project.

No s1 sequence available.

This clone (DKFZp781111183) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerLysGlnGlnLeuGluGluGluGlnGlnLysLysBlaLeuTyrGlyLeuGluAlaAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTGTGCTTGTCGCCGGGGGCCCCAGGGGCCCCGGCTGCCCACTTGGGAGACGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerSerTrpAsnCyaAspGlyGluValLeuHisSerProAlaIleGluVal 513
                                                                                                                                                                                                                                                                                  653
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Matches:
Conservative:
Mismatches:
Indels:
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hlcc4) Homo sapiens cDNA clone
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                                                                                                                                                       GCTTTGCACATCATTATTGGGGACTCACTGGCAATAGACGTGTCCTCTGTGCATTACCAT 240
                                                                                                                                                                                                              LysAspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLys 317
                                                                                                                                                                                                                                                                                                                              ValGlySerProArgAspArgLysProCysArgAlaGlyCysPheValCysArgGlnSer 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerAspLeuileLeuileArgLysCysSerArgPheAsnPheLeuArgPheLeuileArg 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       720
                      237
                                                                             257
                                                                                                                                                                                              SerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspIleIle 297
                                                                                                                                                                                                                                                                                   AAGGACAGTGAAAAGAAACGGTGGATGGGCCTCGTCCGGTATGATTTCTCAGGGTTGAAG 360
                                                                                                                                                                                                                                                                                                                ThrPheLeuSerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThr 337
                                                                                                                                                                                                                                                                                                                                                                                                     ValGluGluTrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSer 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 653)
1 (bases 1, to 653)
1 (bases 1, to 653)
1 (bambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
EST (Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., et al.)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Wolecular Genome Analysis, German Cancer
Research Center (DKE2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGACCTCATCCTTATCCGGAAGTGCTCCAGGTTCANCTTCCTGAGATTCCTCAGG
                      AspGlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIlePro
                                                                             AlaGlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSer
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DKFZp781L11183_r1 781 (synonym: h

DKFZp781L11183_5', mRNA sequence.
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BX952302.1 GI:43428907
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MIPS
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Homo sapiens
Homo sapiens
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AGENCOURT 17899852 NIH MGC_234 Rattus norvegicus cDNA clone IMAGE:7193195 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniels S. Gerhard, Ph.D.
Office of Cancer Genemics
National Cancer Genemics
National Cancer Genemics / MIH
Bldg. 31 Rm.0Ao7 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLANA15055 row: b column: 09
High quality sequence stop: 657.
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                                                                      483 CACACCAACCAGCAGGACCAGTTTGACTTCACTTTTGTTGAAGTTTATCGCGTCAAGAAA 542
                                                                                                                                                                                                                  458 PheGlnPheThrSerLysHisMetGluAspGluAspSerAspLeuLysGlu-GlyGlyLy 477
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                        HisThrAsnGlnGlnAspGlnPheAspPheThrPheValGluValTyrArgValLysLys
 CysalaCysargargSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySer
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/mol type="mRNA"
/db xref="taxon:9606"
/tisuse type="embryonic stem cells, embryoid bodies
derived_from H1, H7 and H9 cells"
/clone lib="GRN EB"
/note="oligo dr primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                 N296312 661 bp mRNA linear EST 16-MAY-2004 17000532197874 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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                                                                                                                                      Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea 1 to 66); Li, Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Control human ES cell growth and differentiation

Radgenerative Medicine
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Fax: 650 473 7760
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Matches:
Conservative:
Mismatches:
Indels:
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Insert Length: 661 Std Error: 0.00.
Location/Qualifiers
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BP224560 Sugano cDNA library, lymphocyte Daudi Homo saplens cDNA
clone DAT01067, mRNA sequence.
                                                                                                                                   GlnValThrPheTrpCysProGluGluGlnLeuCysHisLeuTrpLeuGlnThrLeuArg 120
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Matches:
Conservative:
Mismatches:
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Homo saptens

Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 581)

RS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

AL Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8619, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1. .581

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/clone "Burkitt's lymphoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 AlaValLeuValProSerSerLeuArglleGlyIleIleProAlaGlySerThrAspCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 ValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAlaLeuHis1leValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344
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Search completed: September 6, 2005, 20:29:36 Job time: 5188.87 secs

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| earch,     |   |
| protein se |   |
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| OM protein |   |
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September 3, 2005, 04:10:49; Search time 23.7411 Seconds (without alignments) 2176.332 Million cell updates/sec Run on:

US-10-631-958-10 2888 1 MGATGAAEPLQSVLWVKQQR......QLVRLFARGIEENPKPDSHS 537 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | hypothetical prote | _      | _      | _      | _      | hypothetical prote | _      | _      | ρ      | conserved hypothet | hypothetical prote | conserved hypothet | hypothetical prote | conserved hypothet | hypothetical prote | conserved hypothet | hypothetical prote | conserved hypothet | hypothetical prote | involved in polyke | conserved hypothet | hypothetical prote |        | hyp    | multidrug resistan | cathepsin Q (EC 3. | fibroblast growth | hypothetical prote | protein B0272.5 [i |
|-----------|----------------|--------------------|--------|--------|--------|--------|--------------------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|-------------------|--------------------|--------------------|
| SUMMARIES | QI             | T33517             | T05162 | T38776 | 851398 | T19707 | S67059             | AG1665 | AI1293 | F69795 | AH1 769            | T16422             | AH1528             | A83894             | AE1394             | D83734             | AF1171             | S75948             | G95120             | F84898             | E69678             | C97990             | F71006             | A96719 | A89978 | F69595             | JC7183             | JC1450            | T18688             | 809685             |
|           | DB             |                    |        |        | ~      |        |                    | 7      |        | 7      |                    |                    | ~                  | 7                  | •                  | 7                  | •                  |                    |                    | ~                  |                    | ~                  |                    | •      | •      | ~                  | •                  | -                 | N                  | 0                  |
|           | Length         | 549                | 1240   | 458    | 687    | 473    | 624                | 310    | 310    | 303    | 306                | 732                | 309                | 295                | 306                | 295                | 309                | 433                | 294                | 364                | 345                | 311                | 333                | 1028   | 315    | 297                | 343                | 650               | 1555               | 1973               |
| de        | Ouery<br>Match | 19.7               | 14.5   | 10.1   | 9.8    | •      | 7.3                | 9.9    | 6.1    | 5.1    | 4.7                | 4.7                | ٠                  | 4.5                | ٠                  | 4.3                | 4.3                | 4.2                | •                  | 3.9                | •                  | 3.9                | •                  |        | 3.5    | ٠                  | 3.5                | 3.5               | 3.4                | 3.4                |
|           | Score          | 567.5              | 417.5  |        | 248.5  | 245.5  | 210.5              | 189.5  | 176    | 147    | 136.5              | 136                | 130.5              | 129                |                    | 125.5              | 125.5              | 122.5              | 115.5              | 114                | 112                | 111.5              | 105                | 103.5  | 102.5  | 102                | 102                | 100               | 66                 | 66                 |
|           | Result<br>No.  | 1                  | 7      | m      | 4      | S      | 9                  | 7      | 80     | σ      | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23     | 24     | 25                 | 56                 | 27                | 28                 | 29                 |

| hypothetical prote protein C21F12.1 (hypothetical prote probable membrane conserved hypothet hypothetical prote hypothetical prote hypothetical prote hypothetical prote conserved hypothetical prote conserved hypothetical prote indoleacetamide hypothetical prote indoleacetamide hypothetical prote hypothetical prote hypothetical prote ornithine decarbox | ubiquitin carboxyl<br>hypothetical prote |
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| 118686<br>B89608<br>T15571<br>T15571<br>F72386<br>H70861<br>H70861<br>G71901<br>A81975<br>A81589<br>B83973                                                                                                                                                                                                                                                        | T40647<br>B75125                         |
| 000000000000000                                                                                                                                                                                                                                                                                                                                                   | 7 7                                      |
| 19973<br>23305<br>1511<br>304<br>308<br>309<br>455<br>850<br>850                                                                                                                                                                                                                                                                                                  | 337                                      |
| ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~                                                                                                                                                                                                                                                                                                                            | 3.5                                      |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                             | 92.5<br>91                               |
| ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~                                                                                                                                                                                                                                                                                                                            | 44<br>45                                 |

## ALIGNMENTS

|   | RESULT 1 T33517 hypothetical protein T10B11.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: T33517 R;Minx, P.; Kemp, K. Submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid T10B11. A;Reference number: Z21363 A;Accession: T33517 A;Accession: T33517 A;Accession: T33517 A;Accession: T3517 A;Molecule type: DNA A;Residues: 1-549 <min> A;Residues: 1-549 <min> A;Residues: 1-549 <min> A;Cross-references: UNIPROT:O9TZ11; EMBL:AF088993; PIDN:AAC67466.1; GSPDB:GN00019; CESP A;Experimental source: strain Bristol N2; clone T10B11 C;Genetics: A;Gene: CESP:T10B11.2 A;Map position: 1 A;Introns: Z6/1; 76/2; 109/3; 159/1; 187/3; 229/3; 353/1; 398/2; 434/1; 467/3</min></min></min> | t_change 09-Jul-2004<br>AAC67466.1; GSPDB:GN00019; CESP:<br>1; 398/2; 434/1; 467/3 |
|---|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------|
|   | Query Match 19.7%; Score 567.5; DB 2; Length 549; Best Local Similarity 30.8%; Pred. No. 3.4e-39; Matches 139; Conservative 91; Mismatches 160; Indels 61; Gaps                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Length 549;<br>Indels 61; Gaps 13;                                                 |
|   | Qy 89 VKRARRHRWKWAQVTFWCPEGLCHLWLQTLREMLEKLTSRPKHLLVFINPFCGKGQG 146   : :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SRPKHLLVFINPEGGKGOG 146<br>    ::::         :<br>NRPKNIIIFINPEGGNGKA 180           |
|   | Qy 147 KRIYERKVAPLFTLA-SITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSE :: ::                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | KYDGIVCVGGDGMFSE 202<br>::   :     :  <br>QWSAIDGLVSVGGDGLFNE 240                  |
| · | Qy 203 VLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIV 262 :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | VCYSTVGTSDAETSALHIV 262<br>: S                                                     |
|   | Qy 263 VGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSH<br>  :  :    :    :    :    :    :    :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | RWLGLARYDFSGLKTFLSH 322<br>             :      : <br>RCLGPIRYQWSALRTTIRH 360       |
|   | Oy 323 HCYEGTVSFLPAQHTVGSPRDR-KPCRAGCEVCROSKQQLEEEGKKALYGLEAAEDVEEW 381                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | EEGKKALVGLEAAEDVEEW 381<br>:                                                       |
|   | Qy 382 QVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHT 439  :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | IRKCSRFNFLRFLIRHT 439<br>::   :::  :<br>VPRISRFHNWQFMRKVAMY 463                    |
|   | Qy 440NQDQPPPTFVEVYRVKKPQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNS 497                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | RFGHICSSHPSCCCTVSNS 497                                                            |

16;

228

168

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A;Residues: 1-458 <SKE>
A;Cross-references: UNIPROT:014159; EMBL:298762; PIDN:CAB11477.1; GSPDB:GN00066; SPDB:SP!
A;Experimental source: strain 972h-; cosmid c4A8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Wolecule type: DNA
*Residues: 1-687 «ML»
A;Cross-references: UNIPROT:Q06147; EMBL:U17244; NID:9577171; PIDN:AAB67377.1; PID:957717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | : | : | : | | : | | | : | | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 WKCSIEMDVVSSDRTEIKHMYEKSKNLAPMSESSDSDKTVSTSPESHLLTFEINDLSIFC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSVPVSEIIAVEETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWK-WAQVTFWCPE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 SSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----VCMIPGGSGNAFSYNATGQLKPALTALEILKGRPTSFÜLMTFEQKGK-KAYSFLTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 GYGFYGDIIKDSEKKRWLGLAR-YDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKP- 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QKPD 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 -- CRAGCFVCRQSKQQLEE--EQKKALYGLEAAED-------VEEWQVVC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 GKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHTNQQDQF 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uypornetical protein YLR260w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L8479.7
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S51398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSIPVS----AKNVDLNIPPKNI-LWVDKTGPNSVTLSYVSRSSKVATKCW--VDFVENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 VTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 ADACSVPVSEIIAVEETDVHGKHQGSGKWQKM---EKPYAFTVHCV-KRARRHRWKWAQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQLCHLWLQTLREMLEKLISRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 458;
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                                                                                                                                                                                                                                                                                                                                                                                                                  10.1%; Score 291.5; DB 2; ilarity 23.9%; Pred. No. 2.8e-16; Conservative 72; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.Miller, N. submitted to the EMBL Data Library, November 1994 submitted to the EMBL Data Library, November 1994 A.Pescription: The sequence of S. cerevisiae cosmid A.Reference number: $51395 A.Accession: $51398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 NYGIIADCDIGTĖNWĖFMGENRAYLGFFLRLF----
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| : |:|:||
395 GFYYSKHINYYKVRSFRFT
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A,Cross-references: SGD:S0004250
A,Map position: 12R
                                                                                                                                                                                                                                               A; Gene: SPDB: SPAC4A8.07c
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                      A; Map position: 1
A; Introns: 39/1; 101/1
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simi
Matches 105; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
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A:Introne: 44/3; 117/3; 178/3; 206/1; 237/2; 375/1; 416/1; 449/3; 474/1; 503/1; 529/1;
A:Note: F18E5.160
                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F18E5.160 - Arabidopsis thaliana (Grant Control Protein F18E5.160 - Arabidopsis thaliana (Grant Control Proteins: Arabidopsis thaliana (Grant Control Proteins: Arabidopsis thaliana (Grant Control Proteins: Alpr-1999 #text_change 09-Jul-2004 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cracession: T05162 (Cra
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R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, August 1997
A;Reference number: Z21751
A;Reference conmber: Z21751
A;Reference T38776
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                 SWNCDGEVLHSP---AIEVRVHCQLVRLFAR 525
                                                                                                                                    496 VWNLDGEILEQPKDEPLHFKLHPQLISFFGR 526
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Matches 129; Conservative
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| Qy         372 -LEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKC-S 427           Db         347 LAVGSSDLEETVVIEDNEVNIYAVTLSHIAADGPFAPSAKLEDNRIHLSYILWKDIGT 404           Qy         428 RENFLRFLIRHTNQQDQFDFTFVEVYRVKFQFTSKHWEDEDSDLKEGGKKRFGHIC 484           Db         405 RVNIAKYLLA-IEHETHDLPFVKHVEVSSMKLEVISEGSHVV 446           Qy         485 SSHPSCCCTVSNSSWNCDEVLHSPAIEV 513           Db         447LDGEVVDTKTIEV 459 | RESULT 6 S67059 hypothetical protein YOR171c - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein 03615 C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Species: S67059 R;Bordonne, R.; Camasses, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarassov, I.A.; Winso submitted to the Protein Squence Database, July 1996 A;Reference number: S67059 A;Reference number: S67059 A;Accession: S67059 A;Accession: S67059 A;Residues: 1-674 < BOR> A;Residues: 1-674 < BOR> A;Cross-references: UNIPROT:Q12246; EMBL:Z75078; NID:g1420415; PID:g1420417; GSPDB:GN000 A;Experimental source: strain S288C C;Genetics A;Genetics | Cross-references: SGD:S0005697  Amp position: 15R  Ouery Match  1.3 *, Score 210.5; DB 2; Length 624;  Best Local Similarity 26.3 *, Pred. No. 2.4e-09;  Matches 66; Conservative 46; Mismatches 102; Indels 37; Gaps  1.18 TLREMLEKLTSRPKHILLVFINPFGGKGGKRIYERKVAPLFTLASITTDIIVTEHAN  1.2                                                                                                                                                                                                                                                                         | Oy 292 FVOILIKUSEKKKWIGLARY DESGLKTFLESHOTSELFAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLEAGHTUSEFLA |
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| Qy 103 TFWCPEGLCHLMLQTLREMLEKLTSRPKHLLVFINPFGGKGGKRIYERKVA 155 :::::::::::::::::::::::::::::::::::                                                                                                                                                                                                                                                                                                                                      | Qy         276 HNSTLLRY-SVSLLGYGFYGDIIKDSEKKRWLGLARRYDF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | etical protein C34C6.5 - Caenorhabditis elegans lies: Caenorhabditis elegans: 15-Oct-1999 #sequence_revision 15-Oct-1999 #texssion: T19707  Y, C. Ted to the EMBL Data Library, October 1995 rence number: Z19167 ssion: T19707 ssion: Z19713 sreferences: UNIPROT:Q18425; EMBL:Z66494; PIDN:Crimental source: clone C34C6 tics: CESP:C34C6.5 possition: Z ons: Z26/1; 126/1; 128/3; 276/1; 311/3; 427/3 | Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watch   Watc   |

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Best Local Similarity 21.7%,
Matches 73; Conservative
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Cipportain lmol753 [imported] - Listeria monocytogenes (strain EGD-e)
Cipportecies: Listeria monocytogenes
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipocession: A11293
Cipocession: A11293
Ridlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
K. C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Accession: A11293
A; Reseronce number: AB1077; MUID:21537279; PMID:11679669
A; Accession: A11293
A; Residues: 1-310 - GLAA
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A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1753
                                                                                                    A;Cross-references: UNIPROT:Q92AQ5; GB:AL592022; PIDN:CAC97095.1; PID:g16414366; GSPDB:
A;Experimental source: strain Clipl1262
C;Genetics:
A;Gene: lin1865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD--SEKKR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 WLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIR 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425 KCSRFNFLRFL-----IRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVNLAEFIRLVTLALRGDHIKEPN------VIYVKS-EKVSVHSEDK----- 266
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                                                                                                                                                                                                                                                                                                                                                                131 KHLLVFINPFGGKGGKRIYERKVAPLFTLAS----ITTDIIVTEHANQAKETLYEINID
                                                                                                                                                                                                                                                                                                                                                                                               477 KKRFGHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPD
                                                                                                                                                                                                                                                6.6%; Score 189.5; DB 2; Length 310;
21.8%; Pred. No. 5.3e-08;
tive 57; Mismatches 139; Indels 131;
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91; Conservat
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                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-310 <GLA>
  A; Accession: AG1665
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Best Local S:
Matches 69
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Best Local S:
Matches 91
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A;Experimental source: strain 168
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STVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD--SEKKR 304
                                                                                                                                                                                                                                       WLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEE 364
                                                                                                                                                                                                                                                                                                                                                        -----LKATKVKVEYD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIR 424
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C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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21.7%; Pred. No. 0.00018;
trive 54; Mismatches 120; Indels
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A;Residues: 1-732 <FAV>
A;Cross-references: EMBL:U39850; NID:g1055052; PID:g1055058; PIDN:AAA81060.1; CESP:F52C9
C;Genetics:
A;Genetics: 63/1; 106/3; 148/2; 303/1; 347/1; 408/2; 650/2
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Dates: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
B;Jaccesslon: AH1528
B;Jaccesslon: AH1528
B;Jaccesslon: A,Puchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A,Title: Comparative genomics of Listeria species.
A,Reference number: AB1077; MUID:21537279; PMID:11679669
A,Scatus: preliminary
A,Status: preliminary
A,Pucleul type: DNA
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A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 ADILYVVGGDGTIGTVVTGIFRNREK-------AQLPVGFYPGGYDNLWLKR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 MLPSVFENSDDVRHACETAMAVIEDQKKSVY-----AFELTT--EGSTLAPEYGLGDV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYGFYGDIIKDSEKKRW-LGLAR----YDFSGLK----TFLSHHCYEGTVSFLPAQHTVG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 SPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 VGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 MGGDGTLNETINGL------AIHEKRP------DFGFIPLGTVNDLARSVGIPLK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 -----STDCV----CYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLL-RYSVSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 CRRSPRGLSPAAHLGDGSSDL--ILIRKCSRFNFL----RFLIRHTNQODOFDFTFVEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 YDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----C-AGCEKCR-PKPIIEAPQWR--------WWHVLTG---
                                                                                                                                                                                                                                                                   DB 2; Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indele
                                                                                                                                                                                                                                                               4.7%; Score 136; DB 2; Lv
19.9%; Pred. No. 0.005;
iive 56; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.5%; Score 130.5; DB 2; 22.3%; Pred. No. 0.0044; tive 33; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453 YRVKKFQFTSKHMEDEDSDLKE 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 YSQIRFRAGDPYMPEEEFEWNE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 22.3#
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-309 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289
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Conserved hypothetical protein lin2702 [imported] - Listeria innocua (strain Clip11262)

C) Species Listeria innocua

C; Species Listeria innocua

C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C; Accession: AH1769

R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

C; Accession: AH1769

R; Glaser, P.; Frangeul, L.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUD:21537279; PMID:11679669

A; Reference number: AB1077; MUD:21537279; PMID:11679669

A; Rocossion: AH1769

A; Molecule type: DNA

A; Residues: 1-306 cGLA>

A; Cross-references: UNIPROT:Q927T6; GB:AL592022; PIDN:CAC97928.1; PID:g16415238; GSPDB:G

C; Genetics:
A; Genetics:
C; Genetics:
C; Genetics:
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131 KHLLVFINPFGGKGQGKRI-----YERKVAPLFTLASITTDIIVTEHANQAKE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 GTTNDYARALNFAKDPLEALQIIAKQETIRVDIGKANETEFFINNAAGGRITEITYA--- 150
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hypothetical protein F52C9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16422
R;FaveDlo, T.
R;PaveDlo, T.
R
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4.7%; Score 136.5; DB 2; Length 306;
Best Local Similarity 19.6%; Pred. No. 0.0014;
Matches 62; Conservative 55; Mismatches 91; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 --VKESMKSKW-GRLAYLFSGL------TVLP----TVLP
                                                                                                                                                                                 226 | : | | | | : | | | | 226 KANLAEFIRVATMALRGEHINDQ---HIIYTKANRVK 259
                                                                                                                          425 KCSRFNFLRFLI-----RHTNQODQFDFTFVEVYRVK 456
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                                        184 GK--LFQGEI----
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us-10-631-958-10.rpr

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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and g. A;Reference number: A83650; MUID:20512582; PMID:11058132
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C;Genetics:
                                         A;Molecule_type: DNA
A;Residues: 1-30 c.GLA-
A;Cross-references: UNIPROT:08Y497; GB:NC_003210; PIDN:CAD00635.1; PID:gl6412045; GSPDB:
A;Experimental source: strain EGD-e
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19.1%; Pred. No. 0.0094;
tive 51; Mismatches 94;
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Asmolecule type: DNA
AsResidues: 1-295 <STO>
A;Status: preliminary
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C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 0.1-Bec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A83894
R;Tatkani, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83694
A;Reference number: A83694
A;Ression: A83894
A;Residues: preliminary
A;Residues: 1-295 <STO>
A;Cross-references: UNIPROT:Q9KBH4; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB056
C;Genetics:
A;Gene: BH1953
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AB1394
conserved hypothetical protein lmo2557 [imported] - Listeria monocytogenes (strain EGD-e C)Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Dates: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Datesion: Billing
C;Datesion: Buchieser, C; Amend, A; Baquero, F; Berche, P; Bloecker, G; Dominguez-Bernal, G; Duchaud, E; Durand, L.; Dussurget, O; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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| ò      | AINATINMSCACRRSPRGLSPAAHLGDGSSDL1                              |
| qq     | 179 IEYDGKLFEGEIMMFLVSN-TNSVGGFERLAPNASLRDGMFDFIIVKKTSFPEF 231 |
| ò      | 432 LRFLIRHTNQQDQFDFTFVEVYRVK 456                              |
| q      | 232 LHLAGLALRGEHIKHPKVLYVQANRIK 258                            |
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|               |       | de             |                       |    | SUMMARIES            |                   |
|---------------|-------|----------------|-----------------------|----|----------------------|-------------------|
| Result<br>No. | Score | Query<br>Match | Query<br>Match Length | DB | ID                   | Description       |
| -             | 801.5 | 27.8           | 687                   | 4  | US-09-270-767-45874  | Sequence 45874, A |
| 7             | 585.5 | 20.3           | 359                   | 4  | US-09-270-767-46720  |                   |
| m             | 306   | 10.6           | 490                   | 4  | US-10-053-510-19     |                   |
| 4             | 302.5 | 10.5           | 299                   | 4  | US-09-270-767-61405  |                   |
| ις.           | 301   | 10.4           | 524                   | 4  | US-10-053-510-20     |                   |
| 9             | 271.5 | 9.4            | 618                   | 4  | US-09-970-516-4      | 4                 |
| 7             | 271.5 | 9.4            | 618                   | 4  | US-09-817-676A-14    | 14,               |
| œ             | 267.5 | 9.3            | 617                   | 4  | US-09-817-676A-12    | Sequence 12, Appl |
| 60            | 266.5 | 9.5            | 384                   | 4  | US-09-959-897-2      | 7                 |
| 10            | 264.5 | 9.5            | 384                   | 4  | US-09-970-516-2      |                   |
| 11            | 263.5 | 9.1            | 384                   | 4  | US-09-949-016-7026   |                   |
| 12            | 263.5 | 9.1            | 384                   | 4  | US-09-796-487-3      |                   |
| 13            | 260   | 0.0            | 388                   | 4  | US-09-817-676A-15    | Sequence 15, Appl |
| 14            | 260   | 9.0            | 388                   | 4  | US-09-796-487-2      | 7                 |
| 15            | 255.5 | 8.8            | 368                   | 4  | US-10-053-510-21     | Sequence 21, Appl |
| 16            | 254   | 8.8            | 373                   | 4  | US-09-796-487-5      | 'n                |
| 17            | 254   | 8.8            | 381                   | 4  | US-09-796-487-1      | Sequence 1, Appli |
| 18            | 254   | 8.8            | 381                   | 4  | US-09-796-487-4      | 4                 |
| 19            | 247.5 | 9.6            | 382                   | 4  | US-09-970-516-6      | 9                 |
| 20            | 244.5 | 8.5            | 392                   | 4  | US-09-796-487-6      | 9                 |
| 21            | 242   | 8.4            | 424                   | 4  | US-09-796-487-8      | ω                 |
| 22            | 228   | 7.9            | 536                   | 4  | US-09-248-796A-15859 | 15                |
| 23            | 206.5 | 7.2            | 204                   | 4  | US-09-796-487-9      | σ                 |
| 24            | 198   | 6.9            | 403                   | 4  | US-09-796-487-7      | 7, Ap             |
| 25            | 161.5 | 5.6            | 312                   | 4  | US-09-949-016-9811   | 98                |
| 26            | 153   | 5.3            | 313                   | 4  | US-09-107-532A-7154  | 7154,             |
| 27            | 148   | 5.1            | 119                   | 4  | US-09-205-258-788    | 788, 4            |
|               |       |                |                       |    |                      |                   |

| Sequence 264, App Sequence 38102, A Sequence 328, App Sequence 328, App Sequence 313, App Sequence 5133, App Sequence 5131, App Sequence 3740, App Sequence 6786, App Sequence 4774, App Sequence 45, Appl Sequence 1350, App Sequence 1350, App Sequence 1350, App Sequence 1350, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequence 3616, Appl Sequen                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Drosophila melanogaster                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ### B01.5; DB 4; Length 687;  NO. 1.6e-74;  Matches 206; Indels 129; Gaps 16;  ###################################                                                                                                                                                                                                                                                             |
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| 4 US-09-603-208A-264<br>4 US-09-270-767-38102<br>4 US-09-270-767-5319<br>4 US-09-205-258-328<br>4 US-09-205-258-328<br>4 US-09-107-532-8-33<br>4 US-09-107-532-8-313<br>4 US-09-107-433-3121<br>4 US-09-114-000C-3813<br>5 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774<br>6 US-09-114-001C-4774                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ALIGNMENTS US/09270767 acids and proteins of nee: 7326-094 US/09/270,767 3-17                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | imilarity 31.3%; Score 801.5; DB 4; Length 687; imilarity 31.3%; Pred. No. 1.6e-74; Conservative 97; Mismatches 206; Indels 129; Gaps QSVIMVKQQRCAVSLEPARALLRWMRSPGPGAGADACSVPVSEIIAVETDVHGK QQLVWERLQKIKQSPQGNEAKAPLPPDSPAQPGGICSYGPQSHVLHLDDVVSI HQSGKWQKMCKRAFP                                                                                                             |
| 5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00<br>5.00 | 45874 74, Applicatio 703491 RMATION: RMATION: VENTION: VE | 8 6                                                                                                                                                                                                                                                                                                                                                                            |
| 28<br>29<br>1146<br>30<br>31<br>31<br>31<br>31<br>31<br>31<br>31<br>31<br>31<br>31                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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     Qy       219         Qy       279         Qy       279         Qy       351         Qy       333         Qy       333         Qy       311 |

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                                                          NMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRHTNQQ-DQFDFTFVEVY 453
                                                                                                                      RVKKFOFTSKHMEDEDSDLKEGGKKRFGHIC----SSHPSCCCTVSNSSWNCDGE 504
--EWOVVCGKFLAINAT 394
                                                                                                                                                                                                                                                                                   Sequence 46720, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 46720

LENGTH: 359
                                                                           Gaps
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Patent No. 6830881

GRNEAL INFORMATION:
PAPLICANT: Saba, Julie D.
APPLICANT: Saba, Julie D.
APPLICANT: SYTSE, Henrik
ITILE OF INVENTION: SPHINGCSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
ITILE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.3%; Score 585.5; DB 4; Length 35.5%; Pred. No. 2.4e-52; ive 55; Mismatches 103; Indels
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636 VVTDLDITMRSHCQLIEVFMRGPHSYSKP 664
                                                                                                                                                                                 505 VLHSPAIEVRVHCQLVRLFARGIEENPKP 533
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; ORGANISM: Drosophila melanogaster
US-09-270-767-46720
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Best Local Similarity 35.55
Matches 125; Conservative
374 AAEDVE-
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US-09-270-767-46720
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: 7126-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ 1D NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ 1D NO 61405
LENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 PRAVLVPSSLRIGIIPAGSTDCV-----CYSTVGTSDAETSALHIVVGDSLAMDVSSV
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                                                                                                                                                                                                                                                                                Length 490;
                                                                                                                                                                                                                                                                              10.6%; Score 306; DB 4; L 24.6%; Pred. No. 6.8e-23; rative 68; Mismatches 165;
TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 2001LG.402C2
CURRENT APPLICATION NUMBER: US/10/053,510
CURRENT FILING DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Sequence 61405, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-053-510-19
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US-09-270-767-61405
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29.2%;
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Best Local Similarity 24.6%
Matches 119; Conservative
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Best Local Similarity
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US-09-817-676A-14
; Sequence 14, Application US/09817676A
; Sequence 10. 6800470
; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 14
LENGTH: 618
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; ORGANISM: Homo sapiens
US-09-817-676A-14
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Matches 78; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          618
                                                                                                                                                                                                                                                            RESULT 6
US-09-970-516-4
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                                                                                                                                                                                                                                                                                                                                                                     117 MRNLGNDQWKVVRGNFFMICGANITCACARSPNGISRYSHLGDGCLDLILVKKTSLLNNV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 WLQTLREMLEK-----LTSRPKHLLVFINPFGGKGGGKRIYERKVAPLFTLASIT 164
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                                                                ---PAQHTVGSPRD-----RKPCRAGCFVC----
                                                                                                     RFLIRHTNQQ-DQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHIC-----
   Gaps
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Fatent No. 6830881

GENERAL INFORMATION:

APPLICANT: Saba, Julie D.

APPLICANT: Saba, Julie D.

TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,

TITLE OF INVENTION: PHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,

TITLE OF INVENTION: PLOUSOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,

TITLE OF INVENTION: PLOUSOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,

TITLE OF INVENTION: METHODS OF USE THEREFOR

TITLE OF INVENTION: METHODS OF USE THEREFOR

TITLE OF INVENTION: METHODS OF USE THEREFOR

CURRENT APPLICATION NUMBER: US/10/053,510

CURRENT APPLICATION NUMBER: US/10/053,510

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 20

LENGTH: 524
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   89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKP
   Indels
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   82;
Mismatches
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ORGANISM: Drosophila melanogaster
35;
                                                                317 KTFLSHHCYEGTVSFL-
Conservative
85;
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Sequence 4, Application US/09970516
Fatent No. 6610534
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Induction of blood vessel formation through administration of TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
TITLE REFERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
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APPLICANT: Spiegel, Sarah
APPLICANT: Kohama, Takafumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-04-03
211 TQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYS------TVGTSDAETSALHI
                                                                                428 RFNFLRFLIR---HTNQODOFDFTFVEVYRVKKFQFTSKHMEDEDSD---LKEGGKKRFG
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30.0%; Pred. No. 4e-19;
Live 44; Mismatches 111;
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US-09-959-897-2
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US-09-970-516-2
JS-09-959-897-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----YSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDII 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 AVSHHGGFEQVVGVDLLLNCSLLLCRGGSHPLDLLSVTLASGSRCFSFLSVAWGFLSDVD 309
                                                                                 211 TQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYS-----TVGTSDAETSALHI 261
                                                                                                                                                                                                                                                           262 VVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Takafumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT PEPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2000-04-03
PRIOR PILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 12.
                                   Gaps
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9.3%; Score 267.5; DB 4; Length 617;
Best Local Similarity 28.5%; Pred. No. 1e-18;
Matches 79; Conservative 49; Mismatches 122; Indels 27
 Length 618;
                                 44; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 IHSERFRALGSARFTLGAVLGLASLHTYRGRLSYLPA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 KDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPA 334
9.4%; Score 271.5; DB 4; 30.0%; Pred. No. 4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09817676A Patent No. 6800470 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             333 LHTYRGRLSYLPATVEPASP 352
                                                                                                                                                                                                                                                                                                                         HHCYEGTVSFLPAQHTVGSP 341
                                 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Mus musculus
US-09-817-676A-12
                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-09-817-676A-12
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 Query Match
                                 Matches
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Sequence 2, Application US/09970516
Patent No. 6610534
GENERAL INFORMATION:
APPLICANT: No. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
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                                                                                                                          GENERAL INCORALION STRAIN APPLICANT: PITSON, STRAIN APPLICANT: PITSON, STRAIN APPLICANT: PITSON, STRAIN APPLICANT: PL, XIA
APPLICANT: PL, XIA
APPLICANT: Richard, D'ANDREA J
APPLICANT: Mathew, VADAS A
TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
FILE REFERENCE: PITSON=1
CURRENT APPLICATION NUMBER: US/09/959, 897
CURRENT APPLICATION NUMBER: 2001-11-13
PRIOR APPLICATION NUMBER: PCT/AU00/00457
PRIOR APPLICATION NUMBER: PQ 0339
PRIOR APPLICATION NUMBER: AU PQ 0339
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-07-08
NUMBER: PLE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF
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25.3%; Pred. No. 6.3e-19;
Sequence 2, Application US/09959897
Patent No. 6730480
GENERAL INFORMATION:
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Sequence 7026, Application US/09949016

j Batent No. 6812339
j GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    FILE REPERBENCE: CLOOD.307
    CURRENT APPLICATION NUMBER: 60/241, 755
    PRIOR PILING DATE: 2000-10-20
    PRIOR PILING DATE: 2000-10-20
    PRIOR PILING DATE: 2000-10-03
    PRIOR PILING DATE: 2000-10-03
    PRIOR PILING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 207012
    SOFTHARE: PRESEE FREESEQ for Windows Version 4.0
    SEQ ID NO 7026
                                                                                                                                                                                                                                                                                                                                                                        129 RPKHLLVFINPFGGKGGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 DGIVCVGGDGMFSEVLHGLIGRIQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVC--- 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 SEKKRWIGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQ 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 ---GKGVFA---------VDGELMVSEAVQGQVHPNYFWMVSGCVEPPPS 371
                                                                                                                                                                                                                                                                                                                                                                                                     KEGGKKR FGHI CSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENP-
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases FILE REPEBENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 384
                                                                                                                                                                                                                                                                                9.2%; Score 264.5; DB 4; Length 384; 25.3%; Pred. No. 1e-18;
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Matches 107; Conservative
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ORGANISM:
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NAME/KEY: MISC_PEATURE
LOCATION: (1). (384)
LOCATION: (1). (384)
OTHER INFORMATION: SEQ ID NO 3 is the peptide sequence of hSPHK1 in Fig. 3, correspondence in INFORMATION: nding to amino acid residue 1 to 384 of Homo saplens SPHK-1 of Ge OTHER INFORMATION: nbank sequence Accession Number AAF73423.
PUBLICATION INFORMATION:
AUTHORS: Nava et al.
TITLE: Functional characterization of human spingosine kinase-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Spiegel, Sarah
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
FILE REFERENCE: 07320001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
                                         17;
                                                                                 129 RPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKY 188
                                                                                                                                                                                             | :| :|||: |||: ||::||: |
DALVVMSGDGLMHEVVNGLMERPDWETAIQK-------PLCSLPAGSGNALAASL 120
                                                                                                                                                                                                                                                      ----YSTVGTSDAETSALHIVVGDSLA-MDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD 299
                                                                                                                                                                                                                                                                              300 SEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQ 359
                                                                                                                                                                                                                                                                                                                                                                               181 SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGR-VGSKTPASP-----VVVQQGPV 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 -GVMHLFYVRAGVSRAMILRFFLAMEKGRHM----EYECPYLVYVPVVAFR-----LEPK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSDLKEGGKKRFGHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIE 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVC---
                                         Gaps
                                       87;
Length 384;
                                       Indels
9.1%; Score 263.5; DB 4; 25.1%; Pred. No. 1.3e-18; ative 69; Mismatches 164;
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DATABASE ACCESSION NUMBER: AAF73423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-796-487-3
; Sequence 3: Application US/09796487
; Patent No. 6830916
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
Query Match
Best Local Similarity 25.1<sup>†</sup>
Matches 107; Conservative
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ORGANISM: Homo sapiens
PEATURE:
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LENGTH: 388
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US-09-796-487-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVC--- 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----YSTVGTSDAETSALHIVVGDSLA-MDVSSVHHNSTLLRYSVSLLGYGFYGDIIKD 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 QLEEEQKKALYGLEAAEDV-EEWQVVCGK----FLAINATNMSCACRRSPRGLSPAAHLG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGSSDLILIRK-CSRFNFLRFLI-----RHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDE 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 SEKYRRIGEMRFTIGTFIRLAALRTYRGRLAYLPVGR-VGSKTPASP-----VVVQOGPV 234
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APPLICANT: Spiegel, Sarah
APPLICANT: Kohama, Takatumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
FILE REPERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
PRIOR PILIATION NUMBER: US 60/194,318
PRIOR FILIATION NUMBER: US 60/194,318
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 388
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                                                                                                                                                                                                                                                                                                                                                69; Mismatches 164;
                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                             9.1%; Score 263.5; DB 4 25.1%; Pred. No. 1.3e-18;
DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1)..(384)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AFF73423
DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1)..(384)
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JOURNAL: J. Biol. Chem.
VOLUME: 273
                                                                                                                                                                                                                                                                                                             Best Local Similarity 25.1
Matches 107; Conservative
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PAGES: 23722-23728
DATE: 1998-09-11
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US-09-796-487-3
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US-09-81
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LOCATION: (1). (388)
OTHER INFORMATION: SEQ ID NO 2 is the peptide sequence of SPHKIb in Fig. 1, correspo OTHER INFORMATION: mding to amino acid residue 1 to 388 of SPHKIb of GenBank sequenc OTHER INFORMATION: e Accession Number AAC61698.
PUBLICATION INFORMATION:
AUTHORS: Kohama et al.
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                                                                                                                                                                           13,
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-----QRGVFSVDGELMV 351
                                                                                                                                                                                                                                        104 FWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASI 163
                                                                                                                                                                                                                                                                                                                                                      164 TIDIIVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRIQRSAGVDQNHPR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:----PLCSLPGGSGNALAASVNHYAGYEQVTNEDLLINCTLLLCRRLLSPMNLLSL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 HHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPA 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 VLLHTHLSSELFAAPMGRCEA----GVMHLFYVRAGVSRAALLRLFLAMQKGKHMELDC
                                                                                                                                                                                                                                                                          2 WWC-----CVLFVV----ECPRGLLPRPCRVLVLLNPQGGKGKALQLFQSRVQPFLEEAEI
                                                                                                                                                                              Gaps
                                                                                                                                                                              86;
                                                                                                                 Length 388;
                                                                                                                    9.0%; Score 260; DB 4; Length 3E 23.3%; Pred. No. 3.1e-18; rative 70; Mismatches 173; Indels
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TITLE OF INVENTION: Sphingosin Kinase, Cloni
FILE REFERENCE: 0732001aa (2033957-0001)
CURRENT PELING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.
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; DATABASE ACCESSION NUMBER: AAC61698
; DATABASE ENTRY DATE: 1998-09-26
US-09-817-676A-15
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                                                                                                                                                                              Matches 100; Conservative
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352 CEAVQGQVH 360
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                                                                                                                                                  Similarity
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVLVPSSLRIGIIPAGSTDCVC-----YSTVGTSDAETSALHIVVGDSLA-MDVSSV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPA 334
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                                                                                                                                                                                                                                                           104 FWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASI
                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: Saba, Julie D.

APPLICANT: Saba, Julie D.

APPLICANT: Saba, Julie D.

APPLICANT: Fyret, Henrik

TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REPERRANCE: 200116,4022,510

CURRENT FILING DATE: 2002-01-17

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 21

LENGTH: 368
                                                                                                                                                                                                                           96;
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25.1%; Pred. No. 8.4e-18;
tive 68; Mismatches 167; Indels 79
                                                                                                                                                                                         Length 388;
                                                                                                                                                                                                                           Indels
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lilarity 23.3%; Pred. No. 3.1e-18;
Conservative 70; Mismatches 173;
          DATE: 1998

DATE: 1998

DATABASE ACCESSION NUMBER: AAC61698

DATABASE ENTRY DATE: 1998-09-26

RELEVANT RESIDUES: (1)..(388)

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: AAC61698

MELVANT RESIDUES: (1)..(388)

US-09-796-487-2
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Matches 105; Conservative
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nes 100; Conserv
PAGES: 23722-23728
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US-10-053-510-21
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                419 DLILIRK-CSRFNFLR-FLIRHINQODQFDFTFVBVYRVKKFQFTSKHMEDEDSDLKEGG
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LLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKYDGIV
                                                          193 CVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVC----
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 3, 2005, 04:09:18; Search time 109.661 Seconds (without alignments) 1893.930 Million cell updates/sec Run on:

US-10-631-958-10 2888 Title: Perfect score:

1 MGATGAAEPLQSVLWVKQQR.....QLVRLFARGIEENPKPDSHS 537 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*

geneseqp1980s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20048:\*

#### SUMMARIES

| Human lip<br>Human NOV<br>Human soh |
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| Adn62845 H<br>Abb07857 H            |
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| ABB07857                            |
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| Aae07886 Partial m Abb58465 Drosophil Abr82392 D. melano Abr82390 D. melano Abr82390 D. melano Abb57980 Drosophil Abr82393 D. melano Abu09075 Human sph Abg21144 Novel hum Auu09074 Human sph Abg31587 Human sph Abg31587 Human sph Abd71585 Protein s Add31817 Human pro Add15182 Human sign Add15182 Human sign Add15182 Human sign Add16569 Sphingosi Aau09073 Mouse sph Abb67866 Human sign | Ad£28783 Human sph<br>Aab18659 A human r |
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| AAEO7886 ABB58465 ABR82392 ABR82390 ABR82390 ABR82390 ABR82393 AAU09074 AAU09074 AAEO71597 ABEO715182 ABU52806 AD56569 AAU09073 AAU409073 AAU409073                                                                                                                                                                                                                                             | ADF28783<br>AAB18659                     |
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#### ALIGNMENTS

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Human sphingosine kinase-like protein; intracellular signalling; cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma; autoimmune disease; rheumatoid arthritis; Parkinson's disease.
                                                            Human sphingosine kinase-like protein.
                ABB07856 standard; protein; 537 AA.
                                                                                                                                                        05-OCT-2001; 2001WO-EP011516.
                                                                                                                                                                      06-OCT-2000; 2000US-0238005P.
                                              03-JUL-2002 (first entry)
                                                                                                                                                                                                             Kossida S, Encinas J;
                                                                                                                                                                                                                            WPI; 2002-340094/37.
                                                                                                                                                                                             (FARB ) BAYER AG.
                                                                                                                                                                                                                                     N-PSDB; ABL40828
                                                                                                                          WO200228906-A2
                                                                                                           Homo sapiens.
                                                                                                                                         11-APR-2002.
                              ABB07856;
RESULT 1
ABB07856
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New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous system disorder.

Claim 25; Fig 10; 120pp; English.

The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosline kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g. asthma), autoimmune diseases (e.g. rheumatoid arthritis) and central and peripheral nervous system disorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein

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                                                                                                EETDVHGKHQGSGKMQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEGQLCHLWLQTLR 120
                                                                                                            EMLEKLTSRPKHLLVFINPPGGKGOGKRIYERKVAPLFTLASITTDIIVTEHANOAKETL 180
                                                                                                                                                    EMLEKLISRPKHLLVFINPFGGKGGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL 180
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                                                                     MGATGAAEPLOSVLWYKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                       Gaps
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                  Length 537;
                                       Indels
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                            2e-274;
                                      0; Mismatches
                  100.0%; Score 2888;
100.0%; Pred. No. 2e-
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05-OCT-2001, 2001US-0327435P.
05-OCT-2001, 2001US-0327439P.
09-OCT-2001, 2001US-0328029P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                      Matches 537; Conservative
                            Similarity
Sequence 537 AA;
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2001US-0328849P.
2001US-0329414P.
2001US-0330142P.
2001US-0330309P.
2001US-0331026P.
                                                                              2001US-0343629F.
2001US-0349575P.
2001US-0346357P.
2002US-0373260P.
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2002US-0381037P.
2002US-0381038P.
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2002US-0381642P.
2002US-0383656P.
                                                                                                                                     2002US-0373815P.
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2002US-0391335P.
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            15-0CT-2001;
17-0CT-2001;
18-0CT-2001;
24-0CT-2001;
24-0CT-2001;
29-0CT-2001;
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17-APR-2002;
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## (CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

### WPI; 2003-381626/36. N-PSDB; ADA05679.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

# Claim 1, Page 135; 586pp; English

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule above; (3) an isolated nucleic acid molecule above; (5) a call comprising the nucleic acid molecule described above; (5) a call comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above colypeptide or nucleic acid molecule in a first mammalian subject; (9) a contract of interesting a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aborrant physiological interactions of the polypeptide; (1) a method of corrections of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating correction, antibated and antilipaemic activities, and can be used in gene therapy. The mammal; and (14) a method for producing the above polypeptide in a mannal antilipaemic activities, and can be used in gene therapy. The colypeptide is useful in mannal activities, and can be used in gene therapy. The colypeptide is useful in mannal activity of any polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic acid molecule may be used to diagnose, treat or prevent metabolic acid molecule may be used to diagnose, treat or prevent

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neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
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                                                                                                                             / Match 100.0%; Score 2888; DB 6. Local Similarity 100.0%; Pred. No. 2e-274; Ne 537; Conservative 0; Mismatches 0.
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                                                                        present invention
                                                                                                     Sequence 537 AA;
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This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (FTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polypeptide sequence is a human kinase protein sequence
                                                                                                                                                                                           New nucleic acid molecule encoding a kinase polypeptide, useful for preparing a composition for treating diseases or disorders, e.g., cancer, or neurological, immunological or inflammatory disorders.
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15-JUL-2003; 2003WO-US021730
                                   15-JUL-2002; 2002US-0395632P
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Matches 537; Conservative
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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and condition in human related to the aberrant expression and activity of NOVX polypeptides and conditions. Conversely, antisense NA molecules expression or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of conferentive therapy. NOVX polypeptides may also be used as antigonists and antagonists and in assays to identify modulators the production of antibodies and in assays to identify modulators anti-NOVX polypeptide antibodies, agonists and antagonists may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polypeptide antibodies may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, allabetes, and the various dyslipidaemias, metabolic disorders, and the various dyslipidaemias, metabolic changers.

Masting disorders associated with obesity, the metabolic syndrome X and the various dyslipidaemias, metabolic means an expensity and the various dissipances.
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                                                                                                                                                                                                                                                 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ortr T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGATGAAEPLOSVLWVKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV
                                                                                                                                                                                                                                                                                                                                                                                                      Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 537; Conservative 0
          MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                                                                                            EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                                              AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-213931/20.
                                                                                                                   LEACH M D.
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                                                                                                                                                             human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopojetic disorder; dyslipidaemia; metabolic syndrome X;
                                          ADN62845 standard; protein; 537 AA.
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18-0CT-2001; 20010S-0341039P.
22-0CT-2001; 20010S-0341039P.
24-0CT-2001; 20010S-0339266P.
24-0CT-2001; 20010S-0349562P.
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19-APR-2002; 2002US-0373826P.
19-APR-2002; 2002US-0373884P.
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09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328849P.
12-OCT-2001; 2001US-0328844P.
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2002US-0373260P.
2002US-0373815P.
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16-MAY-2002; 2002US-0381038P.
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2002US-0383831P.
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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ZERHUSEN B D.
ANDERSON D W.
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PATTURAJAN M.
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MILLET I.
PEYMAN J A.
KEKUDA R.
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CATTERTON E.
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19-APR-2002;
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20-MAY-2002
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                           EMLEKUTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
                                                                                                                               EETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLR
                 EMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
                                                                                    TDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDS
                                                                                                    TDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDS
                                                                                                                     EKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQ
                                                                                                                                                      LEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDL
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The
                                                                                                                                                                                                                                                                                                                                                       Human sphingosine kinase-like protein; intracellular signalling; cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma; autoimmune disease; rheumatoid arthritis; Parkinson's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous
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                                                                                                                                                                                                                                                                                                                                       Human sphingosine kinase-like protein.
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intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e sthumber), autoimmune diseases (e.g. rheumatoid arthritis) and central an peripheral nervous system disorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein
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Pred. No. 2.2e-274;
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                                                                                                                                                                                            invention relates to hCERKI, nucleic acids encoding it, expression vectors and host cells containing hCERKI nucleic acids, the recombinant production of hCERKI and antibodies specific for hCERKI. The invention also encompasses methods of isolating hCERKI from samples, the use of hCERKI in drug screening, and the use of hCERKI nucleic acid sequences in gene therapy. hCERKI mediates the ATP-dependent 1-phosphorylation of ceramides and can be used to screen for therapeutic and preventive agents for a wide range of disorders. Such disorders include neurological disease, inflammation, human immunodeficiency virus (HIV) infection, type 2 diabetes, obesity, sepsis, arteriosclerosis and cancer
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                                                                                                                                                                                    sequence represents a human ceramide kinase designated hCERK1. The
                                                                                                                        ceramide kinase gene and the enzyme encoded by it for screening ances as drugs for neurological, inflammatory and other disorders.
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                                                                                                                                                            Claim 1; Page 54-57; 61pp; Japanese.
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            14-JUN-2000; 2000JP-00178039
                                                             Kohama
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                                                            Kono K,
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                                  (SANY ) SANKYO CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKQQLEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSDLILIRKCSRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Platelet derived polypeptides with sphingosine kinase activity treatment of sphingosine related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.6%; Score 2588; DB 6; Length 481;
100.0%; Pred. No. 5.4e-245;
tive 0; Mismatches 0; Indels
                                                                                                             Human, enzyme, haemostatic, sphingosine kinase 4; SPHK4;
platelet transfusion; platelet stabiliser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOKKAIDO TECHNOLOGY LICENSING OFFICE CHEM BIOLOGY INST.
                                                     Human Sphingosine kinase 4-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Fig 4; 39pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                             28-SEP-2001; 2001WO-JP008537.
                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-2001; 2001WO-JP008537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 481; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kihara A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-354917/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 481 AA;
                                                                                                                                                                                                                                                            WO2003031627-A1.
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Igarashi Y,
20-NOV-2003
                                                                                                                                                                                                                                                                                                                    17-APR-2003
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116

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176

236 180 296 240 356 300 416 360

476

ABRS6302 ID ABRS6302 standard; protein; 481

RESULT 7

240 377 300 437 360

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NPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGD 120
                                                                                                                                                                                                                                                                                                                                     361 HINQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; sphingosine kinase; SphK; restenosis; ischaemia; gene therapy; antisense therapy; cancer; sphingolipid; signalling molecule; apoptosis; cytostatic; tumour necrosis factor-alpha; TNF; atherosclerosis; lymphoma; leukaemia; vasotropic; cell proliferative disorder; vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for treating a SphK-
or ischemia in a human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to sphingosine kinase (SphK) polypeptides and nucleic acids encoding them. SphK is useful for treating a SphK-associated disorder especially cancers such as leukaemia, lymphoma, ovarian, breast, lung, colon, testicular, stoomach and skin, atherosis, restenosis or ischaemia and cell proliferative disease or disorder associated with vascular diseases. SphK gene is used in gene
                                                        GMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETS
                                                                                                                         241 TFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQSLGEEGVKXALYGLEAAED
                                                                                                                                                                                                                                     378 VEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIR
                                                                                                                                                                                                                                                        258 ALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLK
                                                                                                                                                                      TFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAED
                                                                                                                                                                                                                                                                                                      HINQQDQFDFTFVEVYRVKKFQPTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNS
                                       GMFSEVLHGLIGRTORSAGVDONHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy and antisense-therapy. Sphingolipids serving as signalling
                                                                                                                                                                                                                                                                                                                                                                                        SWNCDGEVLHSPAIEVRVHCQLVRLFARELEENPKPDSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An isolated Sphingosine kinase polypeptide useful associated disorder especially cancer, restenosis
                                                                                                                                                                                                                                                                                                                                                                       SWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human sphingosine kinase (SphK) protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE07884 standard; protein; 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2000; 2000US-0182360P.
22-MAR-2000; 2000US-0191261P.
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                                                                                                                                                                      318
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New human sphingosine kinase A, B and C polynucleotides and polypeptides useful in e.g. chromosome and gene mapping, and detecting inflammation or disease associated with abnormal levels of sphingosine kinase expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 NPFGGKGGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                   spningosine kinase C; SKC; human; drug screening; infection; antiinflammatory; antiallergic; anticancer; inflammation; allergy; cancer; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                    AAY96059 standard; protein; 460 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 9; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0122516P.
                                                                                                                                                                                                                                                                    Human sphingosine kinase C.
                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gupta A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-572185/53.
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                    421
                                                                                                                                                                                                     AAY96059;
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Matches
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(GETH ) GENENTECH INC

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                                                                                                                                                                                                                                                                                                138 NPFGGKGQGKRIYERKVAPLFTLASITTDII------VTEHANQAKETLYEINID 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEBEQK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQK 300
                                                                                                                                                                                                                                                              9
molecules, have recently emerged as regulators of cell growth, differentiation, diverse cell phenotypes and cell death. Activation of SphK by tumour necrosis factor (FTP)-alpha inhibits apoptosis in human endothelial cells. The present sequence is human sphingosine kinase
                                                                                                                                                                                                                                                                                                                           61 NPFGGKGGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKETLYEINID
                                                                                                                                                                                                                                                                                                                                                                                            121 KYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSS
                                                                                                                                                                                                                          78 MEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFI
                                                                                                                                                                                                                                               1 MEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLREMLEKLISRPKHLLVFI
                                                                                                                                                                                                                                                                                                                                                                       KYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCY
                                                                                                                                                                                                                                                                                                                                                                                                                                              STVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKC
                                                                                                                                                                                         Gaps
                                                                                                                                                                                       11;
                                                                                                                                                   Length 471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS
                                                                                                                                                                                     0; Indels
                                                                                                                                                   DB 4;
                                                                                                                                                 85.1%; Score 2456.5; DB 4
97.5%; Pred. No. 4.4e-232;
                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein sequence SEQ ID NO:1224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP55248 standard; protein; 531
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                                                                                                                                                                                     Conservative
                                                                                                                                                                  Similarity
                                                                                                              Sequence 471 AA;
                                                                          (SphK) protein
                                                                                                                                                                                   Matches 459;
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                                                                                                                                                 Query Match
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                                                                                                                                                                      Local
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human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
                                                                                                                                                                                                                                                                                    28-OCT-2003; 2003WO-US034381
                                                                                                                                                                                virucide; gene therapy
                                                                                                                                                                                                                                WO2004039956-A2
                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                         Homo
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29-OCT-2002; 2002US-0422472P

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The present invention describes an isolated PRO nucleic acid (1). Also described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the cisolated PRO polypeptide; (5) a chimeric molecule comprising the composition of specifically binds to a polypeptide of (4); an agonist or composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the composition of matter of (7); (9) a method of treating an immune related disease in a comprising a container, a label on the container and a composition of marmal; (10) a method for determining the presence of a PRO polypeptide or an ample auspected of having the polypeptide; (11) a method of container and a composition of cin mammal; (12) a method of disease or an inflammatory immune response or antistreatic, antidiabetic, antidial and container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and a container and and an ensed in gene therapy. The nucleic acid (1) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune related disease and in container and immune response. The present sequence represents a human container and a member of a present inpersent because and and a manner of a present inpersent because and and a member of a present inpersent because and and a manner of a present inpersent because and and a manner of a present in the present and
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                                                                                                                                                                    New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.
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                                        Williams
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                                        Schoenfeld J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.1%; Score 2428; DB 8; 85.1%; Pred. No. 3.3e-229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Mismatches
                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1224; 3009pp; English.
                                          Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                      S, Clark H,
Wu TD;
                                                                                                       WPI; 2004-376182/35
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Best Local Similarity
Matches 450; Conserv
                                                                                                                             N-PSDB; ADP55247
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                                          Aggarwal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cyrostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoletic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic protein of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or
                                                                                                                                                                                                                                                                                           antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy.
421 ILIRKCSRFNFLRFLIRHTNQEDQPDFTFVEVYRVKKFPFTSKHVEDEDNDSKEQEKQKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z, Ma Y;
Weng G, Zhou
                                                  ILIRKCSRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
                                                                                                    529
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                                                                                                 GHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEE
                                                                                                             Wang
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Wang J, Ghosh M, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.4%; Score 2350; DB 8; 78.1%; Pred. No. 1.6e-221; ive 2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 1291; 718pp; English.
                                                                                                                                                                                                                                                                   Human therapeutic protein - SEQ ID 1291,
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                                                                                                                                                                                        ADS11054 standard; protein; 536
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                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-2003; 2003WO-US030720
                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2002; 2002US-0416186P.
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                                                                                                                                                                                                                                          (first entry)
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les 452; Conservative
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                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the protein sequence for human sphingosine kinase
                                                        THIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDI I KDSEKKRMLGLARYDFSGLKT
                                                                                                                                                                                                                     EEWOVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRH
                                                                                                              198 HIFTLVTALGCEHRSHPHFMDEDRRTGEHVGPGENAGGLDGSTDCVCYSTVGTSDAETSA
                                                                                                                                                                                                                                                             FLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDV
                                                                                                                                                                                                                                                                                      318 FLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDV
                                                                                                                                                                                                                                                                                                                 EEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLILIRKCSRFNFLRFLIRH
                                       GKRIYERKVAPLFTLASITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLH
                                                                                                                                                   ----GSTDCVCYSTVGTSDAETSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, enzyme; haemostatic; sphingosine kinase 4; SPHK4; platelet transfusion; platelet stabiliser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Platelet derived polypeptides with sphingosine kinase treatment of sphingosine related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS 536
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                                                                                             GLIGRIQRSAGVDQNHPRAVLVPSSLRIGIIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 29-30; 39pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR56301 standard; protein; 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-2001; 2001WO-JP008537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Sphingosine kinase 4.
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82 59

32 LRWWR-----SPGPGAGAPGADACSVPVSEIIAVEEIDVHGKHQGSGKWQKMEKPYAFT 

Best Loca Matches

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86 VHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLREMLEKLISRPKHLLVFINPFGGKGQ 145

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                                                                                                                                                                                                                                                                                          EEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLI 300
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                                                                                                                                                                                                          DCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSE 180
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                                                                                                                                                                                                                                                                                                                                          LIRKCSRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFG 360
                                                                                                                                                                                              DCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDSE 301
                                                                                                                                                                                                                                      KKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQL 361
                                                                                                                                                                                                                                                                                                                      LIRKCSRFNFLRFLIRHTNQQDQFDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRFG 481
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                                                                                                                          MLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLY
                                                                                                                                                       EINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGST
                                                                                                                                                                                                                                                                                                                                                                        HICSSHPSCCCTVSNSSWNCDGEVLASPAIEVRVHCQLVRLFARGIEENPKFDSHS 416
                                                                                                              122 MLEKLISRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETLY
                                                                                                                                                                                                                                                                              EEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDLI
                                                                                                                                                                                                                                                                                                                                                              537
                                                                                          Gaps
4 (SPHK4). The kinase can be used for the diagnosis and treatment caphingosine related disorders. The kinase can also be potentially toor controlling toxicity of platelet transfusion and as a platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations
                                                                                                                                                                                                                                                                                                                                                              HICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                      Length 416;
                                                                                          0; Indels
                                                                     icore 2210; DB 6; L
Pred. No. 6.4e-208;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #13532.
                                                                       Score
                                                                     76.5%; Sco
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23-AUG-2000;
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Best Local Simil
Matches 416; C
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responsible for genetic disorders or other traits and to assess
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420 452 480 512

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New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous system disorder.
GPKQMPAKGQVCRLPLLKLEASGLLRSEGRTCRSPDRLCSSCSIVCVGGDGMFSEVLHGL 120
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23-AUG-2001; 2001US-0314113P.
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                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                      Novel human diagnostic protein #13534.
                                                            ABG13543 standard; protein; 727 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g. asthmat), autoimmune diseases (e.g. rheumatoid arthritis) and central and peripheral nervous system discorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein
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Pred. No. 4.4e-152;
1; Mismatches 0; Indels 11;
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Best Local Similarity 96.3%;
Matches 314; Conservative
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Search completed: September 3, 2005, 04:37:40 Job time : 111.661 secs

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Scoring table:

Minimum DB Maximum DB

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AR541900 Sequence
AB079067 Mus muscu
AX129416 Mus muscu
AX129416 Mus muscu
CX730476 Sequence
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AX477010 Sequence
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AX101269 Drosophil
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AR510156 Sequence
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Novel gen
Homo sapi
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AC008298 Drosophil
AF098993 Caenorhab
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Segulation of human sphingosine kinase-like protein Patent: WO 0228906-A 1 11-APR-2002;
Bayer Aktiengesellschaft (DE)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX457006

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AR122416

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AX457001

AX10203946

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AUTHORS
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JOURNAL
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-MODBL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_epool/US10631958/runat_02092005_165815_4533/app_query.fasta_1.1941
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-NO MAAP -LARGEQUERY -NEG SCORESE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TINEOUT=30 -TRIREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPOXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AX224383 Sequence
CR456404 Homo sapi
AJ457828 Homo sapi
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                          nucleic search, using frame_plus_p2n model
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| Query Match:         100.00\$         Indels:         0           DB:         6         Gaps:         0           US-10-631-958-2         (1-326) x AX456998 (1-979)         (1-979)           QY         1 ProLysHisLeuLeuValPheIleAsnProPheGlyGlyLysGlyGlnGlyLysArglle 20           Db         2 CCAAAGCATTTACTGATTTATCAACCCGTTTGAGGAAAAGGACAAGGCAAAGGGATA 61           QY         21 TyrGluArgLysValAlaProLeuPheThrLeuAlaSerIleThrThrAspIleIleGly 40           CA         1 TyrGluArgLysValAlaProLeuPheThrLeuAlaSerIleThrThrAspIleIleGly 40           CA         2 TATGAAAGAAAAGGAAAAGCAACCAATGAACAACAACAACAACAACAACAACAACAACAACAACAAC | 41 AsniysPheTyrValAsniyvalGluVallleThrGluHisAlaAsnGlnAlaLysGlu 122 AACAAATTCTATGTTAGTAGTAATTACTGAACTGCTAATCAGGCCAGGAG 61 ThrIell                                                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Qy         141 LeuHislleValValGlyAspSerLeuAlaMetAspValSerSerValHisHisAsnSer 160           Db         422 CTGCATATCGTTGGGGACTCGCTGGCCATGGATGTCCTCAGTCCACACACA                                                                                                                                                                                          | 181 AspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThr | Qy         221 GlySerProArgABAPAGLy8ProCy8ArgAlaGlyCy8PheValCy8ArgGlnSerLy8 240           Db         662 GGATCTCCAAGGATAGGAAGCCCTGCCGGCCAGGATGCTTTGTTTG                                                                                                                                                                                                                        | Qy         261 GluGlufrpGlnValValCysGlyLysPheLeuAlaileAsnAlaThrAsnMetSerCys 280           Db         782 GAGGAGGCAAGTCGTGGGAAGTTTCTGGCCATCATGCCACAAACATGTCTGT 841           Qy         281 AlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSer 300           Dh | 301 AspleulleLeulleArglySCysSerArgPheAsnPheLeuArgPheLeulleArgHis |

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1. (basea 1 to 1654)

2. (cle., Goward, M.E., Aguado, B., Mallya, M.P., Grinham, J.A., Gole, G.G., Goward, M.E., Aguado, B., Mallya, M., Mokrab, Y., Huckle, E.J., Beare, D.M. and Dunham, I.

3. (cle., G., Goward, M.E., Aguado, B., Mallya, M., Mokrab, Y., Grinham, J.A., Autherie, E.J., Beare, D.M. and Dunham, I.

3. (cle., G., Goward, M.E., Aguado, B., Mallya, M., Mokrab, Y., Huckle, E.J., Beare, D.M. and Dunham, I.

4. (cle., E.J., Beare, D.M. and Dunham, I.

5. (cle., Goward, M.E., Aguado, B., Mallya, M.)

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Homo sapiens bK29F11.1 full length open reading frame (ORF) cDNA
clone (cDNA clone C22ORF:pGEM.bK29F11.1).
CR456404
CR456404.1 GI:47678338
CDNA, chromosome 22, ORF.
Homo sapiens (human)
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/lab_host="JM109"
/lab_host="JM109"
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/gene="bK29F11.1"
/codon_start=1
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NSTLLRYSVSLLGYGFYGDI IKDSEKKRWLGLARYDFSGLKTFLSHHCYBGTVSFLPA
QHTVGSPRDRKPCRAGCFVCRQSKQQLEBEGKKALYGLEAAEDVEBWQVVCGKFLAIN
ATMSCACRRS PRGLSPAAHLGDGSSDLILIRKCSRFNFLRPLIRHTNQQDGPDFTFV
BVYRVKRFQFTSKHWEDEDSDLKEGGKKRFGHICSSHPSCCTVSNSSWNCDGEVLHS
PAIEVRVKFQPTSKHWEDEDSDLKEGGKKRFGHICSSHPSCCTVSNSSWNCDGEVLHS
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Matches:
Conservative:
Mismatches:
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Gaps:
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                                                                                                                                                                                 ThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspIleIleLys
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AJ457828 AJ457828 GI:20269072
AJ457828 GI:20269072
Homo sapiens (human)
Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                Van Veldhoven, P.P.
A search for lipid kinases
A search for lipid kinases
Unpublished
2 (bases 1 to 2042)
Van Veldhoven, P.P.
Direct Submission
Submitted (18-APR-2002) Van Veldhoven P.P., Farmakologie,
K.U.Leuven, Herestraat, B-3000 Leuven, BELGIUM
Location/Qualifiers
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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FEATURES

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Location/Qualifiers
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Direct Submission

Direct Submission

Direct Submitted (12-NOV-2000) Osamu Ohara, Kazusa DNA Research Institute,

Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0912, Japan (E-mail:cdnainfo@Kazusa.or.jp,

URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens mRNA for KIAA1646 protein, partial cds.
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                                                                                                                                                                                                                                                                                                                           Kossida, S. and Encinas, J. esgulation of human sphingosine kinase-like protein Patent: WO 022896-A 9 11-APR-2002; Bayer Aktiengesellschaft (DE)
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                AND
                                                                                          Sugira, M., Kono, K., Shimizugawa, T., Minekura, H., Spiegel, S.
                                                                                                           Kohama, T. Direct Submission Submitted (29-JNN-2002) Masako Sugiura, Sankyo Co., Ltd., Submitted (29-JNN-2002) Masako Sugiura, Sankyo Co., Ltd., Pharmacology and Molecular Biology Research Laboratories; Hiromachi 1-chome, Shinagawa-ku, Tokyo 140-8710, Japan (E-mail:msugiura@shina.sankyo.co.jp, Tel:81-3-3492-3131, Pax:81-3-5436-8565)
 Spiegel, S. and Kohama, T. Ceramide Kinase. MOLECULAR CLONING FUNCTIONAL CHARACTERIZATION
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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              610 ACTCTGTATGAGATTAACATAGACAAATACGACGCCATCGTCTCTGTGTCGGCGGAGATGGT
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                                                             ThrLeuTyrGlulleAsnIleAspLysTyrAspGlyIleValCysValGlyGlyAspGly
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Sugiura,M., Kono,K., Liu,H., Shimizugawa,T., Minekura,H.,
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Tang, Y.T., Zhou, P., Goodrich, R., Liu, C., Asundi, V., Ren, F.,
Tang, J., Zhao, Q.A., Yang, Y., Xue, A.J., Wehrman, T., Wang, J.-R.,
Wang, J. and Drmanac, R.T.
Nucleic acids and polypeptides
Patent: US 6743619-A 148 01-JUN-2004;
Location/Qualifiers
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ABU/9067 29-JUN-2002 MRNA linear ROD 27-JUN-2002 Mus musculus cerk mRNA for ceramide kinases, complete cds. AB079067
                                                  1018 GACAGTGAGAAGAAACGGTGGTTGGGTTTTGCCAGATACGACTTTTCAGGTTTAAAAGACC 1077
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                AspSerGluLysLysLysLgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThr
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                                                                                                                                                                           PheLeuSerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrVal
       AND
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Sugiura, M., Kono, K., Shimizugawa, T., Minekura, H., Spiegel, S.
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Submitted (29-JAN-2002) Masako Sugiura, Sankyo Co., Ltd.,
Pharmacology and Molecular Biology Research Laboratories;
Hiromachi 1-chome, Shinagawa-ku, Tokyo 140-8710, Japan
(E-mail:meugiura@shina.sankyo.co.jp, Tel:81-3-3492-3131,
Pax:81-3-5436-8565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spiegel, S. and Kohama, T. Ceramide Kinase, MOLECULAR CLONING SPUCTIONAL CHARACTERIZATION J. B.ol. Chem. 277 (26), 23294-23300 (2002)
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/organiam="Mus musculus"
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1. .2830
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Mus musculus
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/gene="cerk"
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WO 0196575-A/1.

Homo sapiens (human)

SM Homo sapiens (human)

ENARTYCLE MELEZCE; CRONGALE; CREMINIE; HOMINIGAE; HOMO.

SM Homo sapiens (human)

ENARTYCLE MELEZCE; CALTATINI; HOMINIGAE; HOMO.

S UGIUTE, M., KONO, K. and Kohama, T.

Ceramide kinase and DNA thereof.

S UGIUTE, M., KONO, K. and KOHAMA, T.

SANKYO CO LTD, MASAKO SUGIURA, KEITA KONO, TAKAFUMI KOHAWA

OS HOMO sapiens (human)

PN WO 0196575-A/1

PP 11-JUN-2001 WO 2001JP004889

PR 14-JUN-2000 UP 00P 178039

PP MASAKO SUGIURA, KEITA KONO, TAKAFUMI KOHAWA

PP MASAKO SUGIURA, KEITA KONO, TAKAFUMI KOHAWA

PP MASAKO SUGIURA, KEITA KONO, TAKAFUMI KOHAWA

PP MASAKO SUGIURA, KEITA KONO, TAKAFUMI KOHAWA
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A61K48/00,
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Matches:
Conservative:
Mismatches:
Indels:
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Key
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/organism="Homo sapiens"
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CC Ceram
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/note="CDS is predicted by in silico analysis. Start codon is not identified.
Start codon is not identified."
Start codon is not identified."
/codon start=2
/evidence=not experimental
/product="mKIAA1646 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Koseki,H., Hiraoka,S., Saga,Y., Nagase,T., Ohara,O. and Koga,H.
Prediction of the coding sequences of mouse homologues of KIAA gene: III. the complete nucleotide sequences of 500 mouse of KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries DNA Res. 10 (4), 167-180 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-JUL-2003) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918) The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing: Kazusa DNA Research Institute; CDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                               281 AlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSer
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                                                            GlnGlnLeuGluGluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspVal
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Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
Direct Submission
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/gene="mKIAA1646"
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THYAADROJCHIMLOTIAGLESLISRYRKHLLVRINPFGKAGGRKITSRTVAPLFTT
ASITTEIITEHAADROJCHSVSTYSTVCVGGGGMFSBVLAGVIGKTQGSAGID
PNHPRAVLVPSTLRIGIIPAGSTDCVCYSTVGTNDAETSALHIIIGDSLAIDVSSVHY
                                                                                                                                                                                                                    HNTLLRYSVSLLGYGFYGDLIKDSEKKRWMGJVRYDFSGLKTFLSHQYYEGTLGFLPA
QHTVGSPRDNKPCRAGCFVCRQSKQQLEEEEKKALYGLENAEEVEEWQVTCGKFLAIN
ATNMSCACPRSPGGLSPFAHLGDGSSDLILIRKCSRFNFLRFLIRHTNQEDQFDFTFV
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                                                                            GCTTGTCCTCGGAGCCCTGGGGCCTGTCCCCATTTGCCCCATCTGGGAGATGGGTCTTCT
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Jane Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2599,
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Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.J.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
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/product="CERK protein"
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                                                                          Contact: MGC help desk
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CTGGCCATGGATGTGTCCTCAGTCCACACAGCACACTCCTTCGCTACTCCGTGTCC 703
                                                                                                                               GlyLeuAlaArgTyrAspPheSerGlyLeuLysThrPheLeuSerHisHisCysTyrGlu 208
                                                                                                                                                                   823
                                                                                                                                                                                                    GlyThrValSerPheLeuProAlaGlnHisThrValGlySerProArgAspArgLysPro 228
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                                                                                           Direct Submission
Submitted (12-MAR-2004) National Institutes of Health, Mammalian
                                                         LeuleuGlyTyrGlyPheTyrGlyAspIleIleLysAspSerGluLysLysArgTrpLeu
                                                                                                                                                    GGGACAGTGTCCTTCCTCCCTGCACACACACGGGGGGATCTCCAAGGGATAGGAACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 1772)
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Editaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallua.

E (bases 1 to 1450)
S Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E., Croning, M.D.F., Davies, R.M., Francis, M.D., Grafham, D.V., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Niblet, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G., Tickle, C. and Wilson, S.A.
Direct Submission
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R Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
                                                                                                                                                    Beguencing project.
This sequence is from the
BBSKC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
from a library constructed by Blizabeth Bosch. cDNA was prepared
from RNA extracted from heads, normalised, and poly A-trimmed.
BCORI.NotI cut cDNA was then ligated into the vector. Vector:
pBluescript II KS(+); Site_I: ECORI; Site_2: NotI Host: Escherichia
coli DH10B.
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/dev_stage="stage 22"
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| 069 | 690 GACAGTGAAAAGAAACGGTGGATGAGATGAGATACGACTATTCAGGCTTCAAGACT 749     |  |
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| 201 | PheLeuSerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrVal 220     |  |
| 750 |                                                                      |  |
| 221 | 221 GlySerProArgAspArgLysProCysArgAlaGlyCysPheValCysArgGlnSerLys 240 |  |

<sup>810</sup> GGATCTCCACGAGATAAGATAGCTGCAGAACAGGATGTTATATTTGCAAGGAAAGTGAG 869 241 GinGinLeuGluGluGluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspVal 260

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| 923 | 280                                                                  | 983                                                                 |
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|     | 261 GluGluTrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSerCys 280 | 924 GAAGAATGGAAGGTATTAAAGGGAAATTTCTAGCCATCAATGTAGTAAATATGTGCTGT 983 |
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Search completed: September 6, 2005, 16:37:43 Job time : 4353.05 secs

<sup>1104</sup> ACAAACAAAGATGACCAG 1121 321 ThrasnGlnGlnaspGln 326 ઠે

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| GenCore version 5.1.6  Copyright (c) 1993 - 2005 Compugen Ltd.  OM nucleic - nucleic search, using sw model Run on: September 5, 2005, 15:12:23 ; Search time 4448.35 Seconds (without alignments) 10664.096 Million cell updates/sec Title: US-10-631-958-1 " "(without alignments) 10664.096 Million cell updates/sec Sequence: 1 accaaagcatttactggtatacaccaaccagcaggaccag 979 Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0 Searched: 4708233 seqs, 24227607955 residues Total number of hits satisfying chosen parameters: 9416466 Minimum DB seq length: 0 Maximum Amatch 00* Post-processing: Minimum Match 00* Total number of hits satisfying chosen parameters: 9416466 Minimum DB seq length: 2000000000 Post-processing: Minimum Match 00* Total number of hits satisfying chosen parameters: 9416466                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Database: GenEmbl:*  1: gb ba:* 2: gb htg:* 3: gb_nn:* 4: gb_pn:* 5: gb_ov:* 6: gb_pat:* 7: gb_pn:* 10: gb_pr:* 11: gb_sts:* 11: gb_sts:* 12: gb_sv:* 13: gb_un:* 14: gb_vi:* 13: gb_un:* 14: gb_vi:* 18: gb_vi:* 18: gb_vi:* 18: gb_vi:* 18: gb_vi:* 19: gb_sv:* 10: gb_sts:* 10: gb_sts:* 11: gb_sts:* 12: gb_sv:* 13: gb_un:* 14: gb_vi:* 15: gb_vi:* 16: gb_vi:* 17: gb_sv:* 18: gb_vi:* 18: gb_vi:* 19: gb_vi:* 10: gb_sts:* 10: gb_sts:* 10: gb_sts:* 11: gb_sts:* 12: gb_sv:* 13: gb_un:* 14: gb_vi:* 14: gb_vi:* 15: gb_sv:* 16: gb_sts:* 17: gb_sts:* 18: gb_vi:* 18: gb_vi:* 19: gb_vi:* 10: gb_sts:* 11: gb_sts:* 12: gb_sts:* 13: gb_sts:* 14: gb_sts:* 15: gb_sts:* 16: gb_sts:* 17: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 19: gb_sts:* 19: gb_sts:* 10: gb_sts:* 10: gb_sts:* 10: gb_sts:* 10: gb_sts:* 10: gb_sts:* 11: gb_sts:* 12: gb_sts:* 13: gb_sts:* 14: gb_sts:* 15: gb_sts:* 15: gb_sts:* 16: gb_sts:* 16: gb_sts:* 17: gb_sts:* 17: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts:* 18: gb_sts: | 100.0 979 6 AX456998<br>100.0 1840 6 AX224383<br>92.2 1654 9 CR456404<br>92.2 4171 9 BD134468<br>92.2 4171 9 AB01433<br>92.2 4413 6 AX457006<br>92.2 4443 6 AX457006<br>92.1 4443 6 AX547006<br>91.7 4463 6 BD102675<br>84.5 1459 6 CQ730476<br>78.1 1779 9 BCC07255<br>65.3 3661 10 AR129416<br>65.1 2830 10 AB079067<br>42.8 1450 5 CR386590<br>37.0 2494 5 BC074110<br>36.0 1520 5 BC074110                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Novel sphingosine kinases
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Curagen Corporation (US); GENENTECH,
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                     ccagaaccacccccccccrcrcrcrccccagraccrccccarrcgaarcarrcccc
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A search for lipid kinases
Unpublished
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Homo sapiens (human)
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Van Veldhoven, P.P.
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/borden_id="CAG30290.1"
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ASITTDIIVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVD
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NSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPA
OHTVGSPRDRKPCRAGCFVCRQSKQQLEEEQKKALYGLEAAEDVEEWQVVCKFLAIN
ATNNSCACRRSPRGLSPAHLGDGSSDLILIRKCSRPYFLRFLIRHTNQQDOFPTFV
EVYRVKKFQFTSKHMEDEDSDLKEGGKKRFGHICSSHPSCCCTVSNSSWNCDGEVLHS
                                                                                    1654 bp mRNA linear PRI 25-MAY-2004 Homo sapiens bK29F11.1 full length open reading frame (ORF) cDNA Clone (CDNA clone C22ORF:pGEM.bK29F11.1).
                                                                                                                                                                                                                                                                                                                                                           Submitted (24 MAY-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript Sanger Institute and : pGEM.bK29F11.1
Homo sapiens CDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see http://www.sanger.ac.uk/HGF/Chr22/.
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                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 1654)

Collins, J.E., Wright, C.L., Edwards, C.A., Davis, M.P., Grinham, J.A., Cole, C.G., Goward, M.E., Agnado, B., Mallya, M., Mokrab, Y., Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 ACCAAAGCATTTACTGGTATTTATCAACCCGTTTGGAGGAAAAGGACAAGGCAAGCGGT
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.larity 96.6%; Pred. No. 6.2e-229;
Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
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CACCAACCAGCAGGACCAG 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="bK29F11.1"
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                                                                                                                                                                        CR456404.1 GI:47678338
CDNA; chromosome 22; ORF.
Homo sapiens (human)
Homo sapiens
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JP 2002345492-A/181
O3-DEC-2002
26-FEB-2002 JP 2002049009
OSAMU OHARA, TAKAHIRO NAGASE, DAISUKE NAKAJIMA
C12N15/09, C07K14/47//A61K31/711, A61K38/00, A61P25/00,
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(hara, O., Nagase, T. and Nakajima, D.

Novel genes and proteins encoded by the genes

RAZUSA DNA RESEARCH INSTITUTE

OS Homo sapiens (human)
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Novel genes and proteins encoded by the genes
Location/Qualifiers
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Novel genes and proteins encoded by the genes.
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Pred. No. 6.9e-229;
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Location/Qualifiers
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JP 2002345492-A/181.
Homo sapiens (human)
Homo sapiens
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Direct Submission
Submitted (18-ARR-2002) Van Veldhoven P.P., Farmakologie,
K.U.Leuven, Herestraat, B-3000 Leuven, BELGIUM
Location/Qualifiers
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Craniata; Vertebrata; Euteleostomi;

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PRI 06-OCT-2001

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Homo sapiens (human)
Memo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HHNSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYBGTVSFL
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                                                                                                                                                       Chases 1 to 4171)
Chara,O., Nagase,T. and Kikuno,R.
Direct Submission
Submitted (122-NOV-2000) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
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Hirosawa,M., Nagase,T., Murahashi,Y., Kikuno,R. and Chara,O. Identification of novel transcribed sequences on human chromosome 22 by expressed sequence tag mapping DNA Res. 8 (1), 1-9 (2001)
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0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=2
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/organism="Homo
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Pred. No. 6.9e-229;
0; Mismatches 0;
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larity 96.6%;
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/mol type="unassigned DNA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Regulation of human sphingosine kinase-like protein
Patent: WO 0228906-A 9 11-APR-2002;
Bayer Aktiengesellschaft (DE)
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (bases 1 to 4463)
E. 1 (bases 1 to 4463)
E. Sugiura, M., Kono, K. and Kohama, T.
Ceramide Kinase and DNA thereof
L. Patent: WO 0196575-A 1 20-DEC-2001;
SANKYO CO LTD, MASAKO SUGIURA, KEITA KONO, TAKAFUMI KOHAMA
OS Homo sapiens (human)
PN WO 0196575-A/1
PD 20-DEC-2001
PF 11-UIN-2001 WO 2001JP004889
PR 14-JUN-2001 WO 2001JP004889
PR 14-JUN-2001 WO 2001JP00489
PR 14-JUN-2001 WO 2001JP00489
PR 14-JUN-2001 JP 00P 178039
PR MASAKO SUGIURA, KEITA KONO, TAKAFUMI KOHAMA
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Key (124). (1734).
Location/Qualifiers
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Pred. No. 1.3e-227
0; Mismatches 3
                                                                                                                                                                                                            DNA
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                      Ceramide kinase and DNA thereof. BD102675.1 GI:22648249 WO 019675.1
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                                                                                                      CACCAACCAGCAGGACCAG 979
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Homo sapiens
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PC A61P3/0
A61P35/00
CC Ceramid
FH Key
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Best Local Similarity
Matches 943; Conserv
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               Tang, Y.T., Zhou, P., Goodrich, R., Liu, C., Asundi, V., Ren, F., Zhang, J., Zhao, Q.A., Yang, Y., Xue, A.J., Wehrman, T., Wang, J.-R., Wang, D. and Dramanac, R.T.
Nuclaic acids and polypeptides
Patent: US 6743619-A 148 01-JUN-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                          ACCAAAGCATTTACTGGTATTTATCAACCCGTTTGGAGGAAAAGGACAAGGCAAGCGGAT
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                                                                                                                                                                              Score 901.4; DB 6;
Pred. No. 1.8e-228;
0; Mismatches 1;
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/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 96.5%;
Matches 945; Conservative (
   (bases 1 to 4432)
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Homo sapiens ceramide kinase, mRNA (cDNA clone IMAGE:6185601), complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                   TTGGGAGGACGCAGAGGAGCGCCGGGGTCGACCAGAACCACCCCCGGGCTGTGCTGGTCC
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                                                                                                       ACGACGCCATCGTCTGTCGCCGCGAGATGGTATGTTCAGCGAGGTGCTGCACGGTCTGA
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    Length 1459;
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  Score 826.8; DB 6;
Pred. No. 1.1e-208;
0; Mismatches 2;
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84.5%;
nilarity 99.8%; 1
Conservative 0;
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                Similarity
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Matches 828;
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
hareof
Patent: WO 02068579-A 16410 06-SEP-2002;

PE Corporation (NY) (US)
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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/organism="Homo sapiens"
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Homo sapiens
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CQ730476
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Pred. No. 3.7e-192;
0; Mismatches 7;
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                    /protein_id="AAH67255.1"
/db_xref="G1:45595583"
/db_xref="LocusID:64781"
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            Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butcow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M., B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 11 Row: d Column: 4
This clone was Belected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21703365
This clone has the following problem: The cds is short compared to the longest cds in the locus.

Location/Qualifiers

1. 1772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="Peripheral Nervous System, dorsal root"
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DKFZp434E0211, FLJ21430, FLJ23239, dA59H18.2, LK4"
/db_xxef="LocusID:64781"
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cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 1772)
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg, R.
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AUTHORS
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AB079067 27-JUN-2002 MNA linear ROD 27-JUN-2002 Mus musculus cerk mRNA for ceramide kinases, complete cds. AB079067
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                           241 TATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGAGCGCCGGGGTCGA
                                                                                                                          229 CATGTTCAGCGAGGTGCTGCATGGGGTGATTGGGAGGACGCAGCAGAGCGCTGGTATCGA
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                                       GACTCTGTATGAGATTAACATAGACAAATACGACGGCATCGTCTGTGTCGCCGGAGATGG
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Spiegel,S. and Kohama,T.
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                                                                                                                                                     Okazaki, N., Kikuno, R., Ohara, R., Inamoto, S., Koseki, H., Hiraoka, S., Saga, Y., Nagase, T., Ohara, O. and Koga, H.
Prediction of the coding sequences of mouse homologues of KIAA gene: III. the complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries 22977043
                                                                                                                                                                                                                                                                                                           Okazaki, N., Kikuno, R., Nagase, T., Ohara, O. and Koga, H.

Direct Submission

Direct Submission

Direct Submission

Bubmitted (23-70L-2003) Hisashi Koga, Kazusa DNA Research

Institute, Laboratory for Genome Informatics; 2-6-7

Kazusas-kamatari, Kisarazu, Chiba 292-0818, Japan

The CREATE program supported by Japan science and technology

corporation; cDNA full insert sequencing: Kazusa DNA Research

Institute; cDNA library construction, clone selection and 5'- &
3'-end one pass sequencing.
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                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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Pred. No. 1.2e-158;
0; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db xref="taxon:10090"
/dlone="mph01246"
/tissue type="embryonic tail"
/note="vector:modified pBC SK+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Start codon is not identified." /codon_start=2
   for mXIAA1646 protein.
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/product="mkTAA1646 protein"
/protein_id="BAC9826.1"
/db_xref="G1:37360496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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/gene="mKIAA1646"
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                                                                  Mus musculus (house mouse)
                                     AK129416.1 GI:37360495
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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               CACACTCCTTCGCTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCATCAAA
                                                                   GGACAGTGAGAAGAACGGTGGTTGGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGAC
                                                                                 GGAGGAGTGGCAAGTCTGTGGGAAGTTTCTGGCCATCAATGCCACAAACATGTCCTG
                                                                                                                       GCAGCAGCTGGAGGAGGAGCAGAAAGCACTGTATGGTTTGGAAGCTGCGGAGGACGT
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Bayer Aktiengesellschaft (DE)
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Pred. No. 2.7e-112;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX457001
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/organism="Homo
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Matches 465; Conservative C
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Sugiuxa,M., Kono,K., Shimizugawa,T., Minekura,H., Spiegel,S.
                                                                                                        Submitted (29-JAN-2002) Masako Sugiura, Sankyo Co., Ltd., Pharmacology and Molecular Biology Research Laboratories; Hiromachi 1-chome, Shinagawa-ku, Tokyo 140-8710, Japan Emallimengiura@shina.sankyo.co.jp, Tel:81-3-3492-3131,
Kinase, a Novel Lipid Kinase. MOLECULAR CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.1%; Score 637.4; DB 10; Length 2830; 79.7%; Pred. No. 3.1e-158; ive 0; Mismatches 166; Indels 33;
 FUNCTIONAL CHARACTERIZATION
J. Biol. Chem. 277 (26), 23294-23300 (2002)
                                                                                                                                                                                                                                                                                                           product="ceramide kinases"
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1. .2830
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/db_xref="GI:21624342"
                                                                                              Direct Submission
Submitted (29-JAN-2002) Masako
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'gene="cerk"
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|            | 128 G                                                     | 419 G                                                     | 188 G                                                     | 479 A                                                       | 248 A                                                  | 539 A                                                     | 308 A                                                       | 599 A                                        | 368 A                                                    | 629                                                | 428 G                                                |  |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

genesegn2004as: \*

| Description                   | Ab140822 Human sph<br>Aad14426 Human sph | Human                | Aaa50510 Human sph | Abl40828 Human sph | Adj96598 Human lip | Adp55247 Human PRO | Abx70921 Novel hum | Aba96945 Human cer | Adn62844 Human NOV | Aas77728 DNA encod | Ads10370 Human the | Aac76031 Human ORF | Aas77731 DNA encod | Aas77730 DNA encod | Abl40823 Human sph | Aas77727 DNA encod | Aas77729 DNA encod | Ab140824 Human sph |
|-------------------------------|------------------------------------------|----------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES                     | ABL40822<br>AAD14426                     | ADA05679<br>ACC70838 | AAA50510           | ABL40828           | ADJ96598           | ADP55247           | ABX70921           | ABA96945           | ADN62844           | AAS77728           | ADS10370           | AAC76031           | AAS77731           | AAS77730           | ABL40823           | AAS77727           | AAS77729           | ABL40824           |
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| *<br>Query<br>Match Length DB | 979                                      | 1740                 | 4231               | 4413               | 4429               | 4445               | 4432               | 4463               | 1740               | 2241               | 4702               | 753                | 1570               | 2186               | 474                | 426                | 411                | 329                |
| %<br>Query<br>Match           | 100.0                                    | 92.2                 | 92.2               | 92.5               | 92.2               | 92.2               | 92.1               | 91.7               | 89.7               | 63.6               | 63.1               | 61.2               | 55.5               | 55.5               | 47.4               | 41.0               | 37.1               | 30.9               |
| Score                         | 979                                      | 903                  | 903                | 903                | 903                | 903                | 901.4              | 898.2              | 878.4              | 622.2              | 618                | 598.8              | 543                | 543                | 464.4              | 401.8              | 362.8              | 302.2              |
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| 55181<br>5185<br>51885<br>51885<br>564<br>153<br>153<br>153<br>1033<br>1050<br>11774<br>1167<br>1167<br>1167<br>1167<br>1167<br>1167<br>116                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | first entry) ine kinase-like ine kinase-like tion; apoptosis; ease; rheumatoid 2.789 /*tag= a /product= "sph /note= "start . 001WO-EP011516.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | I;<br>lating<br>or po<br>ne dis                                                                                                                                                                                        |
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| υυυ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | RESULT ABLA082 10 ABLA082 XX XX XX XX XX XX XX XX XX XX XX XX XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | X 1 X 8 8 X 1 X 1 X                                                                                                                                                                                                    |

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                                                                                                                                                                                                                                             Human sphingosine kinase (SphK) cDNA
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22-MAR-2000; 2000US-0191261P.
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                 The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g. sathmal, autoimmune diseases (e.g. rheumatoid arthritis) and central and peripheral nervous system disorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein
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                                                                                                                                                     100.0%; Score 979; DB 6; Length 9
100.0%; Pred. No. 2.3e-281;
ive 0; Mismatches 0; Indels
Fig 1; 120pp; English
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associated disorder especially cancer, restenosis or ischemia in a human.
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109. .1524
1/tag= a
/product= "Human sphingosine kinase (SphK)
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human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkters RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
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12-0CT-2001; 2
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                                                                 ACCAAAGCATTTACTGGTATTTATCAACCCGTTTGGAGAAAAGGACAAGGCAAGCGGAT
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 Score 979; DB 5; L
Pred. No. 3.1e-281;
0; Mismatches 0;
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VA;

Dipippo

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                   pharmacogenomics
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20; Page 134; 586pp; English. Claim

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit composition or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
ammple; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
CC adaption an agent that binds to the polypeptide acid molecule in a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or
aberrant physiological interactions of the polypeptide; (11) a method of
cc a pathology associated with the polypeptide; (11) a method of
creening for a modulator of activity or of latency or predisposition to
c berrant physiological interactions of the polypeptide; (12) a method of
creening a pathology associated with the above polypeptide in a
mammal; and (14) a method for producing the above polypeptide in a
mannal; and (14) a method for producing the above polypeptide in a
mannal; and (14) a method for producing the above polypeptide in a
mannal; and (14) a method for producing the above polypeptide in a
mannal; and (14) a method for producing the above polypeptide in a
mannal; and (14) a method for producing the above polypeptide or prevent metabolic
conditions associated with a human disease. The polypeptide or the nucleic
acid molecule may be used to diagnose, treat or prevent metabolic
disorders such as diabetes or obesity, infections, cachexia, cancer
and and and and The present sequence encodes a human NOVX protein from dyslipidaemias. The nucleic acids can also be used as hybridisation medicine preventive probes, in chromosome mapping, tissue typing, present invention pharmacogenomics.

Sequence 1740 BP; 389 A; 476 C; 530 G; 345 T; 0 U; 0 Other;

61 ATATGAAAGAAAAGTGGCACCACTGTTCACCTTAGCCTCCATCACCACGACATCATCGG 120 580 180 608 240 668 300 728 360 361 AGGGTCAACGGACTGCGTGTGTTACTCCACCGTGGGCACCAGGACGACGAGAACCTCGGC 420 521 522 ATATGAAAGAAAAGTGGCACCACTGTTCACCTTAGCCTCCATCACCACTGACATCATCG------TTACTGAACATGCTAATCAGGCCAAGGA GACTCTGTATGAGATTAACATAGACAAATACGACGGCATCGTCTGTCGGCGCGCAGATGG GACTCTGTATGAGATTAACATAGACAAATACGACGGCATCGTCTGTGTCGCGGGAGATGG TATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGGCGCCGGGGTCGA TATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGGCGCCCGGGGTCGA CCAGAACCACCCCCGGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGAATCATTCCCGC CCAGAACCACCCCCGGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGAATCATTCCCGC 1 ACCAAAGCATTTACTGGTATTTATCAACCCGTTTGGAGGAAAAGGACAAGGCAAGCGGAT 462 ACCAAAGGATTTACTGGTATTTATCAACCCGTTTGGAGGAAAAGGACAAGGCAAGCGGT TAACAAATTCTATGTTAACTATGTAGAAGTAATTACTGAACATGCTAATCAGGCCAAGGA Gaps 33; Length 1740; Indels .. 92.2%; Score 903; DB 8; I ilarity 96.6%; Pred. No. 1.5e-258; Conservative 0; Mismatches 0; Best Local Similarity Matches 946; Conserv 121 581 609 699 181 301 Query Match 241 셤 g ద g g ઠે g ò ð ઠે à

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                              GCTGCATATCGTTGGTTGGGGACTCGCTGGCCATGGATGTGTCTCTCAGTCCACACAG
                                                                    CACACTCCTTCGCTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCAA
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1. .1251
/*tag= a
/product= "Sphingosine kinase
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New human sphingosine kinase A, B and C polynucleotides and polypeptides useful in e.g. chromosome and gene mapping, and detecting inflammation or disease associated with abnormal levels of sphingosine kinase expression.
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                                                                                                                                                                                                                                                                                                                  GGAGGAGTGGCAAGTCGTCTGTGGGAAGTTTCTGGCCATCAATGCCACAAACATGTCCTG
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71. .1453
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                                                                                                                                                                                                                                                                                                        The present sequence is the coding sequence for human sphingosine kinase of 59HKJ). The Kinase can be used for the diagnosis and treatment of sphingosine related disorders. The kinase can also be potentially used for controlling toxicity of platelet transfusion and as a platelet
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                                                                                                                                                                             Platelet derived polypeptides with sphingosine kinase activity for treatment of sphingosine related disorders.
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BIOLOGY INST
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P-PSDB; ABR56301.
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individuals. Host cells expressing SK can be used in drug screening. Human SK specific antibodies, inhibitors, ligands or their analogues are useful as bioactive agents to treat inflammation or disease including viral, bacterial or fungal infections, allergic responses, mechanical influry associated with trauma, hereditary diseases, lymphoma or carcinoma, and other conditions with activate the genes of kidney, lung, heart, lymphoid or tissues of the nervous system
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New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous system
TGACCTCATCCTCATCCGGAAATGCTCCAGGTTCAATTTTCTGAGATTTCTCATCAGGCA 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human sphingosine kinase-like protein; intracellular signalling; gene; cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma; autoimmune disease; rheumatoid arthritis; Parkinson's disease; ss.
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/note= "see ABB07856"
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Pred. No. 2.5e-258;
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BP.

ADJ96598 standard; DNA; 4429

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This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to buman tyrosine and serine/threonine protein kinases (FrK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polynucleotide sequence is a human kinase DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule encoding a kinase polypeptide, useful for preparing a composition for treating diseases or disorders, e.g., cancer, or neurological, immunological or inflammatory disorders.
                                                                                                                        gene, ds; kinase; human; SNP; single nucleotide polymorphism; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease; cardiovascular disease; brain; neuronal associated disease; metabolic; inflammatory disorder; cytosteatic; neuroprotective; immunomodulator; antiinflammatory; lipid kinse; KIAA1646.
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Sequence 4429 BP; 1020 A; 1115 C; 1213 G; 1081 T; 0 U; 0 Other;

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The present invention describes an isolated PRO nucleic acid (1). Also described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the cisolated PRO polypeptide; (5) a chimeric molecule comprising the composition of matter comprising a polypeptide of (4); an agonist or antibody which specifically binds to a polypeptide of (4); an agonist or antibody which matter comprising a polypeptide of (4); an agonist or antipoptide in combination with a carrier; (8) an article of manufacture comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a mammal; (10) a method for determining the presence of a PRO polypeptide in mammal; (12) a method of flaving the presence of a PRO polypeptide in mammal; (12) a method of identifying a compound that inhibits or minics the activity of or expression of a gene encoding a PRO polypeptide; and (13) a method of stimulating the immune response in a mammal; (22) a method of stimulating the immune response in a mammal. The processive, antipathatic, antidiabedic, antidiabe
                                                                                                                                                                                      human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antisathmatic; antidiabetic; antinflammatory; antipsoriatic; antirheumatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; virucide; gene therapy; gene; ss.
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and treating an immune related disease, e.g. systemic lupus
erythematosus, rheumatoid arthritis, diabetes mellitus or asthma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 1223; 3009pp; English.
                                                                                                                                             Human PRO cDNA sequence SEQ ID NO:1223
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ADP55247 standard; cDNA; 4445 BP
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                                                                                               (first entry)
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Wood WI, Wu TD;
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DB 13;

Score 903;

92.28;

Query Match

PRO nucleotide sequence from the present invention.

immune response.

stimulating an

The present sequence represents

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Huntington's disease; amyotrophic lateral sclerosis; haemophilis; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound; ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke; fibrosis; reperfusion injury; infection; allergic rhinitis; asthma; coagulation disorder; cancer; tumnour; inflammatory disease; septic shock; Crohn's disease; anaphylaxis; proliferation; chemotactic; differentiation; stem cell growth factor; haematopoiseis; chemokinetic; haemostatic; antinflammatory; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptide useful for treating neurodegenerative diseases, myeloid or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.
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                                                                                                                                                                                                                                                                        nervous system disorder; peripheral neuropathy,
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Drmanac RT;
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Wang D,
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Wehrman T, Wang J,
                                  BP.
                                                                                                                                                                                                             Novel human cDNA sequence #146.
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                                  standard; cDNA; 4432
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                                                                                                                                                     (first entry)
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Yang Y,
                                                                                                                                                                                                                                                                        Human; gene; ss;
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                                                                                             ABX70921;
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ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70921 ABX 70
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human polypeptide. The protein encoded by the nucleic acid of the invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic clateral sclerosis); neurodegenerative diseases (e.g. parkinson's disease, amyotrophic clateral sclerosis); neurodegenerative disease (e.g. parkinson's disease, impeloid or lymphoid call disorders (e.g. systemic lupus) crychematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus); wounds, ulcers, burns; bone disorders (e.g. systemic lupus); wounds, ulcers, burns; bone disorders (e.g. osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head trauma); lung or luver fibrosis; preperfusion injury in various tissues; bacterial, viral or fungal infections; allergic conditions such as allergic rhinitis, asthma; cosquiation disorders (e.g. septic shock, Crohn's cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's disease, anaphylaxis). The protein may be used to inhibit the growth, crimiters in the function of infectious agents such as bacteria, fungi, viruses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have completion, immune stimulating or sequence collycensing crecombinant protein for analysis. The present sequence represents a novel crecombinant protein for analysis. The present sequence is an expressing crecombinant protein for analysis. The present sequence is an expressed constitution.

Sequence 4432 BP; 970 A; 1122 C; 1282 G; 1058 T; 0 U; 0 Other;

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                                                                    1 ACCAAAGGATTTACTGGTATTTATCAACCCGTTTGGAGAAAAGGACAAGGCAAGCGGAT
                                  Gaps
                                  33;
 Length 4432;
                                  Indels
Score 901.4; DB 8;
Pred. No. 7.5e-258;
0; Mismatches 1;
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                   96.5%;
                                  945; Conservative
                   Similarity
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 Query Match
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Matches 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569
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                                                                                                                                                                                                                                                                               Human, ceramide kinase, hCERKI, drug screening, gene therapy, neurological disease; inflammation; human immunodeficiency virus; HIV infection; type 2 diabetes; obesity; sepsis, arteriosclerosis; cancer, neuroprotective, antiinflammatory; anti-HIV; antidabetic; anorectic; antibacterial; antiseptic; antiarteriosclerotic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HIV) infection, type 2 diabetes, obesity, sepsis, arteriosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ceramide kinase gene and the enzyme encoded by it for screening substances as drugs for neurological, inflammatory and other disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TAACAAATTCTATGTTAACTATGTAGAAGTAATTACTGAACATGCTAATCAGGGAAGGA
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/product= "Human ceramide kinase hCERK1"
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Pred. No. 6.8e-257;
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124. .1737
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metabolic syndrome X; wasting disorder
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09-OCT-2001, 2001US-0328029P.
09-OCT-2001, 2001US-032804P.
12-OCT-2001, 2001US-032804P.
12-OCT-2001, 2001US-0329414P.
17-OCT-2001, 2001US-0339414P.
17-OCT-2001, 2001US-0339416P.
18-OCT-2001, 2001US-0334105P.
24-OCT-2001, 2001US-0334105P.
24-OCT-2001, 2001US-034105P.
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17-APR-2002, 2001US-034357P.
17-APR-2002, 2002US-0373815P.
19-APR-2002, 2002US-0373815P.
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SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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ZERHUSEN B D.
ANDERSON D W.
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STONE D J.
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SHENOY S G.
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BERGHS C.
DIPIPPO V A.
EISEN A.
GANGOLLI E A.
RIEGER D K.
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MILLET I.
PEYMAN J A.
KEKUDA R.
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CATTERTON E.
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16-MAY-2002;
16-MAY-2002;
16-MAY-2002;
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29-MAY-2002;
                   Homo sapiens
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                                                                                                                                                                                                                                                                                                           The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abbrrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides. For example, NOVX polypeptides and consumer to rectify mutations. Conversely, antisense NA molecules by production or to rectify mutations. Conversely, antisense NA molecules can be daministered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX colymetoleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of the production of antibodies and in assays to identify modulators cancivative therapy. NOVX polypeptides may also be used as anti-NOVX polypeptides and antagonists and antagonists and propertide expression and activity of NOVX polypeptides antibodies, agonists and antagonist may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polynucleotide expression and activity of NOVX polypeptides and polynucleotide may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, immune disorders, chaematopoietic disorders, and the various dyslipidaemias, metabolic disorders, may, also he wasting disorders and the obsity, the metabolic syndrome X and conternant and the various dyslipidaemias, metabolic expenses and various cancers.
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                               Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
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                                                                                                                                                                                                                         Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCAAAGCATTTACTGGTATTTATCAACCCGTTTGGAGGAAAAGGACAAGGCAAGCGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATGAAAGAAAAGTGGCACCACTGTTCACCTTAGCCTCCATCACCACTGACATCATCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAACAAATTCTATGTTAACTATGTAGAAGTAATTACTGAACATGCTAATCAGGCCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGCGCCGGGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTATGTTCAGCGAGGTGCTGCACGGTCTGGATTGGGAGGACGCAGAGGAGGAGCGCCGGGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  may also be used as antibacterial agents. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 1740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 1740 BP; 388 A; 477 C; 530 G; 345 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

89.7%; Score 878.4; DB 12.
Best Local Similarity 96.3%; Pred. No. 3.4e-251;
Matches 944; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represents DNA encoding a human NOVX protein.
                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 39; 395pp; English.
(SPAD/) SPADERNA S K.
                                                                                                                                                                    2004-213931/20.
                                                                                                                                                                                   P-PSDB; ADN62845.
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CGCTGCATATCGTTGGGGACTCGCTGGCCATGGATGTCTCCTCAGTCCACCACAACA
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                                                                                      CAGGGTCAACGGACTGCGTGTGTTACTCCACCGTGGGCACCAGCGACGACGAAAACCTCGG
                                                                                                                                                                                                                                      GCACACTCCTTCGCTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCATCA
                                                                                                                                                                                                                                                                                                                    540 AGGACAGTGAGAAAGGATGGTTGGCTTTGCCAGATACGACTTTTCAGGTTTAAAGA
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                                                                 CAGGGTCAACGGACTGCGTGTTACTCCACCGTGGGCACCAGCGACGCAGAAACCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #13532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1388 ACACCAACCAGCAGGACCAG 1407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                               GTCTTGCCAGATACGACTTTTCAGGTATAAAGACCTTCCTCCTCCCACCACCACTGCTATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCGGCCAGGATGCTTTGTTTGCAGGCAAAGCAAGCAGCAGCAGGAGGAGGAGGAGGAGAAAGA
                                         1376 IGGCCATGGATGTGTCCTCAGTCCACCACAACAGCACACTCCTTCGCTACTCCGGTGTCCC
                                                                                                                                                 1436 TGCTGGGCTACGGCTTCTACGGGACATCATCAAGGACAGTGAGAAACGGTGGTTGG
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447 TGGCCATGGATGTGTCCTCAGCACACACACACTCCTTCGCTACTCCGTGTCCC
                                                                                                                        TGCTGGGCTACGGCTTCTACGGGGACATCATCAAGGACAGTGAGAAAAAACGGTGGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGITCAATTITCTGAGATTTCTCATCAGGCACACCAACCAGGACCAG 1908
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AJ,
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Wang J, Ghosh M,
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Chen R, Zhao QA,
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                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed of the sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed cativity of (II) auseful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in the protein protein and polymers of their traits to assess biodiversity and polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGGAGGACGCAGAGGAGCGCCGGGGTCGACCAGAACCACCCCCGGGCTGTGGTCCC
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                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 183;
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                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 13532; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antiniflammatory, heuropytotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoletic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic DNA of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the MIPO web-site.
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                                                                                                                                                                                                             GGGTCAACGGACTGCGTGTTACTCCACCGTGGGCACCCAGCGACGAGAAACCTCGGCG
                                                                                                                                                                                                                                                        CTGCATATCGTTGGGGACTCGCTGGCCATGGATGTGCTCCTCAGTCCACCACAACAGC
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                                                                                                                                                                                                                                                                                                                                              GACAGTGAGAAAGGATGGTTGGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGACC
                                                                                                                                              Sequence 4702 BP; 970 A; 1226 C; 1364 G; 1118 T; 0 U; 24 Other;
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                                                                                                                                                                  Length 4702;
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                                                                                                                                                                             Pred. No. 3.4e-173;
                                                                                                                                                                   63.1%; Score 618; DB 13;
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Claim 1; SEQ ID NO 607; 718pp; English
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Matches 618; Conservative
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antipositatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; antiviral; antifungal; antithyroid; antidiabetic; hypotensive; sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, cardiovascular disease, disbabetes mellitus, hypertension, hypothyroidism, cholesterol ester strange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 CAGGGTCAACGGACTGCGTGTTACTCCACCGTGGGCACCAGCGACGCAGCAACCTCGG 190
                                 vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiafammatory; antiviral; antibacterial; antifungal; antitheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 CAGGGTCAACGGACTGCGTGTGTTTACTCCACCGTGGGCCACCAGCGACGCAGAAACCTCGG
open reading frame; ORFX; detection; cytostatic; hepatotropic;
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02-APR-1999; 99US-0127636P.

05-APR-1999; 99US-0127728P.

30-MAR-2000; 2000US-00540763.
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Human ORFX ORF1586 polynucleotide sequence SEQ ID NO:3171.

(first entry)

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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed control in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving of (II). (II) and site shidhing partners are useful in medical imaging of supplement. (II) and site shidhing partners are useful in medical imaging of supplement. (II) and site shidhing partners are useful for treating disorders of sites expressing (II). (I) and (III) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in the protein expression or biological activity. The diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and anino acid sequences. Assetlysty-AASS4956 trapresent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the printed specification, but was obtained in the printed specification, but was obtained in the printed specification, but was obtained in the printed specification, but was obtained in the printed specification, but was obtained in the printed specification of mutations.
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                     Claim 1; SEQ ID NO 13535; 103pp; English.
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1 901.4 92.1 4432 4 US-09-774-528-148 Sequence 148, App

2 78.6 8.0 1084 4 US-09-270-767-115155 Sequence 15155, A

4 69.8 7.1 498 4 US-09-270-767-114306 Sequence 15155, A

4 4 1050 4 US-09-220-767-114306 Sequence 175, App

4 4.4 1050 4 US-09-252-991A-11269 Sequence 1769, Ap

4 4.4 1050 4 US-09-252-991A-11269 Sequence 1656, Ap

4 4.2 4.4 1050 4 US-09-252-991A-1269 Sequence 1656, Ap

4 4.2 4.4 1050 4 US-09-252-991A-1269 Sequence 1656, Ap

4 4.2 4.3 1014 4 US-09-902-540-9500 Sequence 1656, Ap

4 4.1 2187 4 US-09-902-540-1080 Sequence 1656, Ap

11 40.4 4.1 2380 4 US-09-902-540-1080 Sequence 117, Appl

12 40.4 4.1 2380 4 US-09-902-540-1080 Sequence 33, Appl

13 39.4 4.0 2698 4 US-09-91A-366 Sequence 31, Appl

14 39.4 4.0 2698 4 US-09-91A-366 Sequence 360, Ap

18 38.4 3.9 327 4 US-09-91A-366 Sequence 360, Ap

18 38.4 3.9 3147 4 US-09-902-540-3150 Sequence 360, Ap

19 18 38.4 3.9 3187 4 US-09-902-540-1169 Sequence 1169, Ap

22 37.8 3.9 4411529 3 US-09-103-840A-1 Sequence 2, Appl

23 37.8 3.9 4411529 3 US-09-103-840A-1 Sequence 62772, A

24 36.8 3.8 103792 4 US-09-949-016-62773 Sequence 22772, A

25 36.8 3.8 103792 4 US-09-949-016-13553, A

27 36.8 3.8 103792 4 US-09-949-016-13553, A

28 36.8 3.8 103792 4 US-09-949-016-13553, A

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20 36.8 3.8 103792 4 US-09-949-016-13553, A

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| Sequence 53419, A Sequence 11782, A Sequence 13280, A Sequence 1941, App Sequence 1944, App Sequence 202, App Sequence 11944, App Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Length 4432; Indels 33; Gaps 1; AAGGACAAGGCAAGCGGAT 60      |
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| 4 US-09-949-016-53419<br>4 US-09-949-016-11782<br>4 US-09-949-016-13280<br>4 US-09-949-016-13280<br>4 US-09-949-016-3948<br>4 US-09-949-016-3948<br>4 US-09-949-016-11944<br>4 US-09-949-016-11944<br>4 US-09-949-016-15690<br>4 US-09-949-016-15690<br>5 US-09-949-016-15690<br>6 US-09-949-016-15690<br>7 US-09-949-016-15690<br>8 US-09-949-016-15690<br>9 US-09-9173-82-7<br>9 US-09-012-540-7500<br>1 US-09-081-351-1<br>1 US-09-081-351-1<br>1 US-09-081-351-1<br>1 US-09-081-517 | ALIGNMENTS  IS/09774528  e T. 743519e1 Nucleic Acids and eptides : US/09/774,528 -01-30 Sion 2.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Score 901.4; DB 4;   Pred: No. 1.4e-266;   0;   Mismatches  |
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Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT FILING DATE: 1995-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14306

LENGTH: 2064
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                                                                         Score 78.6; DB 4; Length 1
Pred. No. 1.5e-13;
0; Mismatches 244; Indels
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US-09-270-767-14306
; ORGANISM: Drosophila melanogaster
US-09-270-767-15155
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Best Local Similarity 48.9
Matches 237; Conservative
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Best Local Similarity
Matches 238; Conserv
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Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15155
LENGTH: 1084
TYPE: DNA
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Query Match
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Matches 113;
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TTGGGAGGACGCAGAGCGCCGGGGTCGACCAGAACCACCCCCGGGGCTGTGCTGGTCC
                           842 TATTCCGTCAAATGCGAGAGTTGGGACTGGACGAGGGCGGCCACCATACATTCCAAGAC
                                                        330 CCAGTAGCCTCCGGATTGGAATCATTCCCGCAGGGTCAACGGACTGCGTGTGTTACTCCA
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Pred. No. 4.8e-11;
0; Mismatches 7;
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APPLICANT: Sheppard, Scott R.
TILLE OF INVENTION MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT PILING DATE: 2001-06-28
PRIOR PILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 329
SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 30448
; Sequence 30448
; Patent No. 6703491
; GENERAL INFORMATION:
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Best Local Similarity 91.4%;
Matches 74; Conservative
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; LOCATION: (1)
US-09-893-737-59
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LENGTH: 498
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Sequence 1269, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ABRUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: A ABRUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 199-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30448
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                                                                                                                                                                                                                                                                                                                                                                                       Length 901;
                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 4; Length 901
Pred. No. 2.5e-06;
0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                        ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.6%;
Best Local Similarity 57.1%;
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Pseudo
US-09-252-991A-1269
                                                                                                                                                                                                                                                                                                                            US-09-270-767-30448
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US-09-252-991A-1269
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RESULT 7

APPLICANT: Homburger et al

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215 GGCATCGTCTGTGTCGGCGGAGATGCTATGTTCAGCGAGGTGCTGCACGGTCTGATTGGG 274
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                                                                                                    155 CWRSYWYCCYYYXRARRWWWKGGSCMYTYRWMRRMCCCCCMRRRRRMCMWKGSYTY 214
                                                                                                                                                                                                                                                    CAATGCCACAAACATGTCCTGTGCTTGTCGCCGGAGCCCCCAGGGGCCTCTCCCCGGCTGC 879
                                                                                                                                                                                                                                                                                                                   CYKSSSMMCMARRWKRARGKKRAMCCYTKGGGRMMRKYCCMRKKGRRACCTGTTCACCTGC 274
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFRENCE: 38-10(15849)8
CURRENT APPLICATION NUMBER: 60/9902,540
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9500
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APPLICANT: Goldman, Barry S.

APPLICANT: Glater, Steven C.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

APPLICANTON: WASCOCCUB Xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (15849) B CURRENT APPLICATION NUMBER: US/09/902,540
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Pred. No. 0.064;
0; Mismatches 157; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             880 CCACTTGGGAGACGGGTCTTC 900
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Matches 135; Conservative
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US-09-902-540-1080/c
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                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE DF INVENTION: AERGICANGE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1179
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Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INFORTION: BSTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16656
LENGTH: 430
                               Sequence 1179, Application US/09252991A
Patent No. 6551795
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Best Local Similarity 49.3%;
Matches 113; Conservative
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US-09-621-976-16656
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Best Local Similarity
Matches 50; Conserv
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US-09-252-991A-1179
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US-09-621-976-16656
US-09-252-991A-1179
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Sequence 13, Application US/09817676A

Patent No. 6800470

GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
APPLICANT: Kohama, Takafumi
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT PILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/194,318
PRIOR PILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFWARE: Patentin Ver. 2.0
SEQ ID NOS: 15
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                                                                                          AGCCTCCGGATTGGAATCATTCCCGCAGGGTCAACGGACTGCGTGTGTTACTCCACCGTG
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DATABASE ACCESSION NUMBER: AF245447
DATABASE ENTRY DATE: 2000-06-27
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: CDS
LCCATION: (7) . (1860)
PUBLICATION:
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VOLUME: 275
ISSUE: 26
PAGES: 19513-19520
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Patent No. 6610534
GENERAL INFORMATION:
APPLICANT. No. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REPERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
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Pred. No. 0.34;
0; Mismatches 157; Indels 0;
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Pred. No. 0.13;
0; Mismatches 266; Indels 9;
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1080
LENGTH: 14101
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Best Local Similarity 44.3%;
Matches 219; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.2%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Myxococcus xanthus
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ORGANISM: Homo sapiens
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US-09-970-516-3
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LOCATION: (1)
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PRIOR FILING DATE: 2000-04-03
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                                                                                                                                                                                                                                                                                                                                            515 TACGGCTTCTACGGGGACATCATCAAGGACAGTGAGAAGAAAACGGTGGTTGGGTCTTGCC 574
                                                                                                                                                                                                                                                                                                                                                                                       907 TGGGGCTTCGTGTCAGATGTGGATATCCAGAGCGAGCGCTTCAGGGCCTTGGGCAGTGCC 966
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                                                                                335 AGCCTCCGGATTGGAATCATTCCCGCAGGTCAACGGACTGCGTGTGTTACTCCACCGTG 394
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Patent No. 6800470.
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Kohama, Takafumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/194,318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 GATCAGTGGAAGGTTGTGCGGGGCAATTTCTTTATGATCTGCGGCGCGAACATAACCTGC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Notleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Notleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 31476
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                                        676 CCCCTGACTGGGAGGAAGCTGTGAAGATG-
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Best Local Similarity
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US-09-270-767-31476/c
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US-09-614-221A-399

Sequence 399, Application US/09614221A

Pattent No. 6723B303

GENERAL INFORMATION:
APPLICANT: Ya. Jachynic
APPLICANT: Wi. Jachynic
APPLICANT: Wishore, Ganesh M.
TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
FILE REFERENCE: 16516.075

CURRENT APPLICATION NUMBER: US/09/614,221A

CURRENT FILING DATE: 1999-07-12

PRIOR APPLICATION NUMBER: US 60/142,981

NUMBER OF SEQ ID NOS: 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.0%; Score 39.4; DB 4; Length 2698;
55.5%; Pred. No. 0.32;
tive 0; Mismatches 61; Indels 0
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4.0%; Score 38.8; DB 4; Length 1875;
Best Local Similarity 54.1%; Pred. No. 0.39;
Matches 79; Conservative 0; Mismatches 67; Indels 0
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                                                                                                                                                                                        LOCATION: (387)..(2237)
PUBLICATION INFORMATION:
TITLE: Molecular cloning and functional characterization
TITLE: novel mammalian sphingosine kinase type 2 isoform
VOLUME: 275
                                                                                                                                                                                                                                                                                                                                                                                                        DATE: 2000-06-30
DATABASE ACCESSION NUMBER: AF245448
DATABASE ENTRY DATE: 2000-06-27
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NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 2698
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                                                                                                    TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                        ISSUE: 26
PAGES: 19513-19520
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5, 2005, 12:52:06 ; Search time 711.691 Seconds (without alignments) 9008.663 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NRW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/US08_BNB_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_BNB_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_BNB_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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CURRENT APPLICATION NUMBER: US/10/631,958
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FRIOR PILING DATE: 2003-08-01
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-06
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NUMBER OF SEQ ID NOS: 16
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; Sequence 1, Application US/10631958 ; Publication No. US20040192580A1 ; GENERAL INFORMATION: ; APPLICANT: Kossida, Sophia ; TITLE OF INVENTION: Regulation of human Sphingosine

RESULT 2 US-10-631-958-1

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Sequence 5. Application US/10876281
| Publication No. US20050123942A1
| GENERAL INFORMATION:
| APPLICANT: RASTELLY, LUCA
| TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
| TITLE OF INVENTION: SAME
| FILE OF INVENTION: SAME
| FILE REFERENCE: 10716-08
| CURRENT FILING DATE: 2004-06-24
| PRIOR APPLICATION NUMBER: US/10/876,281
| PRIOR APPLICATION NUMBER: US/09/784,810
| PRIOR FILING DATE: 2000-02-14
| PRIOR FILING DATE: 2000-02-14
| PRIOR FILING DATE: 2000-02-14
| PRIOR FILING DATE: 2000-02-14
| PRIOR FILING DATE: 2000-03-22
| NUMBER OF SEQ ID NOS: 29
| SEQ ID NO S: 29
| SEQ ID NO S: 29
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Sequence 5, Application US/09784810A

Patent No. US20020082203A1

GENERAL INFORMATION:
APPLICANT: RASTELL: LUCA

TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME

FILE REFERENCE: 1071-6-08

CURRENT PELING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/182,360

PRIOR APPLICATION NUMBER: 60/182,360

PRIOR FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 29

SEQ ID NO S: 29

SEQ ID NO S: 29

LENGTH: 1840
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100.0%; Pred. No. 1.4e-308;
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Best Local Similarity 100.
Matches 979; Conservative
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CORGANISM: Homo sapiens
US-09-784-810A-5
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                                                                                                                                                                                                             Length 1614;
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                                                                                                                                                                                                           Score 903; DB 10;
Pred. No. 9.3e-284;
0; Mismatches 0;
TITLE OF INVENTION: Kinase-Like Protein
FILE REPERRNCE: 004974,00594
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR PILING DATE: 2000-10-06
PRIOR PLILING DATE: 2001-10-06
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 9: SEQ ID NOS: 16
SEQ ID NO 9: SEQ ID NO 9: 16
                                                                                                                                                                                                             Query Match
Best Local Similarity 96.6%;
Matches 946; Conservative 0
                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-969-896-9
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GGAGGAGTGGCAAGTCGTCGGGGAAGTTTCTGGCCATCAATGCCACAAACATGTCCTG

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; Sequence 9, Application US/0996986; Publication No. US20030125533A1; GENERAL INFORMATION: APPLICANT: Kossida, Sophia; TITLE OF INVENTION: Regulation of human Sphingosine

0-968-696-60-SD

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1254 TGACCTCATCCTCATCCGGAAATGCTCCAGGTTCAATTTTCTGAGATTTCTCATCAGGCA 1313
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                                                                                                774 GCTGCATATCGTTGTTGTTGGGGACTCGCTGGCCATGGATGTCTCCTCAGTCCACACAACAG
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            GCTGCATATCGTTGTTGGGGACTCGCTGGCATGGATGTCTCTCAGTCCACCACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 39, Application US/10262511; Publication No. US20040038223A1; GENERAL INFORMATION:
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark E.
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Zerhusen, Bryan D.
Anderson, David W.
Zhong, Mei
Catterton, Elina
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US-10-631-958-9

Sequence 9, Application US/10631958

Publication No. US2000192580A1

GENERAL INFORMATION:

APPLICANT: Kossida, Sophia

TITLE OF INVENTION: Kinase-Like Protein

FILE REFERENCE: 004974.00594

CURRENT FILING DATE: 2001-08-01

PRIOR PILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: US/09/969,896

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2001-06

PRIOR FILING DATE: 2001-06

SOFTWARE OF FILING DATE: 2001-06

SOFTWARE: SEQ ID NOS: 16

SEQ ID NOS: 16

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Best Local Similarity 96.6%; Pred. No. 9.3e-284;
Matches 946; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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                                                                         909 CACACTCCTTCGCTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCATCAA
                                                                                                                                          541 GGACAGTGAGAAGAAACGGTGGTTGGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGAC
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TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Riase-Like Protein
FILE REFERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR APPLICATION NUMBER: US 60/314,113
PRIOR FILING DATE: 2010-10-6
PRIOR FILING DATE: 2010-10-6
SPRIOR FILING DATE: 2010-10-6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 16
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Pred. No. 1.6e-283;
0; Mismatches 0;
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Best Local Similarity 96.6%;
Matches 946; Conservative 0
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US-09-969-896-16
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US-09-969-896-16
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APPLICANT: Berghs, Constance
FILTE OF INVENTION: NOVEL PROYELINS AND NUCLEIC ACIDS ENCODING SAME
FILTE OF INVENTION: NOVEL PROYELING
CURRENT FILING DATE: 2003-05-28
FRIOR PELICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-05-17
PRIOR PLING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR PLING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/373,466
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2001-10-05
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; LOCATION: (76)..(1686)
US-10-262-511-39
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PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-08
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FRAESEQ for Windows Version 4.0
LENGTH: 4413
                                                                                    ; ORGANISM: Homo sapiens
US-10-631-958-16
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Publication No. US20040192580A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Kinase-Like Protein
FILE REFERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/10/631,958
CURRENT PILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US/09/969,896
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US-10-631-958-16
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                                                                 121 TAACAAATTCTATGTTAACTATGTAGAAGTAATTACTGAACATGCTAATCAGGCCAAGGA
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                           33;
  Length 4413;
                            Indels
Query Match 92.2%; Score 903; DB 19;
Best Local Similarity 96.6%; Pred. No. 1.6e-283;
Matches 946; Conservative 0; Mismatches 0;
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| Db   925 CACACTCCTTCGGTACAACAACCTCGTGGGCTACGGCTTCTACGGGACATCAACAACACACAC | PERSURA 11   US-10-120-988-148   Sequence 148, Application US/10120988   Sequence 148, Application No. US2003219745A1   US-10-120-988-148   Sequence 148, Application No. US2003219745A1   Sequence 148, Application No. US2003219745A1   Sequence 148, Application No. US2003019745A1   Sequence 148, Application No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US2003019745A1   No. US200301974 |
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| TGCTTGTCGCCGGGGCCTCTCCCCGGTGCTGCCCATTGGGAGCGGTTTC 900                    | Operaty Match         92.2%; Score 903; DB 19; Length 4429;           Best Local Similarity         96.6%; Pred. No. 1.6e-283;         Indels 33; Gaps 1;           Matches 946; Conservative 0; Mismatches 0; Indels 33; Gaps 1;         Indels 33; Gaps 1;           Oy 1         ACCAAAGCATTACTGGTATTATACAACCGTTTGGAGGAAAGGACAAGGCAAGCGGAT 537           Ob 5         ATATGAAAAGAAAAGTGGCACACTTGACCTTAGCCTCAACACACAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

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S41 GGACAGTGAGAAACGGTGGTTGGCTTTGCCAGATACGACTTTTCAGGTTTAAAGAC 600

1017 GGACAGTGAGAAAAAGGTGGTTGGTTTGCCAGATACGACTTTTCAGGTTTAAAGAC 1076
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                                                                                                                                                                                                                                   Score 898.2; DB 16; Length 4463;
Pred. No. 5.9e-282;
0; Mismatches 3; Indels 33;
FILE REFERENCE: 02658CIP/HG
CURRENT APPLICATION NUMBER: US/10/315,597A
CURRENT FILING DATE: 2002-12-10
FRIOR APPLICATION NUMBER: JP 2000-178039
FRIOR FILING DATE: 2000-66-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 4463
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 96.3%;
Matches 943; Conservative (
                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                NAME/KEY: unsure;
LOCATION: 3371;
CTHER INFORMATION:
US-10-315-597A-1
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1797 TATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGCGCCGGGGTCGA
                                                                                                                                                                                                                       1857 CCAGAACCACCCCCGGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGAATCATTCCCGC
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Publication No. US20030162206A1
GENERAL INFORMATION:
APPLICANT: Sugiura, Masako
APPLICANT: Kono, Keita
APPLICANT: Kohama, Takafumi
TITLE OF INVENTION: Ceramide Kinase and DNA Encoding
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US-10-315-597A-1
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569 120 628 180 959 240 716 300 776 360 836 420 896

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1136

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480

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APPLICANT: Kossida, Sophia
TITLE OF INVENTION: Regulation of human Sphingosine
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99.8%; Pred. No. 1.2e-140;
tive 0; Mismatches 1;
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US-09-969-896-5
; Sequence 5, Application US/0966986
; Publication No. US20030125533A1
; GENERAL INFORMATION:
; APPLICANT: KOSBAGA, Sophia
; TITLE OF INVENTION: Regulation of h
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Matches 465; Conservative
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                                                                                                                                                                                                                                                                                                                               APPLICANT: Kossida, Sophia
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Rinase-Like Protein
FILE REFERENCE: 004974,00594
CURRENT APPLICATION NUMBER: US/09/969,896
CURRENT FILING DATE: 2001-10-04
PRIOR RILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US 60/314,113
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/314,113
PRIOR PILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 464.4; DB 10
Pred. No. 1.2e-140;
0; Mismatches 1;
                                                                                                                                                                                                   1437 CACCAACCAGCAGACCAG 1455
                                                                                                                                                                                                                                                                                        ; Sequence 4, Application US/09969896
; Publication No. US20030125533A1
; GENERAL INFORMATION:
                                                                                                                                                                                  961 CACCAACCAGCAGGACCAG 979
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Best Local Similarity 99.8%;
Matches 465; Conservative 0
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                                                                                                                                                                                                                                                            RESULT 13
US-09-969-896-4
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US-09-969-896-4
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Sequence 4, Application US/10631958
; Bublication No. US20040192580A1
; GENERAL INFORMATION:
APPLICANT: KOGSIGA SOPHIA
; TITLE OF INVENTION: Regulation of human Sphingosine
; TITLE OF INVENTION: Regulation of human Sphingosine
; TITLE REFERENCE: 004974.00594
; CURRENT APPLICATION NUMBER: US/10/631,958
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/238,005
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2001-10-06
; PRIOR FILING DATE: 2001-10-06
; PRIOR FILING DATE: 2001-06-05
; RIUNG FILING DATE: 2001-06-05
; RIUNG FILING DATE: 2001-06-05
; SOFTWARE: FastSEQ for Windows Version 4.0
; SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Kinase-Like Protein
CURRENT APPLICATION UNDER: US/09/969, 896
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-06
SPIOR FILING DATE: 2001-06
PRIOR INFORMATION: n = A,T,C or G
US-09-969-896-5
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Search completed: September 5, 2005, 20:00:08 Job time: 726.691 secs

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Query Match
Best Local Similarity
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COMMENT
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BM479389
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CK000755 AGENCOURT
AK042077 Mus muscu
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CD655311 AGENCOURT
BQ063738 AGENCOURT
BQ063738 AGENCOURT
BP244560 BP224560
CE346749 UI-M-FIO-
BP310011 BP310011
CN296311 170005321
BP309990 BP309990
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CF13875 UI-HF-BNO
CR00525 AGENCOURT
CN296312 170005321
BU430459 UI-HF-BNO
CR00525 AGENCOURT
CN296312 170005321
BU430459 UI-HF-BNO
CR063292 DKFZQ781L
CR135528 UI-HF-BNO
CR6611947 AMGNNUC:N
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10410.363 Million cell updates/sec
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                  34239544 seqs, 19032134700 residues
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                                                                                                          5, 2005, 18:18:34
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Listing first 45 summaries
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BQ057191
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9b_est4::*
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415
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367.8
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Maximum DB
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EST:
Homo sapiens (human)

Momo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

L (bases 1 to 1063)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rômail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI2140 row: c column: 18

High quality sequence stop: 665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGENCOURT 6418742 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502281

5., mRNA Sequence.
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/db_xref="taxon:9606"
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/tisque type="retinoblastoma"
/lab_nof="DH10B (phage-resistant)"
/clone lib="NH1 MGC 67"
/note="Organ: eye; Vector: pGMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Rechnologies."
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56059637H
56059545H
604162346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                   AJ739034
AA355581
BM484519
BM484519
CK36437
CK36437
CK36437
CK3579952
CK531541
CD63156
BU29080
CD63156
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Matches 805, Conservative
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/note="organ: lymph; Vector: priming, Directionally cloned
into EcoR1/XhoI sites using the following 5; adaptor:
into EcoR1/XhoI sites using the following 5; adaptor:
into EcoR1/XhoI sites using the following 5; adaptor:
into EcoR1, Library constructed by Ling Hong in the laboratory
of Garald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.N.A.G.E. Consortium/LLNL at:
http://image.llnl.gov a column: 13
High quality sequence stop: 601.
Location/Qualifiers
I. .1059
//organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.2%; Score 726.4; DB 5; Length 1059; llarity 95.1%; Pred. No. 2e-197; Conservative 0; Mismatches 6; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library."
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Best Local Similarity
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AGENCOURT_6771237 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5803668
5', mRNA sequence.
BQ054406
                                                        272
                                                                        ACGCATCGTCTGTGTCGGCGGAGTGGTATGTTCAGCGAGGTGCTGCACGTCTGATTG 163
                                                                                                                          GGAGGACGCAGAGGAGCGCCGGGGTCGACCAGAACCACCCCCGGGCTGTGCTGGTCCCCA 332
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                                                                                                                                                          GGAGGACGCAGAGGGCGCCGGGGTCGACCAGAACCACCCCCGGGCTGTGCTGGTCCCCA 223
                                                                                                                                                                                                                                GTAGCCTCCGGATTGGAATCATTCCCGCAGGGTCAACGGACTGCGTGTGTTACTCCACCG 283
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Homo sapiens
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Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethead, MD 20892
Email: Gapbba-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM1073 row: c column: 20
High quality sequence stop: 656.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                  CCCACCACTGCTATGAACGGACAGTGTCCTTCCTTCCTGCACAACACACGGTGGGATCTC
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812 720 BQ057191 1047 bp mRNA linear EST 29-MAR-2002 AGENCOURT 6769595 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5812382 5., mRNA sequence. BQ057191 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.

1 (Dases 1 to 1047)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

ORIGIN

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Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630056D11 product:DA59H18.2 (NOVEL PROTEIN SIMILAR TO HUMAN, MOUSE, YEAST, WORM AND PLANT (PREDICTED) PROTEINS) AK042077
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                  -CCAAGGGATAGGAAGCCCTG-CCGGGCAGGATGCTTTG-
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/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone_lib="NNH-MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/KhoI sites using the following 5 adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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                                                                              CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2062 row: I column: 15
High quality sequence stop: 535.
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                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'clone="IMAGE:5812382"
                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
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HNTLLRYSVSLLGYGFYGDLIKDSEKKRWMGLVRYDFSGLKTFLSHQYYEGTLSFLPA
QHTVGSPRDNKPCRAGCFVCRQSKQQLEBEBKKALYGLENAEBNEEWGTCGKFLAIN
AUMSCACPRSPGGLSPFAHLGDGSSDLILIRKCSRFNFLRFLIRHTNGEDGPDFTFV
EVYRVKFHFTSKHPUBEDNDSKEQEKÇKFGKICKDRPSCTCSASRSSWNCDGEVMHS
PAIEVRVHCQLVRLFARGIEEES"
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ASITTEIIITEHANQAKETLYEINTDSYDGIVCVGGDGMFSEVLHGVIGRTQGSAGID
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Xanagawa 230-0045, Japan (E-mail:genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="thymus"
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/dev_stage="3 days neonate"
/sc. 1680
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/note="unnamed protein product; DA59H18.2 (NOVEL PROTEIN
SIMILAR TO HUMAN, MOUSE, YEAST, WORM AND PLANT (PREDICTED)
PROTEINS) (FRAGMENT) homolog [Homo sapiens] (SPTR|Q9UGE5,
evidence: FASTY, 86.5%ID, 100%length, match=945)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
                               Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Solence Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                        RIKEN Genome Exploration Research
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URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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                        Consortium and the
                                                                                   of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1824)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ATATGAAAGAAAAGTGGCACCACTGTTCACCTTAGCCTCCATCACCACTGACATCATCGG
                                                                                                531 CTATGAAAAACAGGGGCGCTCTGTTACCTTGGCTTCCATCACTACGGAGATCATC--
                                                                                                                                                                               738 CCCCAATCACCCCCGAGCCGTGCTGGTGCCCAGTACCCTCAGGATCGGCATCATACCCGC
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                                                                                                                                                       121 TAACAAATTCTATGTTAACTATGTAGAAGTAATTACTGAACATGCTAATCAGGCCAAGGA
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  ACCAAAGCATTTACTGGTATTTATCAACCCGTTTGGAGGAAAAGGACAAGGCAAGCGGAT
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ASITYEI ITTEHANQAKETLYEINTDSYDGIVCVGGDGMFSEYLHGYIGKTQQSAGID
PMHPRAVLVPSTLRIGIIPAGSTDCVCYSTVGTNDAETSALHIIGDSLAIDVSSVHY
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                                   Division of Experimental Animal Research in Riken contributed
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                                                                                               please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNss

L Mature 420, 563-573 (2002)

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S Adachi, J. Alzawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayateu, N., Hiramcto, K., Hiraoka, T., Hirozane, T., Hovia, F., Imchara, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Nathara, K., Nomura, R., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shiba
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                               Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched library, clone:0330016008 product:b559148.2 (NOVEL PROTEIN SIMILAR TO HUMAN, MOUSE, YEAST, WORM AND PLANT (PREDICTED) PROTEINS) (FRAGMENT) homolog [Homo sapiens], full insert sequence.
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Encyclopedia Project of Genome Exploration Research Group in Riken
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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   4248 bp
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics MD 20892
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
CDNA Library Preparation: Yulan Piao and Minoru Ko
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencur Bioscience Corporation
Clone distribution: MGC c lone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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/ Under This is a long-transcript enriched cDNA library (Genome Res. 11: 153-1558 (2001). [PMID: 1154199] from WAO1 cell line. Undifferentiated human ES cell line WAO1/HI was obtained from WiCell Research Institute, Inc., Madison, Wi, cultured according to their instructions, on WEF feeders. They formed according to their instructions, on WEF feeders. They formed colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. FLF3, SSEA-1, TUBB3, NES, GFAP, and EOWES. When confluent (18-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently Scraped off with 5 ml pipette. RNA was purified with TRIZOl Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:11544199]) Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.4g of total RMA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The CDNAs were ligated to Lone-linker LL-Sall4, purified by phenol/chloroform extraction, and separated from free linkers by centricon-100 column. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The CDNAs were digested with Sall and NotI enzymes and cloned into Sall/NotI site of polym-SPORTE plasmid vector. The average insert size is about 3.6kb."
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/lab host="THIOB (T1 phage-resistant)"
/clone lib="NIA Human H1 Embryonic Stem Cell cDNA Library
(Long)"
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BP224560 Sugano cDNA library, lymphocyte Daudi Homo sapiens cDNA clone DAT01067, mRNA sequence.

BP224560.1 GI:52097465
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1. (bases 1 to S1)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
                                                                                                                                                                                                                                                                             447 AGGGTCAACGGACTGCGTGTTACTCCACCGTGGCACCAGCGACGCAAACCTCGGC
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                                                                                                                                                                                                                  CCAGAACCACCCCGGGCTGTGCTGGTCCCCCAGTAGCCTCCGGATTGGAATCATTCCCGC
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/clone_lib="Sugano cDNA library, lymphocyte Daudi"
/note="Burkitt's lymphoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                660 -TGGGATCTCCAAGGGA--TAGGAAGCCCTGCCGGGCAGGATGCTTTGTTTG 708
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site_2:
BCORI; CDNA made by oligo-dT priming. Directionally cloned
into BcoRI/KhoI sites using the following 5' adaptor:
GCGACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                     BQ063738 1078 bp mRNA linear EST 02-APR-2002
AGENCOURT_6873251 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5925382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATATGAAAGAAAGTGGCACCACTGTTCACCTTAGCCTCCATCACCACTGACATCATCGG 120
                                                          491 CCTCTCCCGGCTGCCCACTTGGGAGACGGGTCTTCTGACCTCATCCTCATCCGGAAATG 550
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GAAGITICIGGCCAICAAIGCCACAAACAIGICCIGIGCIIGICGCCGGAGCCCCAGGGG 490
                                        CCTCTCCCCCGGCTGCCCCACTTGGGAGACGGGTCTTCTGACCTCATCCTCATCCGGAAATG 924
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NIH-WGC http://mgc.noi.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapba-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2096 row: p column: 23
High quality sequence stop: 640.
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'db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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                                                                                                                                                                                                                                                                                               mRNA sequence.
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AUTHORS
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| FEATURES  Location/Qualifiers   758                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Query Match 54.9%; Score 537.4; DB 6; Length 758; Best Local Similarity 82.7%; Pred. No. 4.7e-143; Matches 613; Conservative 0; Mismatches 128; Indels 0; Gaps 0; | QY         239         GGTATCTTCACCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGCCCGGGGTC         298                                                   | QY         299         GACCAGAACCACCCCGGGGCTGTGCTGGTCCCCAGTAGCCTCCGGATTGGAATCATTCCC         358 | Oy 359 GCAGGGTCAACGCGTGTGTTACTCCACCGTGGGGACGCGACGCAAAAACGTCG 418 | 0y         419 GCGCTGCATATCGTTGGGGACTCGCTGGCTGGATTGTCCTCAGTCCACCACAAC         478           0b         181 GCTTTGCATCATTTGGGGACTCACTGGCATAGACTGTCCTCTGCACTACCAT         240           0y         479 AGCACCATCATTTGGGGACTCACTGGCATAGACTGTCCTCTGGCATACCAT         240           0y         479 AGCACATCATCTCTCTGCTGGGCTACGGCTTCTACGGGGACTTAATC         300           0y         539 AAGGACGTGGAGAACTCGGTTTCTCTGCTGGCTTTCTACGGGGACTTAATC         300           0y         539 AAGGACAGTGAGAAACGGTGGTTTCTCTCTCTCCTCTCTCAGGGATTAAAC         420           0y         599 ACCTTCTCTCCACCACTGGTAGAGGGCACTGGCGTATCGTTCTCTCCTCCTCCAGGACACACGCACG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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| Query Match         59.2%; Score 579.4; DB 5; Length 581;           Best Local Similarity         99.8%; Pred. No. 3.5e-155;           Matches 580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;           QY           195 TTAACATAGACAAATACGACGACATCGTCTGTCTGGCGGAGATGGTATGTTCAGCGAGG 60           QY         255 TGCTGCACGGTCTGATTGGAGACGCGCGGGGGGGAGATGGTATGTTCAGCGAGG 60           QY         255 TGCTGCACGGTCTGATTGGAGACGCCGCGGGGGGGGACCACCCCC 120           QY         315 GGGTGTGTGTTGATTGGAGACGCCCGGGGGTCGACCAGGGCTCACCCCCC 120           QY         315 GGGTGTGTGTGTTGGAATTGGAATCATTCCCGAGGGTCAACGGACT 180           QY         315 GGGTGTGTGTGTGCTCCCAGTAGCCTCCGGATTGGAATCATTCCCGCAGGTCAACGGACT 180           QY         375 GCGTGTGTTACTCCACGTAGCCTCCGGATTGGAATCATTCCCGCAGGTCAACGGACT 180           QY         375 GCGTGTGTTACTCCACGTGGCCACGGACGCAGAAACCTCCGCAGGTCAACGGACTTCGTTG 190           QY         375 GCGTGTGTTACTCCACGTGGGCACCAGGACGCACACAGACACTCTTCGTT 240           QY         435 GCTGTGTTATTACTCCACCGTGGGCACCAGAAACCTCCACACACA | Oy 555 AACGGTGGTTGGCACATACGACTTTTCAGGTTTAAAGACCTTCCTCTCCCACC 614                                                                                                  | Qy         615 ACTGCTATGAAGGACAGTGTCCTCCTGCACACACACAGGGGTGTGGGGTTCTCCAAGGG 674           Db         421 ACTGCTATGAAGGACAGTGTCCTTCCTCCTGCACACACAC | QY         675         ATAGGAAGCCCTGCCGGCAGGATGCTTTGTTTGCAGGCAAAGCAAGC                          | OY 735 AGGACCAGAAGAAAGCACTGTATGGATTTGGAAGCTGCGGAG 775<br>        | RESULT 10 CB246749 LOCUS LOCUS LOCUS UI.M-FID-cdx-b-10-0-UI.rl NIH BMAP_FIO Mus musculus CDNA clone IMAGE:683595 5', mRNA sequence. ACCESSION CB246749.1 GI:28368393 KEYWORDS ST. SOURCE Nus musculus (house mouse) ORGANISM Mus musculus (house mouse) ORGANISM Mus musculus (house mouse) ORGANISM Mus musculus (house mouse) ORGANISM Mus musculus (house mouse) ORGANISM Musculus (house mouse) ORGANISM Musculus (house mouse) ORGANISM Musculus (house mouse) ORGANISM Musculus (house mouse) ORGANISM Musculus (house mouse) ORGANISM Musculus (house mouse) ORGANISM Musculus (house mouse) ORGANISM Musculus (house mouse) ORGANISM Musculus (house mouse) ORGANISM Musculus (house mouse) ORGANISM Musculus (house noi. nih.gov/. TILLE JOURNAL CONTACT: RObert Strausberg, Ph.D. Email: Gapbarremat: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Library preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Lib. at: http://image.llnl.gov This clone was contributed by the Brain Molecular Anatomy Project (BMAR) Seq primer: pYX-5. |

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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
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foote="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
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I (bases 1 to 541)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., ii, Y., Xu,C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.

I Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Blotechnol. 22 (6), 707-716 (2004)
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17000532199536 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
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Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 541 Std Brror: 0.00.
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99.6%; Pred. No. 1.2e-142;
tive 0; Mismatches 2;
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/organism="Homo sapiens"
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B I (bases 1 to 584)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizuki,Y., Yamashita,R., and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                               584 bp mRNA linear EST 17-SEP-2004
BP310011 Sugano cDNA library, brain Homo sapiens cDNA clone
NRR01274, mRNA sequence.
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                                                                                                                     TCTGACCTCATCCTTATCCGGAAGTGCTCCAGGTTCANCTTCCTGAGATTCCTCATCCGG 720
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TCTGACCTCATCCTCATCCGGAAATGCTCCAGGTTCAATTTTCTGAGATTTCTCATCAGG
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/tissue type="brain"
/clone_lib="Sugano cDNA library, brain"
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Pred. No. 9.6e-143;
0; Mismatches 3;
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                    CACACCAACCAGCAGGACCAG 979
                                                                                                                                                                                                                                                     721 CACACCAACCAGGACCAG 741
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Homo sapiens
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CF138275
UI-HF-BNO-anz-g-11-0-UI.rl NIH MGC_50 Homo sapiens CDNA clone
IMAGE:1094461 5', mRNA sequence.
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Email: bento-soares@uiowa.edu
Tissue Produrement: Louis Standt
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at Seq primer: //genome.uiowa.edu/distribution/humanfl.html
                                                                       268
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 573)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                        147 TACGACGCATCGTCTGTGTCGGCGGAGATGGTATGTTCAGCGAGGTGCTGCACGGTCTG
                                                                                                                                                                        ATTGGGAGGACGCANAGGAGCGCCGGGGTCGACCAGAACCACCCCCGGGCTGTGCTGGTC
                           ATTGGGAGGACGCAGGGGCCGGGGTCGACCAGAACCACCCCCGGGCTGTGCTGGTC
                                                                                                                                                                                                       CCCAGTAGCCTCCGGATTGGAATCATTCCCGCAGGGTCAACGGACTGCGTGTTACTCC
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        GTAATTACTGAACATGCTAATCAGGCCAAGGAGACTCTGTATGAGATTAACATAGACAAA
                                                                       TACGACGCCATCTGTGTCGGCGGAGATGGTATGTTCAGCGAGGTGCTGCACGGTCTG
                                                                                                                                                                                                                                                                         ACCGTGGGCACCAGCGACGCAGAAACCTCGGCGCTGCATATCGTTGTTGGGGACTCGCTG
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Coordinated Laboratory for Computational Genomics
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/organism="Homo sapiens"
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CF138275.1 GI:33253719
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Bukaryota; Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 584)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                       733 GGAGGAGCAGAAAAGCACTGTATGGTTTGGAAGCTGCGGAGGACGTGGAGGAGTGGCA 792
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                                                                       183 CTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCATCAAGGACAGTCAGAA
                                                                                                                  GAAACGGTGGTTGGCTGTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTCTCCCA
                                                                                                                                   243 GAAACGGTGGTTGGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTCTCCCA
                                                                                                                                                                                                                                                      CTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCATCAAGGACAGTGAGAA
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BP309990 Sugano cDNA library, brain Homo sapiens cDNA clone
NRR01216, mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NRR01216"
/tissue type="brain"
/clone_lib="Sugano cDNA library, brain"
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Pred. No. 3.3e-140;
0; Mismatches 2;
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Best Local Similarity 94.2%;
Matches 582; Conservative
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Homo sapiens
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University of lowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA 75 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA 781: 319 315 8260
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                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 550)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
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/lab host="DH10B (LII)"
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                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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/db_xref="taxon:9606"
/clone="IMAGE:3094594"
                                                                                                                                                                                                                               Genome Res. 6 (9), 791-806 (1996)
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1. .550
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Matches 520; Conservative
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ORGANISM
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AUTHORS
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MEDLINE
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UI.HF-BNO-aoc-b-06-0-UI.rl NIH MGC_50 Homo sapiens cDNA clone IMAGE:3094594 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTCCCGCAGGGTCAACGGACTGCGTGTGTTACTCCACCGTGGGCACCAGCGACGCAGAA 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCAAGGAGACTCTGTATGAGATTAACATAGACAAATACGACGGCATCGTCTGTGTCGGC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGATGGTATGTTCAGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGGCGCC 292
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                                                                                                                                                                                                                            /clone lib="NHH MGC 50"
//clone lib="NHH MGC 50"
//note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                           /clone="IMAGE:3094461"
/tissue_type="lymph"
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/lab_nost="DH10B (LTI)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.2%; Score 520.8; DB 7; 93.9%; Pred. No. 2.6e-138; ive 0; Mismatches 4;
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Homo sapiens (human)
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        Db
        482 ATTTTCTGAGATTTCTCATCAGCACCACCAGGAGCAG 525
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L (Jaras J. E., Wright, C.L., Edwards, C.A., Davis, M.P., Grinham, J.A., Collins, J.E., Wright, C.L., Edwards, C.A., Davis, M.P., Grinham, J.A., Cole, C.G., Goward, M.E., Aguado, B., Mallya, M., Mokrab, Y., Huckle, E.J., Beare, D.M. and Dunham, I.

Direct Submission

L Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire, C.B.O. 15A, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript Sanger Institute name: pGEM. DK29F11.1

Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see http://www.sanger.ac.uk/HGP/Chr22/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1654 bp mRNA linear PRI 25-MAY-2004 Homo sapiens bK29F11.1 full length open reading frame (ORF) cDNA clone (CDNA clone C22ORF:pGEM.bK29F11.1).
                                                                                   AB079067 Mus muscu
AK129416 Mus muscu
TR386590 Gallus ga
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CDNA, chromosome 22; ORF.
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AX457006 Sequence
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                ThraspCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAlaLeuHis
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Conservative:
Mismatches:
Indels:
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                                                                                  GluMetLeuGluLysLeuThrSerArgProLysHisLeuLeuValPheIleAsnProPhe
                                                                                                                                       GlyGlyLysGlyGlnGlyLysArglleTyrGluArgLysValAlaProLeuPheThrLeu
                                                                                                                                                         GGAGGAAAAGGACAAGGCAAGCGGATATATGAAAGAAAAGTGGCACCACTGTTCACCTTA
                                                                                                                                                                                             AlaSerIleThrThrAppIleIleValThrGluHisAlaAsnGlnAlaLysGluThrLeu
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     CCTTACGCTTTTACAGTTCACTGTGTAAAGAGAGCACGACGGCACCGCTGGAAGTGGGCG
                               GlnValThrPheTrpCysProGluGluGluLeuCysHisLeuTrpLeuGlnThrLeuArg
                                                                                                GAGATGCTGGAGAAGCTGACGTCCAGACCAAAGCATTTACTGGTATTTATCAACCCGTTT
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ONHPRAVLVPSSLRIGIIPNIDKXDGTVCWGDOMFSEYLHGLGLGRCROWD
ONHPRAVLVPSSLRIGIIPNIDKXDGTVCWGDMSSTALHIVVGDSLAMDVSSVHH
NSTLLRYSVSLLGYGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHLCYEGTVSFLPA
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ATNMSCACRRSPRGLSPAHGDGSSDLILIRKCSRPWFLRFLIRHTNQQDQFDFTFV
BYRVKKROPFTSKHMEDEDSDLKEGGSKRRFGHICSSHPSCCCTVSNSSWNCDGEVLHS
PAIEVRVHCQLVRLFARGIEENPKPDSHS"
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Catarrhini; Hominidae; Homo.
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Van Veldhoven, P. P.
Direct Submission
Submitted (18-APR-2002) Van Veldhoven P.P., Farmakologie,
K.U.Leuven, Herestraat, B-3000 Leuven, BELGIUM
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                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Van Veldhoven,P.P.
A search for lipid kinases
Unpublished
'hases 1 to 2042)
AJ457828
AJ457828.1 GI:20269072
lipid kinase; LK4 gene.
Homo sapiens (human)
Homo sapiens
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AUTHORS
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| GlyaladlyalaProGlyAlaAspalaCysSerValProValSerGluIleIleAlaVal 60 [ | 101 GlnValThrPheTrpCysProGluGluGlnLeuCysHisLeuTrpLeuGlnThrLeuArg 120 | AlaSerileThrThrAspileileValThrGluHisAlaAsnGlnAlaLysGluThrLeu 18                    |                                                                                                                                                                                                                                                                                              | IleValValGiyAspSerLeuhlaMecAspValSerSerValHisHishIshSerThrLeu 28                                                                                                                                                                           | 321 SerHisHisCysfyrGluGlyThrValSerPheleuProAlaGluHisThrValGlySer 340 [ |
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| ThrSerLysHisMetGluAspGluAspSerAspLeuLysGluGlyGlyLysLysArgPhe 480  | 1<br>6-JUL-2                                                         | ans (human) ans i Metazoa; Ch Eutheria; Pr and Encinas 1 of human sp 0 0228906-A 9 | Location/Qualifiers  1441  1441  2. / organism="Homo sapiens"  / organism="Homo sapiens"  / db xref="taxon:9606"  761689  / note="unnamed protein product"  / codon start=1  / protein id="cab38256.1"  / db xref="G1:21715:96"  / translation="MGATGAAEPLQSVLWVKQORCAVSLEPARALLRWWRSPGPGAGA | IAVEETDVHGKAGGSGKWQKUEK<br>LQTLEEMLEKLTSRPKHLLVFIN<br>NQAKETLYEINIDKYDGIVCVG<br>RIGIIPAGSTDCVCYSTVGTSDA<br>RYGFYGDIIKDSEKKRMLGLARYD<br>RYGFYGDIIKDSEKKRMLGLARYD<br>GLSPAAHLGDGSSDLILIBKCSR<br>HMEDEDSDLKEGGKKRFGHICSS<br>LFARGIEENPKPDSHS" | Pred. No.: 8.93e-228   Length: 4413                                    |

| QHTVGSPRDRKPCRAGCFVCRQSKQQLE<br>ATNMSCACRRSPRGLSPAAHLGDGSSDL | EVYRYKKFQFTSKHMEDEDSDLKEGG<br>PAIEVRVHCQLVRLFARGIEENPKPD<br>ORIGIN       | :<br>ty:                                                     | arity: 100.00%<br>100.00%<br>9                                           | US-10-631-958-10 (1-537) x AB079066 (1-4445) Qy 1 MetGlyAlaThrGlyAlaAlaGluProLeuGlnSe | 124                                                                      | 184                                                             | DD 244 GGAGCCGCCCCGGCGCGCGGGAIGCCTCTGT  QY 61 GluGluThrAspValHisGlyLysHisGlnGlySe | Db 364 CCTTACGCTTTTACAGTTCACTGTGTAAAGAGAGC | Oy 101 GlnValThrPheTrpCysProgluGluGluGlnLeuCy | 121                                                                                                                                                     | Db 484 GAGAIGCIGGAGAAGCIGACGICCAGACCAAAGCA                       | 544                  | Oy 161 AlaSerlleThrThrAsplleIleValThrGluHi<br> |                                                                                                                                                | Db 664 TATGAGATTAACATAGACAAAATACGACGGCATC 201 SerGluValLeuHisGlvLeulleGlvArdThr |                                           | Qy 221 HisproArgalaValLeuValproSerSerLeuAr | Db 784 CACCCCGGGCTGTGGTCCCCCAGTAGCCTCCG | Qy 241 ThrAspCysValCysTyrSerThrValGlyThrSe             | Db 844 AcGGACTGCGTGTTACTCCACCGTGGGCACCAG                                             | 261                                                                                                                       | Db 904 ATCGTTGTTGGGGACTCGCTGGCCATGGGTGTCTCGCTGGTGTGTCTCTCTGTGTGTG                                                                                                                      |  |
|--------------------------------------------------------------|--------------------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------------------|---------------------------------------------------------------------------------------|--------------------------------------------------------------------------|-----------------------------------------------------------------|-----------------------------------------------------------------------------------|--------------------------------------------|-----------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------|----------------------|------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------|-------------------------------------------|--------------------------------------------|-----------------------------------------|--------------------------------------------------------|--------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
|                                                              | 421 IleLeuIleArgLysCysSerArgPheAsnPheLeuArgPheLeuIleArgHisThrAsn 440<br> | GINGINASPGINPheAspPheThrPheValGIUVAITYrArgValLysIysPheGINPhe | 461 ThrSerLysHisMetGluAspGluAspSerAspLeuLysGluGlyGlyLysLysArgPhe 480<br> |                                                                                       | 501 CyshapglygluvalLeuHisSerProAlaIleGluValArgValHisCysGlnLeuVal 520<br> | 521 ArgleuPheAlaArgGlyIleGluGluAsnProLysProAspSerHisSer 537<br> | AB079066 AB079066 AB079066 AB079066.1 GI:21624339                                 | Homo sapiens (human)                       |                                               | Sugiura, M., Kono, K., Liu, H., Shimizugawa, T., Minekura, H., Spiegel, S. and Kohama, T., Ceramide Kinase, a Novel Lipid Kinase. MOLECULAR CLONING AND | FUNCTIONAL CHARACTERIZAT<br>J. Biol. Chem. 277 (26),<br>11956206 |                      |                                                | <pre>Hiromachi 1-chome, Shinagawa-ku, Tokyo 140-8710, Japan (E-mail:meugiura@shina.sankyo.co.jp, Tel:81-3-3492-3131, Fax:81-3-5436-8565)</pre> |                                                                                 | /mol_type="mRNA"<br>/db_xref="taxon:9606" |                                            | /gene="cork"<br>/codon start=1          | /product="ceramide kinase"<br>/protein id="BAC01154.1" | /db_xref="G1:21624340"<br>/translation="MGATGAAEPLQSVLWVKQQRCAVSLEPARALLRWWRSPGPGAGA | PGADACSVPVSEI IAVEETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQV<br>TFWCPEEQLCHLWLQTLREMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTL | ASITUDI UYEHANORETUKEIN KIDELUKGOGRAFESUHGULGERUKRSAND<br>ONIPRAUJVPSSILEIGII PAGSILETCVKSTVGTSDAETSALHIVVGDSLAMDVSSVIH<br>NSTLLRYSVSLLGYGFYGDII KDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPA |  |
| QQ                                                           | ර සි                                                                     | g çç                                                         | & B                                                                      | රු සි                                                                                 | දු පු                                                                    | S S                                                             | RESULT 4 AB079066 LOCUS DEFINITION ACCESSION VERSION                              | KEYWORDS<br>SOURCE<br>ORGANISM             | REFERENC                                      | AUTHORS                                                                                                                                                 | JOURNAL                                                          | REFERENCE<br>AUTHORS | TITLE<br>JOURNAL                               |                                                                                                                                                | FEATURES<br>BOUrce                                                              |                                           | gene                                       | 9                                       |                                                        |                                                                                      |                                                                                                                           |                                                                                                                                                                                        |  |

JLEEEOKKALYGLEAAEDVEEWOVVCGKFLAIN ;DLILIIRKCSRFNFLRFLIRHTNQQDQFDFTFV ;KKRFGHICSSHPSCCCTVSNSSWNCDGEVLHS SHS." 120 160 663 200 220 260 243 AlaArgArgHisArgTrpLysTrpAla 100 603 843 ValProValSerGluIleIleAlaVal 60 SerGlyLysTrpGlnLysMetGluLys 80 483 140 543 HisAlaAsnGlnAlaLysGluThrLeu 180 723 783 240 903 280 963 heTyrGlyAspileIleLysAspSer 300 40 LeuargTrpTrpargSerProGlyPro CyshisLeuTrpLeuGlnThrLeuArg HisLeuLeuValPheIleAsnProPhe CATGCTAATCAGGCCAAGGAGACTCTG 4445 537 0 0 0 tive: eB:

| Alignment Scores: 3.39e-227 Length: 4432 Pred. No.: 2881.00 Matches: 536 Score: 2881.00 Matches: 536 Percent Similarity: 99.81\$ Mismatches: 1 Dest Local Similarity: 99.76\$ Indels: 0 Outry Match: 6 Gaps: 0 | 958-10 (1-537) x AR541900 (1-4432)                                      | MecGIVALATITICITYALATITICITYALATITICITYALIANI   MecGIVALIANI   M | 21 CysAlaValSerLeuGlübroAlaArgAlaLeuLeuArgTrpTrpArgSerProGlyPro            | 41 G<br>1324 G                                                      |                                                                                                                                                                  | 81 ProfyralaPheThrValHisCysVallysArgAlaArgArgHisArgTrpLysTrpJla<br> | euArg 1                                                            |                                                                 |                                                                  | ส - ส<br>สเซ                                                         | 7 7                                                             | Oy 201 SerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAspGlnAsn 220 | Qy 221 HisProArgAlaValLeuValProSerSerLeuArgileGlyIleIleFroAlaGlySer 240                                                          | Qy 241 ThrAspCysValCysTyrSerThrValGiyThrSerAspAlaGluThrSerAlaLeuHis 260 | Qy 281 LeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspileIleLysAspSer 300                                                      | Qy 301 GlubysLysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThrPheLeu 320<br> |
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|                                                                                                                                                                                                                | Oy 321 SerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrValGlySer 340 | Qy         341 ProArgAspargLysProCysArgAlaGlyCysPheValCysArgGlnSerLysGlnGln 360           Db         1144 CCAAGGGATAGGAAGCCTGCCGGGCAGGATGCTTTGCAGGCAAGCAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Oy 361 LeuGluGluGluGluGluGluGluLeuTyrGlyLeuGluAaklaGluAspValGluGlu 380<br> | 381 TrpGlnValValCysGlyLysPheLeuAlalleAsnAlaThrAsnMetSerCysAlaCys 40 | Qy         401 ArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSerAspLeu 420           Db         1324 CGCCGGAGCCCCAGGGCCTCCCCGGCTGCCCATTGGGAACGGATCTTCTGACTC | 421 IleLeulleArgLysCysSerArgPheAsnPheLeuArgPheLeulleArgHisThrAsn    | 441 GlnGlnAspGlnPheAspPheThrPheValGluValTyrArgValLysLysPheGlnPhe 1 | 461 ThrSerLysHisMetGluAspGluAspGrAspLeuLysGluGlyGlyLysLysArgPhe | 481 GlyHisIleCysSerSerHisProSerCysCysCysThrValSerAsnSerSerTrpAsn | 501 CysaspGlyGluValLeuHisSerProAlaIleGluValArgValHisCysGlnLeuVal<br> | 521 ArgleuPheAlaArgGly11eGluGluAsnProLysProAspSerHisSer 537<br> | SULT 5<br>541900                                                        | LOCUS ARS41900 4432 bp DNA linear PAT 08-OCT-2004 DEFINITION Sequence 140 from patent US 6743619. ACCESSION ARS41900 GI:53933980 | KEYWORDS . SOURCE Unknown. ORGANISM Unknown.                            | TITLE Nucleic acids and polypeptides JOURNAL Patent: US 6743619-A 148 01-JUN-2004; FEATURES Location/Qualifiers Source 14432 | /organism="unknown"<br>/mol_type="genomic DNA"<br>,                         |

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                                                      TrpGlnValValCysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSerCysAlaCys
                                                                                                                                 CGCCGGAGCCCCAGGGGCCTCTCCCCCGGCTGCCCACTTGGGAGACGGGTCTTCTGACCTC
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                                                                                  LeuGluGluGluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspValGluGlu
                                                                                                                                                           ArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSerAspLeu
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CYCSTVGTSDAETGALHIVVGOSLAMDVSSYHHNSTLARSVSLLGVGFRQDIIKDS
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QQLBEBQKRALYGLBAAEDVBEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andy Chan, Starb Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Parvanch Saecdi, JR Santos, Angelique Schnerch, Ursula Skalska, Bunae Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schnerch, Asim Siddiqui, Rob Holt, Marco Marra.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.J., Halek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.W., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Samailus, D.E., Schnerch, A., Schein, J.E., Jonee, S.J., and Marra, M.A., Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.R. Consortium/LinNL at: http://image.llnl.gov Series: IRAX Plate: 141 Row: d Column: 4 This clone was selected for full length sequencing because it gassed the following selection criteria: matched mRNA gi: 21703365 This clone has the following problem: The cds is short compared to the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (12-Max-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Peripheral Nervous System, dorsal root
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/db xref="LocusID:64781"
579. .1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Janes R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                    human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 1772)
Strausberg,R.
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/protein_id="AAH67255.1"
/db_xref="GI:45595583"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bcvo/255 1772 bp mRNA linear PRI 06-APR-2004
Homo sapiens ceramide kinase, mRNA (cDNA clone IMAGE:6185601),
complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                          1324 CGCCGGAGCCCCAGGGGCCTCTCCCCGGCTGCCCACTTGGGAGACGGGTCTTCTGACCTC 1383
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                    rGlulyslysargTrpLeuGlyLeualaargTyraspPheSerGlyLeuLysThrPheLe
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  CCTTCGCTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGACATCATCAAGGACAG
                                                          uSerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrValGlySe
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Patent: WO 0160990-A 5 23-AUG-2001;
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    /organism="Homo sapiens"
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    /db_xref="taxon:9606"

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Sequence 5 from Patent WO0160990
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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E. 1 (Dases 1 to 4171)
S. Novel genes and proteins encoded by the genes
AZUSA DNA RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002345492-A 181 03-DEC-2002;
RAZUSA DNA RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002345492-A/181
PN JP 2002345492-A/181
PN JP 2002345492-A/181
PN JP 2002345492-A/181
PN JP 2002345492-A/181
PN JP 2002345492-A/181
PN JP 20022459009
PP C - CINNIS/09, COTKL4/4/7//A61K31/711, A61K38/00, A61K48/00, A61P25/00, PC A61P25/18, A61P35/14, A61K31/711, A61K31/702
PC Novel genes and proteins encoded by the genes FH Key
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JP 2002345492-A/181
03-DEC-2002
26-FEB-2002 JP 2002049009
OSAMU OHARA,TAKAHRO NAGASE, DAISUKE NAKAJIMA
C12N15/09,C07K14/477/A61K31/711,A61K38/00,A61K48/00,A61P25/00,A61P25/14,
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                            961 IGCTTTGTTGCAGGCAAAGCAAGCAGCAGCTGGAGGAGGAGCAGCAGAAGAAAGCACTGTAT
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                                                             GlyLeuGluAlaAlaGluAspValGluGluTrpGlnValValCysGlyLysPheLeuAla
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Chara,O., Nagase,T. and Kikuno,R.
Chara,O., Nagase,T. and Kikuno,R.
Direct Submission
Submitted (12-NOV-2000) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
Fax:81-438-52-3914)
Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                     1022 TCCTGTGCTTGTCGCCGGAGCCCCAGGGCCCTCTCCCCGGCTGCCCACTTGGGAGACGGG
AGCAAGCAGCTGGAGGAGGAGCAGAAAGCACTGTATGGTTTGGAAGCTGCGGAG
                                                                  SerCysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGly
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Sugiura, M., Kono, K., Shimizugawa, T., Minekura, H., Spiegel, S. and
                                                           GAGAAGAAAGGGGGGTTTGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTC
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Indels:
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Kohama, T. Submission Submission Submission Submission Submissed (29-JNN-2002) Masako Sugiura, Sankyo Co., Ltd., Pharmacology and Molecular Biology Research Laboratories; Hizomachi 1-chome, Shinagawa-ku, Tokyo 140-8710, Japan (E-mail:msugiura@shina.sankyo.co.jp, Tel:81-3-3492-3131, Fax:81-3-5436-8565)
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S Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.

Direct Submission

Submitted (13-JUL-2003) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics, 2-6-7

Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan

(Razusa-kamatari, Kisarazu, Chiba 292-0818, Japan

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(Remail:mouse@kazusa.or.jp, Tel:1438-52-3918)

The CREATE program supported by Japan science and technology

corporation; cDNA full insert sequencing: Kazusa DNA Research

Institute; cDNA 11brary construction, clone selection and 5'- &

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KFHFTSKHVEDEDNDSKSQUEGGKKFGKICKDRPSCTCSASRSSWNCDGEVWHSPAIEVR
                                                                                                                                                                                                                                                                                                               Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Koseki,H., Hiraoka,S., Saga,Y., Nagase,T., Ohara,O. and Koga,H.
Prediction of the coding sequences of mouse homologues of KIAA gene: III. the complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries 22977043
                                                                                                                      21-NOV-2003
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Mammalia; Eutheria; Rodentia;
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                                                                      LeuGlyTyrGlyPheTyrGlyAspIleIleLysAspSerGluLysLysArgTrpLeuGly
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NFSQLCTPHPSCGCNHVNSIWNCDGETLDQTAIEMRVHCQLIKLFARGIENDAV
NPSKVP"
                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Scries: IRAK Plate: 161 Row: a Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                        Andy Chan, Steve S. Chand, Milliam Chow, Alison Cloutier, Ruth Reatherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Rim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Parka Olson, Diana Palmquist, Anca Petrescu, Anna Litsa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smallus, Joff Stoct, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 AlaieuleuArgTrpArgSerProGlyProGlyAlaGly------AlaPro
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320
81
1117
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="MGC:84197 IMAGE:6954181"
/tissue type="Brain, adult Kenopus"
/clone_lib="NICHD_XGC_Brn1"
/lab_hogt="PH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Vector: pCMV-SPORT6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Xenopus laevis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="MGC84197 protei
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/db_xref="GI:49257665"
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             nfo@bcgsc.bc.ca
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Best Local Similarit
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Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haish, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwant, F.J.,
McKernan, K.J., Malek, J.A., Gunarathe, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                              Z494 bp mRNA linear VRT 03-AUG-2004 Xenopus laevis MGC84197 protein, mRNA (cDNA clone MGC:84197 IMAGE:6954181), complete cds.
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1191 AATGAAAGCAGTGTCACAGACATAGGAAAGAAACATTTTGGCCAGTTCTGCAGAGATCAT 1250
                                                                                                          1311 AGCTCAGCAATTGAAGTGAGGGTTCACTGCCAGTTAATGAAACTGTTTGCAAGGGGAATC 1370
                                                                             ProSerCysCysTyrValSerAsnSerSerTrpAsnCysAspGlyGluValLeuHis 507
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W. and Richardson, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative
                                                                                                                                                                   508 SerProAlaileGluValArgValHisCysGlnLeuValArgLeuPheAlaArgGlyIle
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                                                                                                                                                                                                                                                                                                                                      1371 GAGGAAACTGTAAAGATGAAGCTGCCTACAGCCACAGT 1409
                                                                                                                                                                                                                                                                                      528 GluGluAsnProLysProAsp-----SerHisSer 537
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12454917
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Tissue Procurement:
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Contact: XGC help desk
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                                                                                488
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VERSION
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| 776 CTG 224 Ala 836 GCA 244 Val :::: 896 ATA 956 GGT 1016 TCG 1076 CGT 324 CY8 | créchidéccicatigneanachanagarrergarénagheachantécagr 835 AlavalLeuvalProSerSerLeuarglagliglille |  |
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Search completed: September 6, 2005, 16:38:47 Job time : 7137.33 secs

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AG810370 Human the
AG877728 DNA encod
AB140822 Human Sph
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AG81699 Human Cod
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antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NOV9a encoding cDNA SEQ ID NO:39.
                                                                                                                                                                              ABL40823
ABL25704
AAS77727
ABL25705
AAD14427
AAS77729
ADQ88890
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ABL03296
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ADS10370
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ABT23453
AAD14428
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ABL03297
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76. .1689
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 "MODEL=frame+ parameters".

"MODEL=frame+ parameters".

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPEXT=7
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Ab140828 Human sph
Adj96598 Human lip
Adp55247 Human PRO
Abx70921 Novel hum
                                                                               4; Search time 829.053 Seconds (without alignments) 3834.378 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                           nucleic search, using frame_plus_p2n model
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Scoring table:

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2001US-0327917P.
2001US-0328029P.
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2001US-0328056P.
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2002US-0373826P.
2002US-0373884P.
                                                                       22-OCT-2001; 2001US-0341058P.
24-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0345529P.
29-OCT-2001; 2001US-034557P.
01-NOV-2001; 2001US-0346357P.
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2002US-0373815P.
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112-0CT-2001; 2
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                                                                                                     17-APR-2002;
19-APR-2002;
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     02-OCT-2001;
05-OCT-2001;
05-OCT-2001;
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16-MAY-2002;
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28-MAY-2002;
                                                                                                                                                                               25-JUN-2002;
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## (CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerbusen BD, Anderson DW, Zhong M, Catterton B;
Ji M, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

## WPI; 2003-381626/36. P-PSDB; ADA05680.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

## Claim 20; Page 134; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOVI). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated mucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
collypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or
aborrant physiological interactions of the polypeptide; (11) a method of
carrier physiological interactions of the polypeptide; (12) a method for modulating
cor preventing of the polypeptide described above; (13) methods of treating
cor preventing a pathology associated with the polypeptide; (12) method for modulating
cor preventing a pathology associated with the above polypeptide. NOVX
sequences have antidiabetic, anorectic, antibacterial, virucide,

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Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores:

No.

Gaps:

| US-10-631- | 958-1   | US-10-631-958-10 (1-537) x ADA05679 (1-1740)                       |
|------------|---------|--------------------------------------------------------------------|
| Qy         | Ξ-      | MetGlyAlaThrGlyAlaAlaGluProLeuGlnSerValLeuTrpValLysGlnGlnArg 20    |
| qq         | 76 A    |                                                                    |
| δλ         | 21 0    | CysAlaValSerLeuGluProAlaArgAlaLeuLeuArgTrpTrpArgSerProGlyPro 40    |
| QQ         | 136 T   | GGGCCGTGAGCCTGGGGGCCCGGGGGCTCTGCTGCTGGGGGGGG                       |
| ò          | 41 6    | GlyAlaGlyAlaProGlyAlaAspAlaCysSerValProValSerGluIleIleAlaVal 60    |
| qq         | 196 G   | GAGCCGGCCCCCCGGTGCTGATGCCTGCTCTGTGTCTGTATCTGAGATCATCGCCGTT 255     |
| δλ         | 61 6    | GluGluThrAspValHisGlyLysHisGlnGlySerGlyLysTrpGlnLysMetGluLys 80    |
| qa         | 256 G   | AGGAAACAGACGTTCACGGGAAACATCAAGGCAGTGGAAAATGGCAGAAAATGGAAAAG 315    |
| δλ         | 81<br>P | ProTyrAlaPheThrValHisCysValLysArgAlaArgArgHisArgTrpLysTrpAla 100   |
| qq         | 316     | CTTACGCTTTTACAGTTCACTGTGTAAAGAGAGCACGGGCACGGCACCGCTGGAAGTGGGCG 375 |
| δλ         | 101     | GlnValThrPheTrpCy8ProGluGluGlnLeuCy8HisLeuTrpLeuGlnThrLeuArg 120   |
| qq         | 376 C   | AGGTGACTTTCTGGTGTCCAGAGGAGCAGCTGTGTCACTTGTGGCTGCAGACCTGCGG 435     |
| č          | 121 G   | GluMetLeuGluLysLeuThrSerArgProLysHisLeuLeuValPheIleAsnProPhe 140   |
| qq         | 436 G   | AGATGCTGGAGAAGCTGACGTCCAGACCAAAGCATTTACTGGTATTTATCAACCGGTTT 495    |
| δλ         | 141 G   | GlyGlyLysGlyGlyGlyLysArglleTyrGluArgLysValAlaProLeuPheThrLeu 160   |
| qq         | 496 G   | GAGGAAAAGGACAAGGCAAGGATATATGAAAGAAAAGTGGCACCACTGTTTCACCTTA 555     |
| δ          | 161 A   | AlaSerIleThrThrAspIleIleValThrGluHisAlaAsnGlnAlaLysGluThrLeu 180   |
| Db         | 556 G   | CCTCCATCACCACTGACATCGTTACTGAACATGCTAATCAGGCCAAGGAGACTCTG 615       |
| δ          | 181 T   | TyrGluIleAsnIleAspLysTyrAspGlyIleValCysValGlyGlyAspGlyMetPhe 200   |
| Db         | 616 T   | ATGAGATTAACATAGACAAATACGACGCATCGTCTGTGTTCGGCGGAGATGGTATGTTC 675    |
| ò          | 201 8   | SerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAspGlnAsn 220   |
| QQ         | 676 A   | GCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGACGCCCGGGGTCGACCAGAAC 735    |
| ò          | 221 H   | HisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAlaGlySer 240   |
| QQ         | 736 C   |                                                                    |

protein'

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/product= "sphingosine kinase-like protein"
/note= "see ABB07856"
                               /product= "sphingosine kinase-like |
/note= "see ABB07857"
/**. 1689
                       Location/Qualifiers
1. .1689
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23-AUG-2001; 2001US-0314113P.
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                                                             LeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspileIleLysAspSer
                                                                      CTTCGCTACTCCGTGTCCCTGCTGGGCTACGGCTTCTACGGGGGACATCATCAAGGACAGT
                                                                                                                         SerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrValGlySer
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New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous system disorder.
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                                                                                                                                                                              The invention relates to a human sphingosine kinase-like protein. The polypeptide can be expressed by standard recombinant methodology. The sphingosine kinase-like protein and gene can be used to regulate intracellular signalling and consequently cell proliferation and apoptosis. Such regulation is useful for treating cancer, allergies (e.g. atthmat, autoimmune diseases (e.g. theumatoid arthritis) and central and peripheral nervous system disorders (e.g. Parkinson's disease). The present sequence represents the human sphingosine kinase-like protein
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                                                                                                                                            Claim 1; Fig 9; 120pp; English.
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Human sphingosine kinase-like protein; intracellular signalling; gene; cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma; autoimmune disease; rheumatoid arthritis; Parkinson's disease; ss.

Human sphingosine kinase-like protein encoding cDNA

03-JUL-2002

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preparing a composition for treating diseases or disorders, e.g., cancer, or neurological, immunological or inflammatory disorders.
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Example 1; SEQ ID NO 55; 366pp; English.

This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunemodulator and antiinflammatory activities. This polymucleotide sequence is a human kinase DNA sequence of the invention.

Sequence 4429 BP; 1020 A; 1115 C; 1213 G; 1081 T; 0 U; 0 Other;

| Alignment Sc Score: Score: Score: Percent Simi Best Local S Query Match: DB: US-10-631-95 OY Db 27 OY Db 27 OY Db 27 OY Db 33 OY Db 33 OY Db 33 OY Db 33 | nnt Scorr<br>Similar<br>scal Similar<br>atch:<br>1 p 92 p<br>1 | Alignment Scores: Score: Percent Similarity: Best Local Similarity: Ouery Match: DB: US-10-631-958-10 (1-537 OY 1 MetGlyAla' DD 22 CYSAlaVal DD 22 CGGCGCGC OY 21 CASAlaVal DD 212 GGGCCGCGC OY 21 CHANGAL DD 212 GGGCCGCGC OY 332 CCTTACCCT OY 81 ProTyrAla DD 272 GAGGAAACA OY 81 ProTyrAla DD 332 CCTTACCCT OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr OY 101 GluMalThr | es: 2.61e-254     Length: 2.888.00     Matches: 11arity: 100.00\$     Mismatches: 100.00\$     Mismatches: 100.00\$     Mismatches: 100.00\$     Mismatches: 12.61e-254     Matches: 100.00\$     Mismatches: 12.620.00\$     Mismatches: 13.620.00\$     Mismatches: 14.29) MetGlyAlaThrGlyAlaAlaGluProLeuGlnSerVal MetGlyAlaThrGlyAlaAlaGluProLeuGlnSerVal ArGGGGCGCGGGGGGGGGGGGGCGCTGCAATCCGTG CSTGAGCCTGGAGCCGCGGGGGCGCTGCTGCTGGGG GlyAlaGlyAlaPhrCAlaArgAlaArgAlaCysSerValPro GGAGCGGGCCCCCGGGGGGGGGGGGGGGGGGGGGGGGG | Length: Matches: Conservative: Mismatches: Indels: Gaps: -4429) ProleuglnSerVall | 10 (1-517) x ADJ96598 (1-429)   Matches: 0   0   0   0   0   0   0   0   0   0 | 20<br>151<br>151<br>60<br>271<br>100<br>1120<br>1120<br>1120<br>1140<br>1140<br>1160<br>1160 |
|----------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------|--------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------|
| 8 & 8                                                                                                                                                    | 181 632                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Asnileasplysiyzi                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | AspGlyllevalCyst                                                                 |                                                                                | 200                                                                                          |
| ò                                                                                                                                                        | 201                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | .LevHisGlyLevIle(                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | GlyArgThrGlnArg(<br>                                                             | SerGluvalleuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyvalAspGlnAsn :<br>             | 220                                                                                          |

18-NOV-2004 (first entry)

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| ДQ             | 692                | AGCGAGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGCGCCCGGGGTCGACCAGAAC 751                    |
|----------------|--------------------|--------------------------------------------------------------------------------------|
| ò              | 221                | oSerSerLeuArglleGlyllelleProAlaGlySer 2                                              |
| q              | N                  | 81                                                                                   |
| ò              |                    | rValGlyThrSerAspAlaGluThrSerAlaLeuHis 26                                             |
| qq             | 812                | ACGACTGCGTGTGTTACTCCACCGTGGGCACCAGCGACGCAGAAACCTCGGCGCTGCAT 871                      |
| ò              | 261                | 2                                                                                    |
| QQ             | 872                | ATCGTTGTTGGGGGACTCGCTGGCCATGGATGTCCTCACTCA                                           |
| ò              | 281                | LeuargTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspIleIleLysAspSer 300                     |
| Ор             | 932                | CTTCGCTACTCCGTGTCCCTGCGCTACGGCTTCTACGGGGACATCATCAAGGACAGT 991                        |
| ò              | 301                | 101 GluLystysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThrPheLeu 320                 |
| ф              | 992                | gagaagaaacggtgggttggggtcttgccagatacgacttttcaggtttaaagaccttcctc 1051                  |
| ò              | 321                | $\sim$                                                                               |
| g              | 1052               | teccaccactactatgaagggacagtecttectecetecacacacgetgggatet 1111                         |
| ò              | 341                |                                                                                      |
| g              | 1112               | CCAAGGGATAGGAAGCCCTGCCGGGCAGGATGCTTTGTTTG                                            |
| ò              | 361                | LeuGluGluGluGlnLygLygAblaLeuTyrGlyLeuGluAlaAlaGluAspValGluGlu 380                    |
| ф              | 1172               | crodaggaggagagadaagaggacrorarargarrogaagcrocoggaggaggaggaggaggaggaggaggaggaggaggagga |
| ò              | 381                | TrpGlnValValCysGlyJysPheLeuAlaileAsnAlaThrAsnMetSerCysAlaCys 400                     |
| QQ             | 1232               | TGGCAAGTCGTCTGTGGAAGTTTCTGGCCATCAATGCCACAAGATGTCCTGTGCTTGT 1291                      |
| ò              | 401                | ArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSerAspLeu 420                     |
| qq             | 1292               | 13                                                                                   |
| ò              | 21                 | 440                                                                                  |
| дg             | 1352               | 14                                                                                   |
| ò              | 441                | 46                                                                                   |
| đ              |                    | CCAGTTT 14                                                                           |
| ò              | 461                | PriysHisMetGluAspGluAspSerAspLeuLysGluGlyGlyLysLysArgPhe 4                           |
| qq             | 1472               | GAAGCGCTTT 15                                                                        |
| ò              | -                  |                                                                                      |
| d<br>G         | 1532               | crccreeaac 1                                                                         |
| ઠે             | 501                | sGlnLeuVal 52                                                                        |
| qq             | 92                 | ccaecreerr 1                                                                         |
| ò              | 521                | ArgLeuPheAlaArgGly1leGluGluAanProlysProAspSerHisSer 537                              |
| <u>අ</u> ,     |                    |                                                                                      |
| RESUL<br>ADPSS | T 4<br>247<br>ADP5 | standard: CDNA: 4445 BP.                                                             |
| XX             | 555                |                                                                                      |
| ₹ X I          | F5524              |                                                                                      |

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Human PRO cDNA sequence SEQ ID NO:1223
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human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antiansemic; antiarthritic; antiatsthmatic; antidiabetic; antiallergic; antiantiansemostatic; antidiabetic; antialflammatory; antipsoriatic; antithyroid; CNS; dermatological; gastrointestinal; antirheumatic; haptotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; virucide; gene therapy; gene; ss.

Homo sapiens.

WO2004039956-A2.

28-OCT-2003; 2003WO-US034381 13-MAY-2004

29-OCT-2002; 2002US-0422472P.

(GETH ) GENENTECH INC

Gurney AL, Schoenfeld J, Williams PM; Aggarwal S, Clark H, Wood WI, Wu TD;

WPI; 2004-376182/35. P-PSDB; ADP55248 PRO polynucleotides and polypeptides, useful in useful in diagnosing treating an immune related disease, e.g. systemic lupus hematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response. erythematosus, New and

Claim 2; SEQ ID NO 1223; 3009pp; English.

The present invention describes an isolated PRO nucleic acid (1). Also described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4); (7) a comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a mammal; (10) a method for determining the presence of a PRO polypeptide in a sample suspected of having the presence of a PRO polypeptide in a sample suspected of faving the polypeptide; (11) a method of identifying a compound that inhibits or mammal; (12) a method of identifying a compound that inhibits or minics the activity of or expression of a gene encoding a PRO polypeptide; and (13) a method of stimulating the immune response in a mammal; (12) a method of stimulating the immune response in a mammal; (13) a method of stimulating the immune response in a mammal; (13) a method of stimulating the immune response in a mammal; (14) a method of stimulating the immune response in a mammal; (15) a method of stimulating the immune response in a mammal; (16) a method of stimulating the immune response in a mammal; (17) a method of stimulating the immune response in a mammal; (18) a method of stimulating the immune response in a mammal; (18) a method of stimulating the immune response in a mammal; (18) a method of stimulating the immune response in a mammal; (18) a method of stimulating the immune response in a mammal; (18) a method of stimulating the immune response in a mammal; (18) a method of stimulating the immune response in a mammal; (18) a method of stimulating and subsective antistribution; antistribution; antistribution; antirheumatic, antithyroid, CNS, dermatological, gastrointestinal, haemostatic, hepatotropic, immunostimulant, immunosupressive, muscular, nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid (I) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune related disease and in stimulating an immune response. The present sequence represents a human PRO nucleotide sequence from the present invention.

| S S    | Sequence 4445 BP; 1018 A; 1134 C; 1216 G; 1077 T; 0 U; 0 Other; | 4445 E  | 3P;        | 1018 A  | , 113 | ς; | 1216          | 'n  | 1077 | Ţ, | 0    | <br>0 | ther; |  |
|--------|-----------------------------------------------------------------|---------|------------|---------|-------|----|---------------|-----|------|----|------|-------|-------|--|
| Alic   | nment Scor                                                      | es:     |            |         |       |    |               |     |      |    |      |       |       |  |
| Prec   | Pred. No.:                                                      |         |            | 2.63e   | -254  |    | Length:       | ;;  |      | 4  | 4445 |       |       |  |
| Score: |                                                                 |         |            | 2888.00 | 00    |    | Matches:      | : 8 |      | m  | 537  |       |       |  |
| Perc   | Percent Similarity:                                             | arity:  |            | 100.00% | *0    |    | Conservative: | Z   | ive  |    | _    |       |       |  |
| Best   | : Local Sin                                                     | nilarit | : <u>`</u> | 100.0   | 80    |    | Mismatches    | che | : 83 | 0  | _    |       |       |  |
| One    | Ouery Match:                                                    |         |            | 100.0   | *0    |    | Indels:       |     |      | ٥  | _    |       |       |  |
| , DB:  |                                                                 |         |            | 13      |       |    | Gaps:         |     |      | 0  | _    |       |       |  |
|        |                                                                 |         |            |         |       |    |               |     |      |    |      |       |       |  |

| -10-631- | 958-10 ( | 1-537) x ADP55247 (1-4445)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|----------|----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ò        | 1 MetG   | 1yalaThrGlyAlaalaGluProLeuGlnSerValLeuTrpValLysGlnGlnArg 20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|          | 124 ATGG | 3GGCAACGGGGGGGGGGGGCGCTGCTGTGTGTGTGTGTGTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| È        | 21 CysA  | avalSerLeuGluProAlaArgAlaLeuLeuArgTrpTrpArgSerProGlyPro 40                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|          | 184 TGCG | CCGTGAGCCTGGAGCCCGCGCGCGCTCTGCTGCTGGTGGCCGAGCCCGGGGCCC 243                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| ζ        | 41 GlyA  | IndivalaProGlyAlaAspAlaCysSerValProValSerGluIleIleAlaVal 60                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|          | 244 GGAG | ccecccccceccecececrecrecretrereraterradatearcerer 303                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| ζ        | 61 GluG  | luThrAspValHisGlyLysHisGlnGlySerGlyLysTrpGlnLysMetGluLys 80                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|          | 304 GAGG | aaacagacettcacgggaaacatcaaggcagtggaaaatggcagaaaatggaaaag 363                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|          | 81 ProT  | yralapheThrValHisCysValLysArgAlaArgArgHisArgTrpLysTrpAla 100                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|          | 364 CCTT | ACGCTTTTACAGTTCACTGTGTAAAGAGAGCACGACGGCACCGCTGGAAGTGGGCC 423                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|          | 101 GlnV | alThrPheTrpCysProGluGluGlnLeuCysHisLeuTrpLeuGlnThrLeuArg 120                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|          | 124 CAGG | IGACTTICTIGGIGICCAGAGGAGCAGCTGTGTCACTTGTGGCTGCAGACCCTGCGG 483                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| <u>ئ</u> | 121 GluM |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|          | 184 GAGA | rgcrggagaagcrgacgaccaagaccarrracrggrarrrarcaacccgrr 543                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|          | 141 G1yG | yLysGlyGlnGlyLysArglleTyrGluArglysValAlaProLeuPheThrLeu 160                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|          | s44 GGAG | saaaagaacaagacaagagararargaaagaaagagagaacaacrarcaccrra 603                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|          | 161 Alas | prileThrThrAspIleIleValThrGluHisAlaAsnGlnAlaLysGluThrLeu 180                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|          | so4 GCCT | ccarcaccacreacarcarracreaacarecraarcaeeccaaeeacare 663                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|          | 181 TyrG | UI  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASII  BASIII   BASIII   BASIII  BASIII  BASIII  BASIII  BASIII  BASIII  BASIII  BASIII  BASIII  BASIIII  BASIIII  BASIII  BASIII  BASIIII  BASIII  BASIII  BASIII  BASIII  BASIII  BASIIII  B |
|          | s64 TATG | Agarriaacaragacaaaracgacgcarcgrcrccrcccgcgggggargrarcrrc 723                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|          | 201 SerG |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|          | 724 AGCG | AGGTGCTGCACGGTCTGATTGGGAGGACGCAGAGGAGCGCCGGGGTCGACCAGAAC 783                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|          | 221 HisP | roArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAlaGlySer 240                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|          | 784 CACC | ccedacraracracracracracraca atraca atraca atraca at 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|          | 241 ThrA | ppCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAlaLeuHis 260                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|          | 844 ACGG | Acrecereierracrececeresecaeceaeaeaeaeaeaeaeaeaeaeaeaeae 903                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| ζ        | 261 11eV | 261 IleValValGlyAspSerLeuAlaMetAspValSerSerValHisHisAsnSerThrLeu 280                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|          | 904 ATCG | ITGITGGGGACTCGCTGGCCATGGATGTGTCCTCAGTCCACCACACAGCACACTC 963                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|          | 281 LeuA | rgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAspIleIleLysAspSer 300                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|          | 964 Crrc | acracicerererecrecrescraceerrerererescarcarcarcaererere                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|          | 301 Glub | ysbysArgTrpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThrPheLeu 320                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 1        | 024 GAGA | AGAAACGGTGGTTGGGTCTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTC 1083                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ٥٠       | 321 SerH | IsHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrValGlySer 340                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 7        | 384 ŤČČĆ | ACCACTGCTATGAAGGGACAGTGTCCTTCCTCCCTGCACAACACACGGTGGGATCT 1143                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 'n       | 341 ProA | rgAspArgLysProCysArgAlaGlyCysPheValCysArgGlnSerLysGlnGln 360                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |

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(GOOD/) GOODRICH R W.
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this invention relates to the CDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system disease. Givention is useful for treating central and peripheral nervous system disease, amyotrophic diseases (e.g. peripheral nervopathy, Huntington's disease, amyotrophic clateral sclerosis); neurodegenerative disease (e.g. parkinson's disease, amyotrophic content of particles of systemic lupus services, burns; bone disorders (e.g. systemic lupus) certhematosid arbhritis, insulin-dependent diabetes mellitus); wounds, ulcers, burns; bone disorders (e.g. osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head trauma); lung or liver fibrosis; reperfusion injury in various tissues; cancer and tumours; and inflections; allergic conditions such as allergic rhinitis, asthma; coagulation disorders (e.g. septic shock, Crohn's disease, anaphylaxis). The protein may be used to inhibit the growth, inflection or function of infections agence such as bacteria, fungi, viruses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have

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Cycles of thythms sequences of the invention are useful for expressing recombinant protein for analysis. The present sequence is an expressed of human cDNA sequence of the invention, this sequence is an expressed of sequence tag (EST) and was identified using subtractive hybridisation
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                                                                                                     Novel polypeptide useful for treating neurodegenerative diseases, myeloid or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.
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    Ren F;
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  Zhao QA, R
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Zhou P, Asundi V,
Wehrman T, Wang J,
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This sequence represents cDNA encoding a human ceramide kinase designated hCERKI. The invention relates to hCERKI, nucleic acids encoding it, expression vectors and host cells containing hCERKI nucleic acids, the recombinant production of hCERKI and antibodies specific for hCERKI. The invention also encompasses methods of isolating hCERKI from samples, the use of hCERKI in drug screening, and the use of hCERKI nucleic acid sequences in gene therapy. hCERKI mediates the ATP-dependent 1 phosphorylation of ceramides and can be used to screen for therapeutic and preventive agents for a wide range of disorders. Such disorders include neurological disease, inflammation, human immunodeficiency virus (HIV) infection, type 2 diabetes, obesity, sepsis, arteriosclerosis and
                                                                                                                                                                                                                                                                                                               Human, ceramide kinase, hCERKI; drug screening, gene therapy; neurological disease; inflammation; human immunodeficiency virus; HIV infection; type 2 diabetes; obesity; sepsis; arteriosclerosis; cancer; neuroprotective; antiinflammatory; anti-HTV; antidiabetic; anorectic; antibacterial; antiseptic; antiarteriosclerotic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ceramide kinase gene and the enzyme encoded by it for screening substances as drugs for neurological, inflammatory and other disorders.
                                                             CysAspGlyGluValLeuHisSerProAlaIleGluValArgValHisCysGlnLeuVal
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/product= "Human ceramide kinase hCERK1"
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18-OCT-2001; 2001US-0339105P.
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24-OCT-2001; 2001US-034362P.
25-OCT-2001; 2001US-034362P.
29-OCT-2001; 2001US-03436357P.
01-NOV-2001; 2001US-03436357P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UW; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B; Ji M, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenborg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen A, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2004-213931/20. P-PSDB; ADN62845 Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

Claim 20; SEQ ID NO 39; 395pp; English.

GAGATGCTGGAGAAGCTGACGTCCAGACCAAAGCATTTACTGGTATTTATCAACCGTTT 495

436 141

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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abbrrant expression and activity of NOVX by supplementing the patient our polymucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptides antibodies, agonists and antagonists may also be used as antigens in the antigenides. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polypeptide antibodies may be used in this way to prevent, clagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymucleotide may be used in this way to prevent, disquesse, nancers, cancer, dispecters, diabetes, obesity, infectious dispense, anorexia, cancer, cancer associated cachexia, meurodegenerative discuters, associated cachexia, meurodegenerative chaematopoietic disorders, and the various dyslippidaemias, metabolic wasting disorders associated with obesity, the metabolic syndome X and various cancers. They may also be used as antibactorial agents. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetGlyAlaThrGlyAlaAlaGluProLeuGlnSerValLeuTrpValLySGlnGlnArg
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents DNA encoding a human NOVX protein
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Human; sphingosine kinase; SphK; restenosis; ischaemia; gene therapy; antisense therapy; cancer; sphingolipid; signalling molecule; apoptosis; cytostatic; tumour necrosis factor-alpha; TNF; atherosclerosis; lymphoma; leukaemia; vasotropic; cell proliferative disorder; vascular disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated Sphingosine kinase polypeptide useful for treating a SphK-associated disorder especially cancer, restenosis or ischemia in a human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to sphingosine kinase (SphK) polypeptides and nucleic acids encoding them. SphK is useful for treating a SphK-sesociated disorder especially cancers such as leukaemia, lymphoma, ovarian, breast, lung, colon, testicular, stomach and skin, atherosclerosis, restenosis or ischaemia and cell proliferative disease or disorder associated with vascular diseases. SphK gene is used in gene therapy and antisense-therapy. Sphingolipids serving as signalling molecules, have recently emerged as regulators of cell growth, diverse cell phenotypes and cell death. Activation of SphK by tumour necrosis factor (TMF) -lipha inhibits apoptosis in human endothelial cells. The present sequence is human sphingosine kinase
 Location/Qualifiers
109. .1524
/tag= /
/product= "Human sphingosine kinase (SphK)
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22-MAR-2000; 2000US-0191261P.
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                                                    TyrGlulleAsnIleAsplysTyrAspGlyIleValCysValGlyGlyAsp-GlyMetPh
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protein #2"

61 AlaGlyAlaProGlyAlaAspAlaCysSerValProValSerGluIleIleAlaValGlu

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| 1081 ATCAATGCCACAAACATGTCCTGTGCTTGTCGCCGGAGCCCTCTCCCCGGCT 1140   | 531 ProbysProAspSerHisSer 537  [ | KW cancer; therapy; diagnosis; ds.  XX  XX  XX  Homo sapiens.  Y11453  FT CDS 711453  XX  XX  W0200052173-A2.  XX  O8-SEP-2000.  XX  Y2 02-MAR-2000; 2000WO-CA000223.  XX  XX  XX  XX  XX  XX  XX  XX  XX                                                                                                                                                                                                                                                                                                                                                                                                  | (ALLX ) NPS ALLELIX CORP.  Munroe D, Gupta A, Falzone GR;  Munroe D, Gupta A, Falzone GR;  WPI; 2000-572185/53.  P-PSDB; AAY96059.  New human sphingosine kinase A, B and C polynucleotides and polypeptides useful in e.g. chromosome and gene mapping, and detecting inflammation or disease associated with abnormal levels of sphingosine kinase expression.  Disclosure; Fig 7; 81pp; English.  The present sequence is that of an isolated polynucleotide encoding human cypingosine kinase C (SKC, see AAY96059), an enzyme that phosphorylates |
|------------------------------------------------------------------|----------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 60<br>81<br>120<br>101<br>180<br>121<br>240<br>141<br>300<br>161 | 1                                | ThrserasphlaguthrsexhlaLeuHislleValValGlyAspSerLeuAlaMetAsp 270  ThrserasphlaguthrsexhlaLeuHislleValValGlyAspSerLeuAlaMetAsp 270  ACCAGCGACGACAAACCTCGCGCGCTGCTGTTGTTGTGTGGGGCTCGCTGGCCATGGT 720  ValSerSerValHisHisMasnSerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyr 290  GTGTCCTCAGTCCACACACACACTCCTTCGCTACTCCTGCTGCTCGCTGGGCTAC 780  GJyPheTyrGlyAspIleIleIleLySaspSerGluLySLySArgTrpLeuGlyLeuAlaArg 310  GJyPheTyrGlyAspIleIleIleLySaspSerGluLySLySArgTrpLeuGlyLeuAlaArg 310  GGCTTCTACGGGGACATCATCAAGGACAGTGAGAAACGGTGGTTGGGTTTGCCAGA 840  TyrAspPheSerGlyLeuLysThrPheLeuSerHisHisCySTyrGluGlyThrValSer 330 | 1acly 350<br>      <br>Cacca 960<br>      <br>      <br>TGTAT 1020<br>euala 390<br>      <br>TGGCC 1080                                                                                                                                                                                                                                                                                                                                                                                                                                                |

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sphingosine to form sphingosine 1-phosphate. The polynuclectide was isolated from an HeLa cDNA library by PCR amplification. The invention provides polynuclectides (see AAX50508-10) and polypeptides (see AAX96057-59) for the human sphingosine kinase (SK) homologues SKA, SKB and SKC. The polynuclectides may be used as hybridization probes, in the construction of PCR primers for chromosome and gene mapping, in the recombinant production of SKA, SKB and SKC, and in the generation of antisense DNA or RNA. They can be used to detect inflammation or disease differences in gene sequence between normal and carrier or affected individuals. Host cells expressing SK can be used in drug screening. Human SK specific antibodies, inhibitors, ligands or their analogues are useful as bioactive agents to treat inflammation or disease including curstly bacterial or fungal infections, allergic responses, mechanical injury associated with trauma, hereditary diseases, lymphoma or carcinoma, and other conditions with activate the genes of kidney, lung,
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                                                                                                                                                  A Y;
                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic DNA of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
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                                                                                                                                                                                                                                               New polynucleotide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
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Chen R, Zhao
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P-PSDB; ADS11054.
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LeuAlaArgTyrAspPheSerGlyLeuLysThrPheLeuSerHisHisCysTyrGluGly
                                              crifeccadaracdacriricaderriraaadaccrirerereceaecaeracrardaaggg
                                                             ThrValSerPheLeuProAlaGlnHisThrValGlySerProArgAspArgLysBroCys
                                                                                                    ArgalaGlyCysPheValCysArgGlnSerLysGlnGlnLeuGluGluGluGlnLysLys
                                                                                                                                       AlaLeuTyrGlyLeuGluAlaAlaGluAspValGluGluTrpGlnValValCysGlyLys
                                                                                                                                                                           PheLeuAlaIleAsnAlaThrAsnMetSerCysAlaCysArgArgSerProArgGlyLeu
                                                                                                                                                                                      TTTCTGGCCATCAATGCCACAAACATGTCCTGTGCTTGTCGCCGGAGCCCCAGGGGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #13532.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 13532; 103pp; English.
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Drmanac RT, Liu C,
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Seguence 2241 BP; 453 A; 627 C; 700 G; 461 T; 0 U; 0 Other;

| Alignment S<br>Pred. No.:                | Scores:                                       | 2.73e-205                                    | Length:<br>Matches.          | 2241<br>471                                                          |     |
|------------------------------------------|-----------------------------------------------|----------------------------------------------|------------------------------|----------------------------------------------------------------------|-----|
| Percent Similarity<br>Best Local Similar | Percent Similarity:<br>Best Local Similarity: | 64.50%<br>63.82%                             | Conservative:<br>Mismatches: |                                                                      |     |
| Query Match:<br>DB:                      |                                               | 81.35%<br>5                                  | Indels:<br>Gaps:             | 255<br>5                                                             |     |
| US-10-631-9                              | 58-10 (1-537                                  | US-10-631-958-10 (1-537) x AAS77728 (1-2241) | -2241)                       |                                                                      |     |
| ολ                                       | 1 MetGlyAla                                   | ThrGlyAlaAlaGluE                             | ProLeuGlnSerVal              | MetGlyAlaThrGlyAlaAlaGluProLeuGlnSerValLeuTrpValLysGlnGlnArg 2       | 20  |
| qa                                       | 83 ATGGGGGCG                                  | ACGGGGGGGGGGAGC                              | CCGCTGCAATCCGTG              | ATGGGGGGGGGGGGGGGGGGGGGGGGGTGCATCCGTGGGTGTGGGGGGGG                   | 42  |
| ò                                        | 21 CysAlaVal                                  | SerLeuGluProAla                              | ArgAlaLeuLeuArg              |                                                                      | 40  |
| Db 1                                     | 143 TGCGCCGTG                                 | AGCCTGGAGCCCGCGC                             | GGGCTCTGCTGCGC               |                                                                      | 202 |
| ò                                        | 41 GlyAlaGly.                                 | AlaProGlyAla                                 |                              | GlyAlaGlyAlaProGlyAla                                                | 47  |
| Db 2                                     | 203 GGAGCCGGC                                 |                                              | CTCACCAAGGCCCAG              | ACCT                                                                 | 261 |
| δ                                        | 47                                            |                                              |                              | 4 4                                                                  | 47  |
| Dp 5                                     | 62 AGCACTGGT                                  | TATTTGCAGTATGTT                              | rccaagactgggcag              | 262 AGCACTGGTTATTTTGCAGTATGTTCCAAGACTGGGCAGCGTTTACACCTTCTGTTTAGC 3   | 321 |
| ò                                        | 47                                            |                                              |                              | 4                                                                    | 47  |
| 3<br>3                                   | 22 TGGTTTCTC                                  | TGGCACTGCTCCAGCA                             | AGGGAACGCCGCTGG              | 322 TGGTTTCTCTGGCACTGCTCCAGCAGGGAACGGCGCTGGTACTGCCAGGGGCCTGCACCC 381 | 81  |
| ò                                        | 47                                            |                                              |                              | 4                                                                    | 47  |

 

| Qy 274 ValHisHisAsnSerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyr 2 | 294                                                 | Qy 314 SerGlyLeuLysThrPheLeuSerHisHisCysTyrGluGlyThrValSerPheLeuPro 3 | Qy         334 AlaGlnHisThrValGlySerProArgAspArgLy8ProCysArgAlaGlyCysPheVal 3 | Oy 354 CysArgGlnSerLysGlnGlnLeuGluGluGluGluGlnLysLysAlaLeuTyrGlyLeuGlu 3 | Oy 374 AlaAlaGluAspValGluGluTrpGlnValValCysGlyLysPheLeuAlaIleAsnAla 3 | Oy 394 ThrAsnMetSerCysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeu (                                                    | Oy 414 GlyAspGlySerSerAspLeuIleLeuIleArgLyScysSerArgPheAsnPheLeuArg 4 | Qy         434 PheLeuileArgHisThrasnGlnGlnAspGlnPheAspPheThrPheValGluValTyr | Oy 454 ArgValLysIysPheGlnPheThrSerLysHisMetGluAspGluAspSerAspLeuLys ( | Qy         474 GluGlyGlyLysLysLysPheGlyHisIleCysSerSerHisProSerCysCysCysThr ' | Qy 494 ValSerAsnSerSerTrpAsnCysAspGlyGluValLeuHisSerProAlaIleGluVal 4 | Qy 514 ArgValHisCysGlnLeuValArgLeuPheAlaArgGlylleGluGluAsnPro 531 | RESULT 12 ACC70838 ID ACC70838 standard; DNA; 3975 BP. XX | AC ACC70838;<br>XX XX DT 20-NOV-2003 (first entry) | Ē                                                                           | <pre>KW Human; enzyme; haemostatic; sphingosine kinase 4; SPHK4; KW platelet transfusion; platelet stabiliser; gene; ds. XX</pre> | sapiens. | FH Key Location/Qualifiers FT CDS 1. 1251 FT /*tag a /*tag a /*tag a /*roduct = "Sphinoosine kinase 4" | / product                                                              |
|-----------------------------------------------------------------------|-----------------------------------------------------|-----------------------------------------------------------------------|-------------------------------------------------------------------------------|--------------------------------------------------------------------------|-----------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------|-----------------------------------------------------------------------------|-----------------------------------------------------------------------|-------------------------------------------------------------------------------|-----------------------------------------------------------------------|-------------------------------------------------------------------|-----------------------------------------------------------|----------------------------------------------------|-----------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|----------|--------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------|
| 47                                                                    | CAGCTGCTGACTCTGCAGGCTTGCAGCGAGCGGGCCTGCTGTGGATCTCTG | GTGTCCCCGGTTCACTGCCTGTTTCTTGTTCTTGTCCAGAGCTATCAGTCATAGCGGGA           | 562 CGGGAGCTGATGCAGGTTTCCCGCGACCTGACAGGATGGGGACGGCGCGGTTC 621  48             | SerGlullelleAlaValGluGluThrAspValHisGlyLySHisGlnGlySerGlyLyS<br>         | TrpGlnLysMetGlutysProTyralaPheThrValHisCysValLysArgArgArg             | IGGCRGMARIGGRANGCCIIACGCIIICCAGIGIRANGGRANGCCACGACGG<br>HisArgTrpLySTrpAlaGlnValThrPheTrpCysProGluGluGlnLeuCysHisLeu<br> | TrpLeuGlnThrLeuArgGluMetLeuGluLygLeuThrSerArgProLysHisLeuLeu          | TGGCTIGCAGACCCTGCGGGAGATGCTGGAAGCTG                                         | 89/                                                                   | GlnAlaLysGluThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIleValCysVal 19               | hrGlnArgSer 21                                                        | Leuargilegly 234                                                  |                                                           |                                                    | 1156 GÁCTGCGTGTGTTACTCCACGTGGGCACCAGCAGGAAACCTGGGGCTGCATATC 1215 262 ValVal |                                                                                                                                   | 263 263  | 1276 AGTGGGCACGGGCAGCTGTGGCTGCCAGCTGTGGAACGCATGCCTGTGAGGCC 1335 264                                    | 1336 TCGAGGCTTCAGTCCAGGATGCAGAGCCCCGGGGACTCGCTGGCCATGGATGTGTCCTCA 1395 |

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                                                                                                                                                                                                                The present sequence is the coding sequence for human sphingosine kinase 4 (SPHK4). The kinase can be used for the diagnosis and treatment of sphingosine related disorders. The kinase can also be potentially used for controlling toxicity of platelet transfusion and as a platelet
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                                                                                                                                                                                                                                                                      The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, ollowers, and for chomosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving abberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations capposed and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patient did not appear in the printed specification, but was obtained in constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of
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                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                  Human sphingosine kinase-like protein; intracellular signalling; gene; cell proliferation; apoptosis; cancer; allergy; cytostatic; asthma; autoimmune disease; rheumatoid arthritis; Parkinson's disease; ss.
              New reagent for modulating the activity of sphingosine kinase-like protein polypeptide or polynucleotide and treating cancer, asthma, allergy, an autoimmune disease, or a central or peripheral nervous disorder.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                           AGCAGCATCCCCCCACACACGTGTGTGGACATGCCACAGCATCCGCGGGAGAAAAC 496
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                                    161 AlaSerIleThrThrAspIleIleValThrGluHisAlaAsnGlnAla-LysGluThrLe 180
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                                                                                                    uTyrGluIleAsnIleAspLysTyrAspGlyIleValCysValGlyGlyAspGlyMetPh
                                                                                                                                                                                            572 AAACCACCCGCGTCCCGCCATACTGCCT--------GTGGCAGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed centers. (I) is useful in gene therapy techniques to restore normal certifying of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, foreanise, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Matches:
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ACCAACCAGCAGGACCAG 979
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Best Local Similarity:
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23-AUG-2000;
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                                                                                                                     AAS77731;
                   962
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Search completed: September 6, 2005, 11:25:27 Job time : 893.053 secs This Page Blank (uspto)

5, 2005, 23:41:54 ; Search time 1512.64 Seconds (without alignments) 2324.913 Million cell updates/sec OM protein - nucleic search, using frame\_plus\_p2n model September Run on:

2888 1 MGATGAAEPLQSVLWVKQQR......QLVRLFARGIEENPKFDSHS 537 US-10-631-958-10 **BLOSUM62** Perfect score: Scoring table: Sequence:

0.5 0.5 0.0 0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

14677368 Total number of hits satisfying chosen parameters: 7338684 segs, 3274456166 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE-pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=cbc -NORM=ext -HEAPSIZE=500 -MINLEN-0
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-NCPUG=6 -IPCUP=3 -NO MMAP -LARGEQUERY -NGG\_SCORES=0 -WAIT -DSPBLOCK=100
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:\*

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11: /cgn2\_6/ptodata/1/pubpna/USO9\_PUBCOMB.seq:\*
12: /cgn2\_6/ptodata/1/pubpna/USO9\_PUBCOMB.seq:\*
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15: /cgn2\_6/ptodata/1/pubpna/USO9\_PUBCOMB.seq:\*
16: /cgn2\_6/ptodata/1/pubpna/USO9\_PUBCOMB.seq:\*
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18: /cgn2\_6/ptodata/1/pubpna/USO9\_PUBCOMB.seq:\*
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27: /cgn2\_6/  Pred. No. is the number of results predicted by chance to have a

/cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seg:\*

prodata/1/pubpna/US11A FUBCOMB.seq: prodata/1/pubpna/US11 NEW PUB.seq:\* prodata/1/pubpna/US60\_NEW\_PUB.seq:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result<br>No.    | Score                                                        | i i                   | Len           | 08             | SUMMARIES                                 | Description       |
|------------------|--------------------------------------------------------------|-----------------------|---------------|----------------|-------------------------------------------|-------------------|
| -                | ıa                                                           | 10                    | 15            |                | 908-090-0                                 |                   |
| 1 72             | 2888                                                         |                       | 1614          | 13             | )-631-958<br>)-631-958                    | 25                |
| e                | - σο                                                         | 00                    | 74            | 18             | 0-262-511-3                               | equence           |
| ₹ 1              | Φ,                                                           | 99                    | 41            | 01             | 968-696-6                                 | equence 1         |
| ח ע              | pο                                                           | 9 6                   | 4 T           | 7 5            | 7-631-958-1<br>7-618-941-5                | equence           |
| 7                | 000                                                          | 6                     | 43            | 17             | 0-120-988-1                               | equence 1         |
| 80               | 28                                                           | 6                     | 46            | 16             | -315-597A-1                               | Sequence 1        |
| σ,               | 649                                                          | <u>.</u>              | 84            | 6              | .784-810A                                 | -                 |
| 0:               | 00 0                                                         | ٠,                    | 8 8           | 5 5            | 0-876-281                                 | .,,               |
| 11               | 940                                                          |                       | 7 6           | 9 6            | 7-964-896<br>7-621-958                    |                   |
| 7 7              | ֓֞֜֞֜֜֜֜֜֜֓֓֓֜֜֜֜֜֜֓֓֓֓֜֜֜֜֜֓֓֓֡֜֜֜֓֓֓֡֓֜֜֡֓֡֓֡֓֜֡֡֡֓֡֓֡֡֡֡֡ |                       | 7.18          | 7 -            | 7-631-936<br>7-115-635                    | , ·               |
| 14               | 200                                                          |                       | 550           | 101            | 8-968-696-6                               | ·w                |
| 15               | 871                                                          | 6                     | 550           | 13             | -631-958                                  | ·w                |
| 16               | 811                                                          | ω.                    | 474           | 10             | 968-696-6                                 | v.                |
| -                | 811                                                          |                       | 474           | 13             | 1-631-958                                 | Seguence 4        |
| 0 t              | 929                                                          |                       | 522           | ດ ເ            | .784-810A                                 |                   |
| ٦ ،              | ع ه                                                          | · -                   | 2 2           | 20             | )-8/6-281-/<br>)-425-115-1764             |                   |
| 21               | 573.5                                                        | . 6                   | 2079          | 18             | 0-425-114-34530                           |                   |
| 22               | 73                                                           | 6                     | 6             | 20             | 0-425-115-8621                            | w                 |
| 23               | 525                                                          | 18.2                  | 329           | 10             | US-09-969-896-5                           | Sequence 5, Appli |
| C 25             | . 6                                                          |                       | 2189          | 1 6            | )-631-336-3<br>)-437-963-9                | , 0               |
| N                | 437.5                                                        | 'n.                   | 56            | 22             | 1-477-445-46                              | Α.                |
| 27               | 99                                                           | ٠.<br>ش               | 83            | 13             | 0-437-963-306                             | 4.1.              |
| 8 6              | 389                                                          |                       | 96            | 2 6            | )-424-599-4 <i>1</i> 39<br> -425-115-6489 | 4. 4              |
| 30               | 371.5                                                        |                       | 1869          | 18             | )-425-113-8489<br>)-425-114-3480          | , i.,             |
| 31               | c.                                                           | ď.                    | 33            | σ              | -783-590-5271                             | .,                |
| 32               | 363                                                          | ∾.                    | 3362          | 50             | 0-425-115-29                              | -                 |
| 2,5              | 7                                                            | · -                   | 7 7           | 2 5            | 1-424-599-594I<br>1-425-115-6489          |                   |
| 35               | . 5                                                          |                       | 38            | i o            | -784-810A-9                               | ંજે               |
| 36               | 343.5                                                        | ä                     | 382           | 22             | 0-876-281-9                               | Sequence 5        |
| 37               | ന                                                            | ä,                    | 77            | 18             | 0-425-114-3408                            | -                 |
| 38               | 33                                                           | d.                    | 38            | 13             | 0-437-963-9514                            | ٠, ١              |
| ν c              | 330.5                                                        |                       | 200           | J -            | 1-43/-963-/<br>1-435-114-3                | - (-              |
| 41               | 26                                                           | ; ;                   | 2 2           | 202            | 125-115-9784                              |                   |
| 4.2              | 3                                                            |                       | 91            | 13             | 0-437-963-5870                            |                   |
| 43               | 319                                                          | ä                     | 2609          | 17             | -348-052-25                               |                   |
| 44               | n                                                            | ή.                    | 9             | 13             | -622-011-25                               | -                 |
| 45               | 316.5                                                        | ή.                    | 28            | 70             | )-425-115-7                               | 41                |
|                  |                                                              |                       |               |                | ALIGNMENTS                                |                   |
| RESULT           | 1                                                            |                       |               |                |                                           |                   |
| Sedne :          | US-09-969-896-9<br>; Sequence 9, Application                 | ,<br>pplicat          | ion US/       | 660            | 96869                                     |                   |
| ; Publi<br>GENER | cation N                                                     | Io. US2003<br>MATION: | )0301255<br>: | 333A]          |                                           |                   |
| , APPL           | , APPLICANT: Kossida, Sophia                                 | cossida,              | Sophie        |                |                                           |                   |
| TITE             | E OF INV                                                     | ENTION:               | Kinas         | 10171<br>36-Li | n or numan spaingosine<br>ike Protein     |                   |
| FILE             | REFEREN                                                      | CE: 004               | 1974.005      | 594            | 9                                         |                   |
| CURR             | ENT FILL                                                     | NG DATE               | 3: 2001       | 100            | 60'60                                     |                   |
| , PRIC           | R APPLIC                                                     | ATION N               | VUMBER:       | Sn             | 50/238,005                                |                   |
| ; PRIC           | R FILING                                                     | DATE:                 | 2000-10       | 90-0           |                                           |                   |
| PRIC             | R FILING                                                     | DATE:                 | 2001-08       | 3-23           | 1,                                        |                   |
| , NUMB           | ER OF SE                                                     | N OI O                | )S: 16        |                |                                           |                   |

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LeuGluGluGluGlnIysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspValGluGlu 380
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Publication No. US20040192580A1

GENERAL INFORMATION:

TITLE OF INVENTION: Regulation of human Sphir

TITLE OF INVENTION: Kinase-Like Protein

TITLE OF INVENTION: Kinase-Like Protein

TITLE OF INVENTION: Kinase-Like Protein

FILE REFERENCE: 004974 00598

CURRENT APPLICATION NUMBER: US/10/631,958

CURRENT FILING DATE: 2001-06

PRIOR FILING DATE: 2001-06

PRIOR FILING DATE: 2001-06

PRIOR APPLICATION NUMBER: US 60/238,005

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2001-06

PRIOR FILING DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 1614
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                        ; TYPE: DNA
; ORGANISM: Homo sapiens
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                                   SerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrValGlySer
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US-10-262-511-39
Sequence 39, Application US/10262511
Sequence 39, Application US/10262511
Sublication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Peyman, John A.
APPLICANT: Li, Li Lingfang
APPLICANT: Li, Li Lingfang
APPLICANT: Li, Li Lingfang
APPLICANT: Batturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Blerman, Karen
APPLICANT: Blerman, Karen
APPLICANT: Gorman, Linda
APPLICANT: Cort, Taciana
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Zerhusen, Bayan D.
APPLICANT: Zhong, Mei
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| 376 CAGGTGACTTTCTGGTGTCCAGAGGAGCAGCTGTGTCACTTGTGGCTGCAGACCCTGCGG 435  121 GluMetLeuGluLysLeuThrSerArgProLysHisLeuLeuValPhelleAsnProPhe 140 | TyrGlulleAsnileAspLysTyrAspGlylleValCysValGlyGlyAspGlyMetPhe 2  | 201 SerGIUVAILENINGSYLEUIGEIGYAFGFINGSINARGSERTAGILYANGSGINASN 220 [                                                                                                                                                                           | 241 ThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAlaLeuHis 260                                                                                                                                                                   | LeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAsplle1leLysAspSer 300                                                                                                       | 976 GAGAAGAAGAAGATGGTTGGGTTGCCAGATACGACTTTTCAGGTTTAAAGACCTTCCTC 1035 321 SerHiaHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrValGlySer 340                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 361 LeuGluGluGluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspValGluGlu 380                                                | ArgargSerProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSerAspLeu                                                                      | 441 GlnGlnAspGlnPheAspPheThrPheValGluValTyrArgValLysLysPheGlnPhe 460                                                                         |
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| Db   1396 CAGCAGGACCAGTTTGACTTTGTTGAAGTTTATCGCGTCAAGAATTCCAGTTT 1455                                                                       | 521 ArgLeupheAlaArgGlyIleGluGluAsnProLysProAspSerHisSer 537<br> | NS-09-969-896-16 ; Sequence 16, Application US/09969896 ; Fublication No. US2000125533A1 ; GENERAL INFORMATION: ; APPLICANT: Kossida, Sophia ; TITLE OF INVENTION: Regulation of human Sphingosine ; TITLE OF INVENTION: Regulation of Protein | FILE REFERENCE: 004974.00594 ; CURRENT APPLICATION NUMBER: US/09/969,896 ; CURRENT FILING DATE: 2001-10-04 ; PRIOR APPLICATION NUMBER: US 60/238,005 ; PRIOR APPLICATION NUMBER: US 60/314,113 ; PRIOR APPLICATION DATE: 2001-10-08-23 | ; NUMBER OF SEQ ID NOS: 16 ; SCFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 16 ; LENGTH: 4413 ; TYPE: DNA ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-969-896-16 | Alignment Scores:  Pred. No.:  Score:  Score:  Percent Similarity:  Dest Local Similarity:  100.00\$  Mismatches:  Ouery Match:  100.00\$  Gaps:  Ogaps:   10-531-958-10 (1-537) X US-U9-959-895-16 (1-4413)    MetGlyAlaThrGlyAlaAlaGluProLeuGlnSerValLeuTrpValLysGlnGlnArg 2 | 136 TGCGCCGTGAGCCCGCGCGGGGCTCTGCTGCGCTGGTGGCGGGGCCCGGGGCCC 19  41 GlyAlaGlyAlaProGlyAlaAspAlaCysSerValProValSerGluIleIleAlaVal 60 | Oy 81 ProfyralaPheThrValHisCysValLysArgAlaArgArgHisArgTrpLysTrpAla 100   81 ProfyralaPheThrValHisCysValLysArgAlaArgArgHisArgTrpLysTrpAla 100 |

| 436 GAGATGCTGGAGGTGACGACGAAGCATTTACTGGTATTTATCAACCGGTTT 495 141 GlyGlyLysGlyGlnGlyLysArglleTyrGluArgLysValAlaBroLeuPheThrLeu 160                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CATAGACAATACGACGCATCGTGTGTGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 856 ATCGTTGTTGGGGCATGGATGTGTCCTCAGTCCACAACAGCACACACA                                                                                                                                                                                                                          | 1096   CCAAGGGATAGGAAGCCCTGCCGGCCAGGATGCTTGTTTGCTGGGGCAAGCAA                                           | 421 IleLeuIleArgLysCysSerArgPheAsmPheLeuArgPheLeuIleArgHisThrAsn 440 1336 ATCCTCATCCGGAAATGCTCCAGGTTCAATTTTCTGAGATTTCTCATCAGGCACCCAAC 1395 441 GlnGlnAspGlnPheAspPheThrPheValGluValTyrArgValLysPheGlnPhe 460                                                                                                                                                                                                   |
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| Qy         481 GlyHisIleCysSerSerHisProSerCysCysCysThrValSerAsnSerSerTrpAsn 500           Db         1516 GGGCACATTGCAGCCACCCCTCCTGCTGCTGCTCCTCCACACACTCCTGGAAC 1575           Qy         501 CysAspGlyGluValLeuHisSerProAlaileGluValArgValHisCysGlnLeuVal 520           Db         1576 TGCGACGGGAGGTCCTGCACACCCTGCCATCGAGGTCACACTGCCACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTTTTGCACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTACTGCTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTAC | RESULT 5 US-10-611-958-16 Sequence 16, Application US/10631958 Publication No. US2004019280A1 GENERAL INFORMATION: TITLE OF INVENTION: Regulation of human Sphingosine TITLE OF INVENTION: Regulation of human Sphingosine TITLE OF INVENTION: Regulation of human Sphingosine TITLE OF INVENTION: Regulation of human Sphingosine CURRENT APPLICATION NUMBER: US/10/631,958 CURRENT APPLICATION NUMBER: US/10/631,958 PRIOR APPLICATION NUMBER: US/09/969,896 PRIOR PILING DATE: 2000-10-04 PRIOR PILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: US 60/314,113 | PRIOR FILING DATE: 2010-0.3 NUMBER OF SEQ ID NOS: 16 SOFTWARE: FastSEQ for Windows SEQ ID NO 16 LENGTH: 4413 TYPE: DNA ORGANISM: Homo sapiens S-10-631-958-16 Lignment Scores: 0 core: 2888.00 ercent Similarity: 100.00\$ est Local Similarity: 100.00\$ est Match: 100.00\$ | 8-10 (1-537) x US-10-631-958-16 (1-4413)  MetGlyAlaThrGlyAlaAlaGluProLeuGlnSerValLeuTrpValLysGlnGlnArg | Db 196 GGAGCCGCCCCGGCGCGCATGCTCTGTGCCTGTATCTGAGATCATCGCCGTT 255  Qy 61 GluGluThrAspValHisGlyLy8HisGlnGlySerGlyLy8TrpGlnLy8MetGluLy8 80  256 GAGGAAACAGCTTCACGGGAAACATCAGGCAAAATGGAAAATGGAAAATGGAAAAGA 315  Qy 81 ProfyralaPheThrValHisCy8ValLy8AxgAlaArgAHisAxgTrpLy8TrpAla 100  Db 316 CCTTACGCTTTTACAGTTCACTGTGAAAGAGACCACGCCTGGAAGTGGAAGTGGAAGTGAAACGAGAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATTAAAAGAAAAAA |

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                                                                                 Sequence 55, Application US/10618941
Publication No. US20040197792A1
GERERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: CAENBEREL, SEAN
ITILE OF INVENTION: NOVEL KINASES
FILE REPERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
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LENGTH: 4429
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RESULT 7

US-10-120-988-148

Sequence 148, Application US/10120988

Sequence 148, Application US/10120988

SPUDICALION US/20030219745A1

SPUDICANT: Tang, Y: Tom

APPLICANT: Tang, Y: Tom

APPLICANT: Liu, Chenghua

APPLICANT: Liu, Chenghua

APPLICANT: Ren, Feiyan

APPLICANT: Drmanac, Paronic Title OF INVENTION: No. US20030219745A1e1 Nucleic Acids and

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 802CON

CURRENT APPLICATION NUMBER: US/10/120,988

FILE REPERENCE: 802CON

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: 09/774,528

PRIOR APPLICATION NUMBER: 09/774,528

PRIOR APPLICATION NUMBER: 09/774,528

SEQ ID NO 348

LENGTH 4432

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Best Local Similarity:
Query Match:
DB:
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LOCATION: (11
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Matches:
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                                        JOS-10-315-974-1

Sequence 1, Application US/10315597A

Publication No. US20030162206A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUGIULEA.
APPLICANT: Kohama, Takafumi
TITLE OP INVENTION: Ceramide Kinase and DNA Enc.
FILE REFERENCE: 02658CIP/HG
CURRENT APPLICATION NUMBER: US/10/315,597A
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US/2009-178039
PRIOR PILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 4463
TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: Unsure
LOCATION: 3371
OTHER INFORMATION:
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2880.00
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Query Match:
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Pred. No.:
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; Sequence 5, Application US/10876281
; Publication No. US20050123942A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA 1141 1201 1321 541 231 601 251 661 271 721 291 781 311 331 901 351 431 451 1261 531 1501 유 셤 8 8 8 용 a 셤 원 장 g ∂ g 8 ద ò g 8 ያ ያ ò ♂ S G 8 ò a 8 8 a ò ద ઠે

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                                              ValSerSerValHisHisHsnSerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyr
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US-09-969-969-1
; Sequence 1, Application US/0996986
; Publication No. US20030125533A1
; GENERAL INFORMATION:
; APPLICANT: Kossida, Sophia
; TITLE OF INVENTION: Regulation of human Sphingosine
; TITLE OF INVENTION: Regulation of human Sphingosine
; TITLE OF INVENTION: Rinase-Like Protein
; FILE REFERENCE: 004974.00594
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/238,005
; PRIOR FILING DATE: 2000-10-06
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TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
FILE REFERENCE: 10716-08
CURRENT APPLICATION NUMBER: US/10/876,281
CURRENT FILING DATE: 2004-06-24
FRIOR PELING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-12
SOFTWARE: PALENTIN VOY: 2.1
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; ORGANISM: Homo sapiens
US-10-876-281-5
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Query Match:
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Pred. No.:
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Sequence 1, Application US/10631958
; Sequence 1, Application US/10631958
; Publication No. US2004012580A1
; GENERAL INFORMATION:
; APPLICANT: Kossida, Sophia
; TITLE OF INVENTION: Regulation of human Sphingosine
; TITLE OF INVENTION: Kinase-Like Protein
; FILE REPRENCE: 004974.00594
; FILE REPRENCE: 004974.00594
; CURRENT APPLICATION NUMBER: US/10/631,958
; CURRENT FILING DATE: 2001-00-04
; PRIOR FILING DATE: 2001-10-04
; PRIOR FILING DATE: 2001-10-06
; PRIOR FILING DATE: 2001-10-06
; PRIOR FILING DATE: 2001-10-06
; RIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO!
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Best Local Similarity:
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: US 60/314,113
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SEQ TO NO 1
LENGTH: 979
                                                                                                                                 1,27e-183
1640,50
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                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-896-1
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Query Match:
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Pred. No.:
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; Publication No. US20030125533A1
; GENERAL INFORMATION:
; APPLICANT: Kossida, Sophia
; TITLE OF INVENTION: Regulation of human Sphingosine
; TITLE OF INVENTION: Regulation of human Sphingosine
; FILE REFERENCE: 004974.00594
; CURRENT APPLICATION NUMBER: US/09/969,896
; CURRENT FILING DATE: 2001-10-04
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2001-06
; NUMBER OF SEQ ID NOS: 16
                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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100.00$
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TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No.:
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Percent Similarity:
Best Local Similarity:
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Query Match:
                                        ; NAME/KEY: CDS
; LOCATION: (90)
US-10-115-635-247
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US-09-969-896-8
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Publication No. US200401374341
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Ran, Feiyan
APPLICANT: Zhao, Qing A
APPLICANT: Zhao, Qing A
APPLICANT: Zhao, Qing A
APPLICANT: Wehrman, Tom
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APPLICANT: PUBMENT: 09/196914,936
FILE REFERENCE: 797COM
CURRENT APPLICATION NUMBER: US/10/115,635
FRIOR FILING DATE: 2000-11-17
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SOFTWARE: pt_PL_genes Version 2.0
SEQ ID NO 247
LENGTH: 817
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PAPLICANT:

TITLE OF INVENTION: Regulation of human Sphingosine;

TITLE OF INVENTION: Rinase-Like Protein;

FILE REPERENCE: 004974,00594

CURRENT APPLICATION NUMBER: US/10/631,958

CURRENT FILING DATE: 2003-08-01

PRIOR APPLICATION NUMBER: US/09/969,896

PRIOR APPLICATION NUMBER: US 60/238,005

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2001-10-04

PRIOR FILING DATE: 2001-10-04

SPIOR FILING DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 550
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8 LENGTH: 550
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; Publication No. US20040192580A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-631-958-8
                                 TYPE: DNA
, ORGANISM: Homo sapiens
US-09-969-896-8
                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
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Mismatches:
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Perfect score:

Sequence:

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Scoring table:

Minimum DB Maximum DB

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Sequence 1756, Ap Sequence 399, App Sequence 340, App Sequence 12677, A Sequence 263, App Sequence 261, App Sequence 11772, A Sequence 11772, A Sequence 1479, Ap Sequence 1479, App Sequence 1179, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1164, App Sequence 1112, App Sequence 1113, App Sequence 1112, App Sequence 2112, Appli
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Sequence 5908, Ap
Sequence 5922, Ap
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APPLICANT: Liu, Chenghua
APPLICANT: Ren, Felyan
APPLICANT: Ren, Felyan
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Xne, Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REPERRNCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILLING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: PL_FL_genes Version 2.0
SEQ ID NO 148
US-09-248-796A-1756
US-09-614-21A-399
US-09-614-21A-399
US-09-620-312D-796
US-09-107-532A-350
US-09-107-532A-350
US-09-107-532A-350
US-09-207-767-6490
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Patent No. 6743619
GENERAL INFORMATION:
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Ren, Feiyan
Zhang, Jie
Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
Wang, Jian-Rui
Wang, Jian-Rui
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US-09-774-528-148
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APPLICANT:
APPLICANT:
    228
210.5
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    -MODEL-frame+ p2n.model -DEV=x1h
-Q=/Cgn2_1/USPTO spool/US10631958/runat_02092005_165811_4432/app_query.fasta_1.1941
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-D=168ued_Patents_NA -QFWT=fastap_SUPFIX=ni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Ebits -STRATS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL_OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10631958_GCM_1_1_397_erunat_02092005_165811_4432 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCR=100 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1155, Ap
Sequence 90, Appl
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 148, App
                                                                                                                                                              4 ; Search time 303.735 Seconds (without alignments) 2892.921 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                            537
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2888
1 MGATGAAEPLQSVLWVKQQR......QLVRLFARGIEENPKPDSHS
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/pcTuS_COMB.seq:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                  nucleic search, using frame plus p2n model
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US-09-270-767-14306
US-09-270-767-15155
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US-09-970-516-3
US-09-817-676A-11
US-09-817-676A-11
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Listing first 45 summaries
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Score

Result Š.

Database :

| 232   Serifishis CystyrGlucityThrvalserPhetasProlateInHisThrivalGlySer 140 |                                                                                                                                               |
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| 1.18e-317   MacChel.   536                                                 | Db 2044 CTTCGCTACTCCCTCCTCTGGGCTACGGCTTCTACGGGGGATCATCAAGGACAGT 2103  Qy 301 GluLysLysArgTTpLeuGlyLeuAlaArgTyrAspPheSerGlyLeuLysThrPheLeu 320 |

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433 ArgPheLeuIleArgHisThrAsnGlnGln---A8pGlnPheAspPheThrPheValGlu 451
  385 CysGlyLysPheLeuAlaIleAsnAlaThrAsnMetSerCysAlaCysArgArgSerPro
                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ArgLysProCysArgAlaGlyCysPheValCys----
                                                                                                                                                                                                                                                                                                                                                    317 LysThrPheLeuSerHisHisGysTyrGluGlyThrValSerPheLeu
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Matches:
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Mismatches:
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                                       ArgGlyLeuSerProAlaAlaHisLeuGlyAspGly
                                                  AATGGCATCTCCCGTTACAGTCATCTGGGTGATGGT
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CRGANISM: Drosophila melanogaster
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                                                                                                                                       AspGly11eValCysValGlyGlyAspGlyMetPheSerGluValLeuHisGlyLeu11e 208
                                                                                                                                                                                                                   GlyargThrGlnargSeralaGlyValaspGlnAsnHisProArgAlaValLeuValPro 228
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                                                                                                                             149 IleTyrGluArgLysValAlaProLeuPheThrLeuAlaSerIleThrThrAspIleIle 168
                                                                                                                                                                   ValThrGluHisAlaAsnGlnAlaLysGluThrLeuTyrGluIleAsnIleAspLysTyr 188
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CTGAGAATGTTAGAAGAGCCCGATCTTCTACTGACCACGCCGCTGGAGGACATTCCGCAG
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|327 CAGCGCTGCAGCTTCGCCAGCATACAGGAACAGCGATCCTCATTGTTCATCCAAGAG
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                    Conservative:
Mismatches:
Indels:
   Length:
Matches:
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35.51%
20.27%
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Best Local Similarity:
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                                                                                                                                                                                                    Sequence 70.1-0.7-15.

Sequence 70.6749.

Sequence 70.6749.

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

FILE REFERENCE: File Reference: 7326-094.

CURRENT APPLICATION NUMBER: US/09/270,767.

NUMBER OF SEQ ID NOS: 62517.

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 30448.
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967 ACACTGGGCAGGTGCTGGCCTCGCCACACTGCACCCTACCGGGGAGGCCTCTCCTAC 1026
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                                                                                                                 GlyGlyLysGlyGlnGlyLysArgIleTyrGluArgLysValAlaProLeuPheThrLeu 160
                                                                                                                                                                             AlaSerIleThrThrAspIleIleValThrGluHisAlaAsnGlnAlaLysGluThrLeu 180
                                                                                                                                                                                                                                                                                                              201 SerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAspGlnAsn 220
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APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
Tarahan Takahanian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REPERBNCE: 00170/HG
FILE REPERBNCE: 00170/HG
CURRENT PILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/194,318
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PAGENTIN VET. 2.0
SEQ ID NOS: 15
                                                                                                                                                                                                                                            TyrGlulleAsnlleAspLysTyrAspGlylleValCysValGlyGlyAspGlyMetPhe
                                                  GluMetLeuGluLysLeuThrSerArgProLysHisLeuLeuValPheIleAsnProPhe
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| GAGATCACCCCTGACCTGCTACCTCGGCCCCCGGTTGCTTCTATTGGTCATCCCTTT
                                                                                                                                               GGGGGTCGGGCCTGGCAGGGTGTAAGAACCACGTGCTTCCCATGATCTCTGAA
                                                                                                                                                                                                                                                                                                                                                                              221 HisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAlaGlySer
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                     CTCACCTGTCTG-
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NAME/KEY: CDS
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Patent No. 6610534
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. 6610534artis AG
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE: 4-31617
CURRENT APPLICATION WUMBE: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 3
LENGTH: 1857
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590 GTATATCCCAGCACAGAGAATTCCGGTTCAGAACTTTTTTCTGCCAGGAGGAGGACTACAGC 649
                                                                                                                                                                                                GAAATGACCGCCCACTCCTCC-----TCGACGGAGTTTTCCAGCTGGAACTGTGAT 736
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                                               ValTyrArgValLysLysPheGlnPheThrSerLysHisMetGluAspGluAspSerAsp 471
                                                                                                                                             650 TTGGCAGGGTCT--------------TGTCAGCCGATTACACCGCCTGAA 685
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     ----SerSerHisProSerCysCysCysThrValSerAsnSerSerTrpAsnCysAsp
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Conservative:
Mismatches:
Indels:
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44.24%
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ORGANISM: Homo sapiens
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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NAME/KEY: CDS
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Pred. No.:
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US-09-970-516-3
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973 ACACTGGGCACGGTGCTGGCCTCGCCACACCGCACGCGGACGCCTCTCCTAC 1032
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                                                                                                                                                                          312 AspPheSerGlyLeuLysThrPheLeuSerHisHisCysTyrGluGlyThrValSerPhe 331
   APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 2698
                                                           19 GlnArgCysAlaValSerLeuGluProAlaArgAlaLeuLeuArgTrpTrpArgSerPro
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                                                                                                      292 PheTyrGlyAspIlelleLysAspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyr
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                                       SerSerValHisHisAsnSerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGly
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                             ; Sequence 11, Application US/09817676A; Patent No. 6800470; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATABASE ACCESSION NUMBER: AF245448
DATABASE ENTRY DATE: 2000-06-27
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269.00
41.64%
25.99%
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LOCATION: (387)..(2237)
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL: J. Biol. Chem.
VOLUME: 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
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Query Match:
DB:
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PAGES: 19513-19520
DATE: 2000-06-30
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PUBLICATION INFORMATION:
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APPLICANT: Richard, D'ANDREA J
APPLICANT: Jennifer, BAMBLE R
APPLICANT: Jennifer, BAMBLE R
APPLICANT: Jennifer, BAMBLE R
APPLICANT: Mathew, VADAS A
TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
FILE REFERENCE: PITSON=1
CURRENT APPLICATION NUMBER: US/09/959,897
CURRENT FILING DATE: 2001-11-13
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PRIOR PILING DATE: 1999-05-13
PRIOR PILING DATE: 1999-05-13
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  547 ATGGTCTA-GTCTCTCTGGATGAGGTCTCGGGCTGTGGCACCCTGCAGAGCCGTAGCCCC 605
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                                                               008 ACTGTCTGGAGACGGGCTGCTTTACGAGGTGCTGAATGGCCTCCTTGATCGG-----
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                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                 NAME/KEY: CDS
LOCATION: (33)..(1184)
OTHER INFORMATION:
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Best Local Similarity:
Query Match:
DB:
SEQ ID NO 1
LENGTH: 1205
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Sequence 1, Application US/09959897 Patent No. 6730480 GENERAL INFORMATION: APPLICANT: PITSON, SLUATE APPLICANT: Brian, WATTERBERG W

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                                                                                                                                                                                                                                              CTCTTCCGGAGTCACGTGCAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATG 156
                                                                                                                                                                                                                                                                                     ValThrGluHisAlaAsnGlnAlaLysGluThrLeuTyrGluIleAsnIleAspLysTyr 188
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Patent No. 6610534
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Induction of blood vessel formation through administration of TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REFERENCE: 4-31677
CURRENT APPLICATION NUMBER: US/09/970,516
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 3.1
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                                                                                                          SerProArgAspArgLysProCysArgAlaGlyCysPheValCysArgGlnSerLysGln 359
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                                               LeuSerHisHisCysTyrGluGlyThrValSerPheLeuProAlaGlnHisThrValGly
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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; OTHER INFORMATION:
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| dy 434PheLeulleArgHisThrAmGinGlndhapGlnPheAspPheThrPheValGluVal 452                                                                | Db 553<br>Qy 209  | 3 GACGCTCTGGTGGTCATGTCTGGAGACGGGTGATGCACGAGGTGGTGAACGGGCTCATG 612<br>6 GlyargThrGlnArgSerAlaGlyValAspGlnAsnHisProArgAlaValLeuValPro 228                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|                                                                                                                                    |                   | GAGCGGCCTGACTGGGAGACCGCCATCCAGAAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Db 964 GTGCCCGTCGCCTTCCGCTTGGAGCCCAAGGAT 999                                                                                       | Qy 229            | 9 SerSerLeuArglleGlyIleIleProAlaGlySerThrAspCysValCys 245                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| 473 LysGluGl                                                                                                                       | Db 646            | ססכ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 1000GGGAAAGGTGTTTGCA                                                                                                               |                   | TyrSerThrValGlyThrSerAspAlaGluThrSerAlaLeuHis                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| VY 493 INIVALSERABNSERVERITPABNCYBABDGIYGIUVALLEUHIBSSERFROALAILEGIU 512<br>                                                       | DD 697            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 513 ValArgValHisCysGlnLeuValArgLeuPheAlaArgGlyIleGluGluAsnPro                                                                      |                   | TIGGREGACGCGGCTGCTGTCACCCATGAACCTGCTCTCTGCACACGGCTTCGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Db 1054 GGCCAGGTGCACCAAACTACTTCTGGATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGC 1113                                                           | Qy 280            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Qy 532LysPro 533                                                                                                                   | Db d0             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Db 1114 TGGAAGCC 1122                                                                                                              | Qy 300            | 0 SerGluLysLysArgTrpLeuGlybeuAlaArgTyrAspPheSerGlybeuLysThrPhe 319                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| RESULT 10<br>US-09-949-016-1155                                                                                                    | Db da             | 7 AGIGAGAAGTATCGGCGTCTGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTG 936                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <ul><li>; Sequence 1155, Application US/09949016</li><li>; Patent No. 6812339</li><li>; GENERAL INFORMATION:</li></ul>             | Oy 320            | 0 LeuSerHigHisCygTyrGluGlyThrValSerPheLeuProAlaGlnHigThrValGly 339 :::                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| KNOWN GENES ASSOCIATED                                                                                                             |                   | SerProArgAspArgLysPrcCy8ArgAlaGlyCysPheValCy8ArgGlnSerLysGln                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF. T. FILE REFERENCE: CLOODSON NUMBER. 115/MC/AG 015 | Db 994            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ; CUKRENT FILING DATE: 2000-04-14; PRIOR APPLICATION NUMBER: 60/241,755                                                            |                   | GlnLeuGluGluGluGlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspVal                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| ; PRIOR FILING DATE: 2000-10-20<br>; PRIOR APPLICATION NUMBER: 60/237,768                                                          | п                 | GATGCACACGAGCCAGTGCCACTGGAGGAGCCAGTGCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <pre> ; PRIOR FILING DATE: 2000-10-03 ; PRIOR APPLICATION NUMBER: 60/231,498 ; PRIOR FILING DATE: 2000-09-08 </pre>                | Qy 379<br>Db 1075 | 9 GluGlufrpGlnValValCysGlyLysPheLeuhlallaAsnAlarhr 394<br>        :::     :::         :::                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| ; NUMBER OF SEQ ID NOS: 207012; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 1155                                          |                   | AsnMetSerCysAlaCysArgArgSerProArgGlyLeuSerProAlaAlaHisLeuGly                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| ; LENGTH: 1783<br>; TYPE: DNA                                                                                                      | Db 1135           | CACCTGGGCAGTGATGTTTGCTGCACCCATGGGCCGCTGTGCAGCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| ) ORGANISM: Human<br>US-09-949-016-1155                                                                                            | Qy 415<br>Db 1183 | 5 AspGlySerSerAspLeuIleLeuIleArgLysCysSerArgPheAsnPheLeuArg 433                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ent Scores: 2.15e-19 Length:                                                                                                       | Qy 434            | PheLeulleArgHisThrAsnGlnGlnAspGlnPheAspPheThr 448                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
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| 9.12% Indels:<br>4 Gaps:                                                                                                           | Qy 449            | PheValGluValTyrArgValLysLysPheGlnPheThrSerLysHisMetGluAspGlu<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| .10-631-958-10 (1-537) x US-09-949-016-1155 (1-1783)                                                                               | Db 1288           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Oy 129 ArgProLysHisLeuLeuValPhelleAsnProPhellyGlyGlnGlyLysGlyGlnGlyLysArg 148                                                      | Oy 469            | 9 AspSerAspLeuLysGludlydlyLysLysArgPhedlyHisIleCysSerSerHisPro 488                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Db 373 CGCCCTGCCGCGTGGTGCTGCTGAACCCGCGGGGGAAGGGCAAGGCCTTGCAG 432                                                                   |                   | 120 The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of t |
| 149 IleTyrGluArgLygValAlaProLeuPheThrLeuAlaSerIleThrThrAspIleIle                                                                   | QY 489<br>Db 1354 | 9 SerCy8Cy8ThrValSerABhSerSerirpaBhCy8ABbLyALhvalalLeuntsBer 508<br>4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Db 433 CTCTTCCGGAGTCACGTGCAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATG 492                                                            | VO VO             | ProAlaIleGluValArqValHigCvsGlnLeuValArqLeuPheAlaArqGlvIleGlu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 169 ValThrGluHisAlaAsnGlnAlaLyGGluThrLeuTyrGluIleAsnLleAspLysTyr                                                                   |                   | GAGGCCGTGCAGGCCAGGTGCACCCAAACTACTTCTGGATGGTCGGTGGTTGCGTGGAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| DD 493 CTCACTGAGCGGGAACCACGCGGGGAGGTGCGGTCGGAGGAGCTGGGCCGCTGG 552                                                                  | Qy 529            | 9 GluAgnProLysPro 533                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |

us-10-631-958-10.rni

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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
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BEARLIER APPLICATION NUMBER: OF/048,885

BEARLIER FILING DATE: 1997-06-06

BEARLIER APPLICATION NUMBER: 60/049,375

BEARLIER APPLICATION NUMBER: 60/049,375

BARLIER APPLICATION NUMBER: 60/049,881

BARLIER APPLICATION NUMBER: 60/049,881

BARLIER FILING DATE: 1997-06-06

BEARLIER FILING DATE: 1997-06-06

BEARLIER PELLICATION NUMBER: 60/049,99

BARLIER APPLICATION NUMBER: 60/049,902

BARLIER PELLING DATE: 1997-06-06

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A APPLICATION NUMBER: 60/048,916

A APPLICATION NUMBER: 60/049,373

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,875

R FILING DATE: 1997-06-06

A PPLICATION NUMBER: 60/048,374
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,974
APPLICATION NUMBER: 60/048,974
FILING DATE: 1997-06-06
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APPLICATION UMBER: 60/048,964
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,882
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APPLICATION NUMBER: 60/048,899
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,893
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APPLICATION UNMBER: 60/048,900
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,901
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APPLICATION NUMBER: 60/048,892
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APPLICATION NUMBER: 60/048,915
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APPLICATION NUMBER: 60/049,019
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APPLICATION UNMBER: 60/048,970
ELING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,972
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APPLICATION NUMBER: 60/048,917
                                1438 CCCCCCCCCAGCTGGAAGCCC 1458
                                                                                                                                                                Sequence 90, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
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EARLIER PELING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 1227 υ υ υ LOCATION: (1522) OTHER INFORMATION: n equals a,t,g, or ö OTHER INFORMATION: n equals a,t,g, or ö APPLICATION NUMBER: 60/048,883 LOCATION: (123) OTHER INFORMATION: n equals a,t,g, n equals a,t,g, 8.02e-19 257.50 41.75% 26.65% 8.92% ORGANISM: Homo sapiens 349 GGA-----Percent Similarity: Best Local Similarity: NAME/KEY: SITE FEATURE: NAME/KEY: SITE NAME/KEY: SITE FEATURE: NAME/KEY: SITE Alignment Scores: SEQ ID NO 90 509 LOCATION: Query Match DB: FEATURE Score: ò 셤 8 요 g 셤 g ଚ ò ઠે

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SENERAL INFORMATION:
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                                                                                               260 sIleValValGlyAspSerLeuAla---MetAspValSerSerValHisHisAsnSerTh
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                                                  ------TyrSerThrValGlyThrSerAspAlaGluThrSerAlaLeuHi
                                                                  553 GCTGCGCCTCTTCTCTGTGCTCAGCCTGGGGCCTTCATTGCTGATGTGGACCTAGA
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          -SerSerLeuArgIleGlyIleIleProAlaGlySerThrAspCysValCys-
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Sequence 5, Application US/09970516 Patent No. 6610534

RESULT 12 US-09-970-516-5

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APPLICANT: NO. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE PERENENCE: 4-31610 CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
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100
67
179
56
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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247.50
41.65%
24.94%
8.57%
                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (1)..(1149)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                 LENGTH: 1149
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US-09-970-516-5
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|                                                                                                               | Qy 159 ThrLeuAlaSerIleThrThrAspIleIleValThrGluHisAlaAsnGlnAlaLysGlu 178 | Oy 179 ThrLeuTyrGluIleAsnIleAspLysTyrAspGlyIleValCysValGlyGlyAspGly 198                                             | Qy 199 MetPheSerGluValLeuHisGlyLeuIleGlyArgThrGlnArgSerAlaGlyValAsp 218 ::: | Qy 219 GlnAsnHisProArgAlaValLeuValProSerSerLeuArgIleGlyIleIleProAla 238 ::: ::: ::: ::: | Qy 239 GlySerThrAspCysValCysTyrSerThrValGlyThrSerAspAlaGluThrSerAla 258                                                      | Qy 259 LeuHisIleValValGlyAspSerLeuAlaMetAspValSerSerValHisHis 276 | Qy 277AsnSerThrLeuLeuArgTyrSerValSerLeuLeuGlyTyrGlyPheTyrGlyAsp 295 ::: | Qy 296 IleIleLysAspSerGluLysLysArgTrpLeuGlyLeuAlaArgTyrAsp 312 | Qy         313PheSerGlyLeuLysThrPheLeuSerHisHisCys         324           Db         1021 ATACAAAAAGTGTTCTCGGGGCAAAATATCCTTGTGACTATTTGTGAAATACAAG         1077 | OY 325 TyrGluGlyThrValSerPheLeuProAlaGlnHisThrValGlySerProArgAspArg 344                                                           | Qy 345 LysProCysArgAlaGlyCysPheValCysArgGlnSerLysGlnGlnGlnGluGluGluGluGluGluGluGluGluGluGluGluGluG                                                                                                               | Qy 365 GlnLysLysAlaLeuTyrGlyLeuGluAlaAlaGluAspValGluGluTrpGln-Va 383 :::         :::         :::                                              | Oy 383 IValCysGlyLysPheLeualaIIeAsnAlaThrAsnMetSerCysAlaCysArgArgSe 403 :                      | Qy 403 rProArgGlyLeuSerProAlaAlaHisLeuGlyAspGlySerSerAspLeull 421 ::: |       | ; Patent No. 672837<br>; GENERAL INFORMATION:               |
|---------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|-------------------------------------------------------------------------|----------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------|-------|-------------------------------------------------------------|
| Oy 337 ThrValGlySerProArgAspArgLysProCysArgAlaGlyCysPheValCysArgGln 356         :::::::           ::::::::::: | 377 AspValGludluTrpGlnValValCysGlyLysPheLeuAlaIle                       | 392 AsnalaThrAsnMetSerCysAlaCysArgArgSerProArgGlyLeuSerProAlaAla 787 CTACACCACCTGAGCTCCGAGCTGTTTGCAGGCACCGCTGAGACTC | 412 HisLeuGlyAspGlySerSerAspLeulleLeulleArgLysCysSerArgPheAsn               | 4 431 F                                                                                 | 450 ValgluvalTyrargValLystysPheGlnPheThrSerLysHisMetGluAspGluAsp<br>1:: :: : 952 CTGGTTCATGTGGTTGCTTGGAGCCCAGAGCCAGAGGGGGGGG | 470 SerAspLeuLysGluGlyGlyLysLysArgPheGlyHislleCysSerSerHisProSer  | 490 CysCysCysThrValSerAsnSerSerTrpAsnCysAspGlyGluValLeuHisSerPro        | 510 Ala 510                                                    | DD 1109 GCC 1111<br>RESULT 13<br>US-09-248-796A-1756                                                                                                          | ; Sequence 1756, Application US/09248796A<br>; Patent No. 6747137<br>; GENERAL INFORMATION:<br>; APPLICANT: Keith Weinstock et al | TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 107196.132 CURRENT APPLICATION NUMBER: US/09/248,796A | CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR FILING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: US 60/096,409 | PRIOR FILING DATE: 1998-08-13<br>NUMBER OF SEQ ID NOS: 28208<br>SEQ ID NO 1756<br>LENGTH: 1611 | ; TYPE: DNA<br>; ORGANISM: Candida albicans<br>US-09-248-796A-1756    | tive: | <br>US-10-631-958-10 (1-537) x US-09-248-796A-1756 (1-1611) |

us-10-631-958-10.rni

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APPLICANT: VEWTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN SOOP 9949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
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Gacgggttgatgcacgaggtggtgaacgggttcatggagggggcctgactgggacggcc
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Matches:
Conservative:
Mismatches:
Indels:
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1258 AAATATGCTGCCAAATCTAAAAAGGAATTAAAA 1290
                        PhevalCysArgGlnSerLysGlnGlnLeuGlu 362
                                                                                                                    Sequence 3940, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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203.50
40.48%
24.34%
7.05%
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Pred. No.:
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LENGTH: 1764
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871 TCGGGTGATGGTATTCCATACGAAGTAATTAATGGCTTTATAGAAGACCCGACAGA--- 927
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APPLICANT: Yu, Jaehyuk
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: NUCLECLE ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
FILE REFERENCE: 16516.075
CURRENT APPLICATION NUMBER: US 60/9/614,221A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/142,981
PRIOR PLING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 626
SEQ ID NO 399
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|TCATTATTAATCCCCACGGTGGTAAAGGTACTGCTAAAAATTTATTCCTGACAAAAGCA
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Mismatches:
Indels:
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Matches:
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44.62$
26.29$
7.29$
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Pred. No.:
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Search completed: September 6, 2005, 02:34:14 Job time : 349.735 secs

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3025
1 HEAANGPAPLGVRAPPAWRT......QLVRLFARGIEENPKPDSHS 562
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6959266 segs, 1168006243 residues
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/cgn2_6/ptodata/1/paa/US60_
                                                                                                                                                                                          September 3, 2005, 03:56:52
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match
Best Local Similarity
Matches 537; Conserv
 Best Local Similarity
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                                                                                                                                                                GVDQNHPRAVLVPSSLRIGIIPAGSTDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVH 300
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                                          Length
                                       100.0%; Score 3025; DB 25; Length
100.0%; Pred. No. 1e-292;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORTATION:
APPLICANT: KOSSIGA, Sophia
TITLE OF INVENTION: Regulation of human Sphingosine;
TITLE OF INVENTION: Rasa-Like Protein;
FILE OF INVENTION: Riasa-Like Protein;
FILE REFERENCE: 004974.00594
CURRENT APPLICATION NUMBER: US/10/631,958
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US/09/969,896
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-08-13
NUMBER: US 60/314,113
NUMBER: OF SEQ ID NOS: 16
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HCQLVRLFARGIEENPKPDSHS 562
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US-10-631-958-11
Sequence 11, Application US/10631958
GENERAL INFORMATION:
                                                                    Conservative
ORGANISM: Homo sapiens
                                                     Similarity
                                      Query Match
Best Local Simi:
Matches 562;
    US-10-631-958-11
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DB 32; Length 562;

100.0%; Score 3025;

Query Match

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Sequence 13, Application PC/TUS0224623
Sequence 13, Application PC/TUS0224623
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SPHKE AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
TITLE OF INVENTION: SPHKE AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
TITLE OF INVENTION NUMBER: PCT/US02/24623
CURRENT APPLICATION NUMBER: PCT/US02/24623
CURRENT FILING DATE: 2002-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 13
SSEQ ID NO 13
SSEQ ID NO 13
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                                Indels
; Pred. No. 1e-292; 0; Mismatches 0;
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                                562; Conservative
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; ORGANISM: CG143216-01
PCT-US02-31373-40
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PCT-US03-21730-121
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SEQ ID NO 40
LENGTH: 537
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                                                                                                                                                                                                                                                                          361 LEEEQKKALYGLEAAEDVEEWQVVCGKFLAINATNMSCACRRSPRGLSPAAHLGDGSSDL 420
                                                                                                                                                                                                                                                                                                                                                                 GHICSSHPSCCCTVSNSSWNCDGEVIASPAIEVRVHCQLVRLPARGIEENPKPDSHS 562
                                                                                                                                                                                                                                                                                                                              421 ILIRKCSRFNFLRFLIRHTNQQQQPDFTFVEVYRVKKFQFTSKHMEDEDSDLKEGGKKRF
            61 EETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLR
                                                               TDCVCYSTVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLGYGFYGDIIKDS
EETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLR
                                                EMLEKLTSRPKHLLVFINPFGGKGOGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
                                                                                                    YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS
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PRELICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-462C-061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/USO2/31373
CURRENT FILING DATE: 2003-09-28
PRIOR APPLICATION NUMBER: 10/262,511
PRIOR FILING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40, Application PC/TUS0231373 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zerhusen, Bryan D.
Anderson, David W.
Zhong, Mei
Catterton, Elina
Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
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Leach, Martin D.
Agee, Michele L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smithson, Glennda
Millet, Isabelle
Peyman, John A.
Kekuda, Ramesh
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Li, Li
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Best Local Similarity 100.0%; Pred. No. 5e-279;
Matches 537; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR PILING DATE: 2001-10-02
PRIOR PLING DATE: 2001-10-02
PRIOR PLING DATE: 2001-10-09
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2001-10-09
PRIOR PPLICATION NUMBER: 60/321,917
PRIOR PELING DATE: 2001-00-09
PRIOR PILING DATE: 2002-05-17
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2001-00-09
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265 240 325 300

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; ORGANISM: Homo sapiens
US-09-969-896-10
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TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Rinase-Like Protein
FILE OF INVENTION: Kinase-Like Protein
FILE OF INVENTION: Kinase-Like Protein
FILE OF INVENTION: RUBBER: US/09/969,896
CURRENT APPLICATION NUMBER: US 60/238,005
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR FILING DATE: 2000-10-06
PRIOR PILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NOS: 16
           FILE REFERENCE: 034526/0461
CURRENT APPLICATION NUMBER: PCT/US03/21730
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 153
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 121
LENGTH: 537
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18-09-969-996-10
i Sequence 10, Application US/09969896
i GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL KINASES
                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 537; Conservative
                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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PCT-US03-21730-121
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                                                                                      EMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
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   Length 537;
                                   Indels
   DB 25;
                   5e-279
Query Match 95.5%; Score 2888; D
Best Local Similarity 100.0%; Pred. No. 5e-
Matches 537; Conservative 0; Mismatches
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Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
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Li, Li
Guo, Xiaojia (Sasha)
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Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
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Anderson, David W.
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Miller, Charles E.
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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95.5%; Score 2888;
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APPLICANT: Smithson, Glennda APPLICANT: Millet, Isabelle APPLICANT: Peyman, John A. APPLICANT: Kekuda, Ramesh
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
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Ort, Tatiana
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Anderson, David W.
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Catterton, Elina
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Li, Li
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US-10-262-511A-40
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US-10-262-511A-40
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                                                        APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
ITILE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2000-40-19
PRIOR PELING DATE: 2000-20-17
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PILING DATE: 2002-10-09
PRIOR PELING DATE: 2002-10-09
PRIOR PELING DATE: 2002-10-09
PRIOR PELING DATE: 2002-06-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR PELING DATE: 2001-10-09
PRIOR PELING DATE: 2001-10-09
PRIOR PELING DATE: 2001-00-09
PRIOR PELING DATE: 2002-04-17
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PRIOR PELING DATE: 2
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Shimkets, Richard A.
                        Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
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; ORGANISM: Homo sapiens
US-10-262-511-40
APPLICANT:
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APPLICANT: Stunkets, Martin D.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Applicant: Leach, Martin D.
APPLICANT: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: 
506 GHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS
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                                 EMLEKLISRPKHLLVFINPFGGKGGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
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              EMLEKLTSRPKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIVTEHANQAKETL
                                                                              YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS
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Best Local Similarity 100.0%; Pred. No. 5e-279;
Matches 537; Conservative 0; Mismatches C
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APPLICANT: WANNING, GERARD
APPLICANT: CARENEESEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT APPLICATION NUMBER: 60/395,632
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SEQ ID NO 121
SEQ ID NO 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 121, Application US/10618941; GENERAL INFORMATION:
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US-10-618-941-121
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US-10-486-306-13

i Sequence 13, Application US/10486306

i GENERAL INFORMATION:

APPLICANT: EXELIXIS, INC.

i TITLE OF INVENTION: SPHEA SA MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

FILE REPRENCE: EX02-104C-US

CURRENT APPLICATION NUMBER: US/10/486,306

CURRENT APPLICATION NUMBER: US 60/310,362

PRIOR FILING DATE: 2001-08-06

PRIOR PLIAGO DATE: 2001-08-06

PRIOR PLIAGO DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.1

SEQ ID NO 13
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                                                                                                                               EETDVHGKHQGSGKWQKMEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQLCHLWLQTLR 145
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                                                                                                                                                                                                                                                                   YEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGS 265
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                                                                                1 MGATGAAEPLQSVLWVKQQRCAVSLEPARALLRWWRSPGPGAGAPGADACSVPVSEIIAV 60
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5e-279;
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100.0%; Pred. No. 5e-279;
ive 0; Mismatches 0
            100.0%; Pred. No. 5e-
ive 0; Mismatches
                            537; Conservative
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Les 537; Conservative
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US-10-486-306-13
          Best Local Similarity
Matches 537; Conserv
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                                                                            GHICSSHPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS 562
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APPLICANT: Kono, Keita
APPLICANT: Kono, Keita
APPLICANT: Kono, Keita
TITLE OF INVENTION: Ceramide Kinase and DNA Encoding It
FILE REFERENCE: 02658CIP/HG
CURRENT APPLICATION NUMBER: US/10/315,597A
CURRENT APPLICATION NUMBER: UP 2000-178039
PRIOR APPLICATION NUMBER: JP 2000-178039
PRIOR PILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
LENGTH: 537
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Pred. No. 3.2e-278;
1; Mismatches 1;
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Best Local Similarity 99.6%;
Matches 535; Conservative 1
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US-10-315-597A-2
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US-10-315-597A-2
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GENERAL INFORMATION:
APPLICANT: Kossida, Sophia
TITLE OF INVENTION: Regulation of human Sphingosine
TITLE OF INVENTION: Rinase-Like Protein
FILE REFERENCE: 004974.00594
CURRENT FILING DATE: 2003-001
PRIOR APPLICATION NUMBER: US/09/969,896
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR APPLICATION NUMBER: US 60/238,005
PRIOR APPLICATION NUMBER: US 60/314,113
PRIOR FILING DATE: 2001-00-06
PRIOR APPLICATION NUMBER: US 60/314,113
SOFTWARE: PSECSEC for Windows Version 4.0
SEQ ID NO 10
LENGTH: 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 95.5%; Score 2888; DB 32; Il Similarity 100.0%; Pred. No. 56-279; 537; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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US-10-631-958-10
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Best Local S:
Matches 537
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Sequence 12, Application US/10486306
GENERAL INFORMATION:
APPLICANT: EXELIXES, INC.
TITLE OF INVENTION: SPHKE AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/486,306
CURRENT FILING DATE: 2004-02-05
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
TYPE: PRI
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100.0%; Pred. No. 4.8e-249;
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PRIOR APPLICATION NUMBER: US 60/357,501
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 481
                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 481; Conservative
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ORGANISM: Homo
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GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SPHKS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF FILE REFERENCE: EX02-104
CURRENT PRILIGGATION NUMBER: PCT/US02/24623
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/310,362
PRIOR FILING DATE: 2001-08-06
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                                                                                    APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISEI
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CLOO1381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 15652
LENGTH: 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2874.5; DB 2
Pred. No. 1.2e-277;
0; Mismatches 0;
                                  ; Sequence 15652, Application US/10170205E; GENERAL INFORMATION:
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Best Local Similarity 98.7
Matches 537; Conservative
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US-10-170-205E-15652
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PCT-US02-24623-12
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                                                                                                      241 IKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQ 300
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Best Local Similarity 100.0%; Pred. No. 4.8e-249; Matches 481; Conservative 0; Mismatches 0;
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